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1361 TGAAGATGATCGGGAAACACAA 1382
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                       1 rcaagragaraccaragaarc 22
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ORGANISM: Artificial Sequence
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Publication No. US20030162796A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boohringer Ingelheim International GmbH
TITLE OF INVENTION: Pharmaceutical composition for the treatment of disorders of TITLE OF INVENTION: non-human mammals
FILLE REFERENCE: Case 12.21
CURRENT APPLICATION NUMBER: US/10/259,451
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 11
LENGTH: 22
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                                                                                                                       Query Match 0.4%; Score 15.6; DB 1; Length 21; Best Local Similarity 93.8%; Pred. No. 6e+02; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1081, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT BRISCIAL Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT APPLICATION NUMBER: 60/251,015
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR PILING DATE: 2000-12-03
PRIOR FILING DATE: 2000-10-03
PRIOR RELING DATE: 2001-01-23
PRIOR RELING DATE: 2001-01-23
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 15.6; DB 1; Length 22; Best Local Similarity 81.8%; Pred. No. 6.3e+02; Matches 18; Conservative 0; Mismatches 4; Indels
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                       ; OTHER INFORMATION: DNA excision repair protein BRCC5; OTHER INFORMATION: The letter "s" stands for g or c. US-09-782-837-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-005-956-1081
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US-10-259-451-11
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FEATURE:
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1748 TGAAGTGGATGCCCCTGAGGC 1769

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APPLICANT: YANAI, Yoshiaki
APPLICANT: YANAMOTO, Kozo
APPLICANT: YAMAMOTO, Kozo
APPLICANT: YAMAMOTO, Kozo
APPLICANT: YAMAMOTO, Kozo
TITLE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
TITLE OF INVENTION: factor
FILE REFERENCE: YANAI=3
CURRENT APPLICATION NUMBER: US/10/409,107A
CURRENT FILING DATE: 2003-04-19
NESULY 64-66-79

US-10-094-466-79

Sequence 79, Application US/10094466

Sequence 79, Application US/10094466

Publication No. US20030203333A1

GENERAL INFORMATION:

APPLICATURY: Syptck et al.

ITITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM

ITITLE OF INVENTION: AND METHODS OF USING

TITLE OF INVENTION: AND METHODS OF USING

TITLE OF INVENTION: THE SAME

CURRENT FILING DATE: 2002-03-07

PRIOR PELING DATE: 2001-03-07

PRIOR FILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-13

PRIOR PILING DATE: 2001-12-03

PRIOR PILING DATE: 2001-13-13

PRIOR PILING DATE: 2001-13-13

PRIOR APPLICATION NUMBER: 60/275,579

PRIOR PILING DATE: 2001-10-13

PRIOR PILING DATE: 2001-10-13

PRIOR APPLICATION NUMBER: 60/275,601

PRIOR PILING DATE: 2001-10-13

PRIOR PILING DATE: 2001-10-13

PRIOR PILING DATE: 2001-10-13

PRIOR PILING DATE: 2001-03-13

PRIOR PILING DATE: 2001-03-03

PRIOR PILING DATE: 2001-03-03-03

PRIOR PILING D
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; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-094-466-79
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0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels
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PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 100
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                       Gaps
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                                          CTHER INFORMATION: Description of Artificial Sequence: Synthetic in OTHER INFORMATION: Oligonucleotide US-10-219-195-35
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                                                                                                                                                    Length 39
                                                                                                                                                                                                       Indels
                                                                                                                                                  Score 15.6; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 9;
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PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-65
SEQ ID NOS: 15752
SEQ ID NO 7996
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLILING DATE: 2000-10-0-6
PRIOR PLILING DATE: 2000-10-0-0
PRIOR PLILING DATE: 2000-10-0-3
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7996, Application US/09866108 Patent No. US20020048800A1
ORGANISM: Artificial Sequence
                                                                                                                                                       Query Match 0.4%;
Best Local Similarity 70.0%;
Matches 21; Conservative
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Sequence 22, Application US/10455470

Publication No. US20040170613A1

GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Le Couter, Jennifer
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR LIVER GROWTH AND LIVER PROTECTION FILE REFERENCE: P1849R1US
CURRENT APPLICATION NUMBER: US/10/455,470

CURRENT FILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: US 60/386,637

PRIOR FILING DATE: 2002-06-05

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 22

LENGTH: 22
                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of ERK1 mRNA
US-10-409-107A-55
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ilarity 81.8%; Pred. No. 6.38+02;
Conservative 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PCR primer
LOCATION: Full
SOTHER INFORMATION: bFGF forward
US-10-455-470-22
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ORGANISM: Artificial sequence
       SOFTWARE: PatentIn version 3.2
SEQ ID NO 55
LENGTH: 22
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Matches 18; Conserva
                                                                                       TYPE: DNA ORGANISM: Artificial
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
FILE REPERRINCE: MBH800-958-I (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: Patentin version 3.0
SEQ ID NO 3493
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
TILE REFERENCE: MBHB00-864-A (400/006)
CURRENT APPLICATION NUMBER: US 60/006)
CURRENT FILING DATE: 2000-12-05
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897
SEQ ID NO 155
LENGTH: 17
                                                                                               Gaps
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                              Score 15.4; DB 1; Length 17;
Pred. No. 5.1e+02;
8; Mismatches 1; Indels
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76.5%; Pred. No. 5.1e+02;
ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3493, Application US/09848754A; Publication No. US20030073207A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          US-09-730-289B-155; Sequence 155, Application US/09730289B; Publication No. US20030050259A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 649, Application US/10163552
; Publication No. US20030105051A1
                                                                                                                                                       3003 AGTTTTGTTTAAAACT 3019
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1 GUUUAGUUUUAAAACUG 17
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                              Query Match

Best Local Similarity 47.1%;
Matches 8; Conservative 8
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Best Local Similarity 76.5%;
Matches 13; Conservative
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US-09-848-754A-3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-730-289B-155
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US-US-ES-BO-7/11

US-US-ES-BO-7/11

Sequence 711, Application US/0985805

Publication No. US200300004122A1

GENERAL INFORMATION:

APPLICANT: Religablan, Leo

APPLICANT: Religablan, Leo

APPLICANT: Religablan, Leo

APPLICANT: Religablan, Leo

APPLICANT: Arapisky, Alex

APPLICANT: Amenic, Jasenka Matulic

APPLICANT: Amenic, Jasenka Matulic

APPLICANT: Amenic, Jasenka Matulic

APPLICANT: Amenic, Jasenka Matulic

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

CURRENT APPLICATION NUMBER: US/09/825, 805

CURRENT APPLICATION NUMBER: 09/476, 330

PRIOR FILING DATE: 1999-04-28

PRIOR FILING DATE: 1999-04-29

PRIOR PLILING DATE: 1999-04-29

PRIOR PLILING DATE: 1999-04-29

PRIOR PLILING DATE: 1998-04-29

PRIOR PLILING DATE: 1998-04-29
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US-09-730-289B-154

Squence 154, Application US/09730289B

Publication No. US20030050259A1

GENERAL INVENDATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
FILE REPERENCE: MRH800-864-A (400/006)
CURRENT APPLICATION NUMBER: US/09/730,289B

CURRENT FILING DATE: 2000-12-05
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897

SOFTWARE: Patentin Version 3.0

SOFTWARE: Patentin Version 3.0
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1992 CACCTTCAAGCAGCTGG 2008
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                                                          1 CACCATCAAGCAGCTGG 17
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Best Local Similarity 76.5%;
Matches 13; Conservative 3
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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PAPPLICANT: RESKENDAN, BEINDARD

APPLICANT: ROSCHORZ, Birgit
APPLICANT: ROSCHORZ, Birgit
APPLICANT: Madreas
TITLE OF INVENTION: UNCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATIONS.
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
TITLE OF TABLE TO BE T
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Sequence 1977, Application US/10138674

Publication No. US20040077565A1

GENERAL INFORMATION:
APPLICANT: Relocyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Bacobedo, Jaim
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin Version 3.0

SEQ ID NO 1977
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             Sequence 28, Application US/10454224 Publication No. US20040010814A1 GENERAL INFORMATION:
APPLICANT: HERRMANN, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1609 AAGTGCATCCACAGGGA 1625
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ORGANISM: Homo sapiens
US-10-138-674-1977
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                       APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
TITLE OF INVENTION: HER2
CURRENT REFERENCE: MBHR01-1653-A (400/014)
CURRENT APPLICATION NUMBER: US/10/163,552
CURRENT PILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: Patentin version 3.0
SEQ ID NO 649
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publication No. US20030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 20
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US-10-061-201-442
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US-10-163-552-649
GENERAL INFORMATION:
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US-10-138-674-2009
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RESULT 685

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APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Strindtondb, Dan
APPLICANT: Strindtondb, Dan
APPLICANT: Strindtondb, Dan
APPLICANT: Bscobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MRH800-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6731
LENGTH: 17
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i Sequence 6762, Application US/10138674
i Publication No. US20040077565A1
i Publication No. US20040077565A1
i Publicant Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF SEQUENCE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DAE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6730
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O.4%; Score 15.4; DB 1;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1;
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
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CORGANISM: Homo sapiens
US-10-138-674-6730
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CORGANISM: Homo sapiens
US-10-138-674-6731
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                                                                                               APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Raco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Bacobed, Jam
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTMARE: Patentin Version 3.0
SEQ ID NO 2009
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US-10-138-674-6729
Sequence 6729, Application US/10138674
Sequence 6729, Application US/10138674
Sequence 6729, Application US/10138674
Sequence 6729, Application US/10138674
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICAN
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Scoobedo, Jaine
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
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82.4%; Pred. No. 5.1e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 0.4%; Score 15.4; DB 1; Length 17; Local Similarity 58.8%; Pred. No. 5.1e+02; nes 10; Conservative 6; Mismatches 1; Indels
Sequence 2009, Application US/10138674 Publication No. US20040077565A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1798 AGTGACGTCTGGTCCTT 1814
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Best Local Similarity 82.4%;
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-2009
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; ORGANISM: Homo sapiens
US-10-138-674-6729
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: APPL
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APPLICANT: MCSWIGGEN, Jim
APPLICANT: MCSWIGGEN, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re-
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re-
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 8260
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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US-10-138-674-8510/c
; Sequence 8510, Application US/10138674
; Publication O. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8261, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION:
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1 GUGUGUGUGUGGGUG 17
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CRGANISM: Homo sapiens
US-10-138-674-8261
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-10-138-674-8261
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US-10-138-674-8260
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US-10-118-674-7615

Sequence 7615, Application US/10138674

Sequence 7615, Application US/10138674

Sequence 7615, Application No. US20040077565A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: PavCo, Pam
APPLICANT: Bacobedo, Jaim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Bescobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/10/138,674
CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SEQ ID NOS: 20822

SEQ ID NO 7615
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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Best Local Similarity 76.5
Matches 13; Conservative
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US-10-138-674-8259
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; ORGANISM: Homo sapiens
US-10-138-674-7615
                           ; ORGANISM: Homo sapiens
US-10-138-674-6762
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287, 949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 2003-2
SOFTWARE: PatentIn version 3.0
FEM ID NO 1977
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APPLICANT: Ravoc, Pam
APPLICANT: Ravoc, Pam
APPLICANT: Ravoc, Pam
APPLICANT: Ravochoomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobed, Jam
APPLICANT: Escobed, Jam
APPLICANT: Becobed, Jam
APPLICANT: Becobed, Jam
APPLICANT: Becobed, Jam
APPLICANT: Levels of Vascular Endothelial Growth Factor Receptor FILE REFRENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 8985
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Pred. No. 5.1e+02;
6; Mismatches 1; Indel8
                                                                                                                                                                                                                                                        Score 15.4; DB 1; Length 17; Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8988, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8954
LENGTH: 17
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Best Local Similarity 58.8'
....hes 10; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-138-674-8954
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US-10-138-674-8985
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APPLICANT: Baccob, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-875-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138;674
CURRENT APPLICATION NUMBER: US/10/138;674
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARE: Patentin version 3.0
SEQ ID NO 8949
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Brobedo, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
                                                                                         APPLICANT: ESCOBEGO, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2997 CACCGCAGITITIGITIT 3013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1585 GGCATGGAGTACTTGGC 1601
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Matches 12; Conservative
                                      McSwiggen, Jim
Stinchcomb, Dar
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674-8949
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APPLICANT:
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Sequence 6730, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Baccobedo, Dan
APPLICANT: Secobedo, Jaime
APPLICANT: Secobedo, Jaime
APPLICANT: Sinchcond, Dan
APPLICANT: Sinchcond, Dan
APPLICANT: Sinchcond, Dan
APPLICANT: Secobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Religious FINE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE PATENTIN Version 3.0
SEQ ID NO 6730
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Sequence 6731, Application No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
FRAVEO, Pam
APPLICANT:
FRICANT:
FRICANT:
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FRICANT:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/287,943A

CURRENT APPLICATION NUMBER: US/10/287,943A

CURRENT FILING DATE:
CURRENT FILING DATE:
CONTRIBUTION:
FRICANTION NUMBER:
FRICANTION NUMBE
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; Sequence 6762, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1611 GTGCATCCACAGGGACC 1627
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-287-949A-6730
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; Sequence 6729, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
; APPLICANT: Stinchroumb, Dan
; APPLICANT: Stinchroumb, Dan
; APPLICANT: Stinchroumb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REPERENCE: MBHB00-876-N (400/049)
; CURRENT FILIG DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ALCOLOGY.

APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Brinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT PILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 2002-2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2009
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1; Indels
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   82.4%; Pred. No. 5.1e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                      Sequence 2009, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1610 AGTGCATCCACAGGAC 1626
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Best Local Similarity 82.4
Matches 14; Conservative
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Matches 10; Conservative
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CRGANISM: Homo sapiens
US-10-287-949A-2009
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ORGANISM: Homo sapiens
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Sequence 8260, Application US/10287949A

Fublication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Baccobed, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobed, Jaime
APPLICANT: Becobed, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stocked, Jaime
APPLI
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Sequence 8261, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
Harmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobed, Jaime
APPLICANT: Escobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions RefirtLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MENBOO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin version 3.0

SEG ID NO 9261
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Pred. No. 5.1e+02;
7; Mismatches 1;
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1 GUGUGUGUGUGGGGUG 17
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 52.9%;
Matches 9; Conservative
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         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8259
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US-10-287-949A-8261
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US-10-287-949A-8260
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Subjection No. US20040102389A1
Subjection No. US20040102389A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Racco, Pam
APPLICANT: Strinchcomb, Dam
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Publication No. US20040102389A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobedo, Dam
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
UNMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 7615
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions 1
TITLE REFERENCE: MEHBOO-876 of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEHBOO-876 vol (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 15.4; DB 1; Length 17; 52.9%; Pred. No. 5.1e+02; ive 7; Mismatches 1; Indels
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-287-949A-7615
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US-10-287-949A-8259
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LENGTH: 17
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APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Bacobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Religible FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REPERENCE: MBHBO0-976-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

SOFTWARE: PatentIn version 3.0

SEQ ID NOS 954

LENGTH: 17
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; Bublication No. US20040102389A1
; Bublication No. US20040102389A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ravco, Pam
; APPLICANT: Berochedo, Jaime
; APPLICANT: Escobedo, Jaime
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rell
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rell
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases
; TUBENT REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9985
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| Sequence 7996, Application US/10723361
| Publication No. USZ0040137589A1
| GENERAL INFORMATION:
| APPLICANT: GU, Yizhong
| APPLICANT: FEAN: Sharron G. APPLICANT: HANZEL, David R. APPLICANT: RANK, David R. APPLICANT: SHANKON, Mark
| APPLICANT: SHANNON, Mark
| APPLICANT: SHANNON, Mark
| TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
| FILE REFERENCE: PB0105
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 5.1e+02;
Matches 10; Conservative 6; Mismatches 1; Indels
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Pred. No. 5.1e+02;
1; Mismatches 1;
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Best Local Similarity 88.2%;
Matches 15; Conservative 1
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CORGANISM: Homo sapiens
US-10-287-949A-8985
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
, ORGANISM: Homo sapiens
US-10-287-949A-8954
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; Sequence 8949, Application No. US20040102389A1
; Sequence 8949, Application No. US20040102389A1
; Publication No. US20040102389A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Bacobed, Jaim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobed, Jaim
; APPLICANT: Bacobed, Jaim
; APPLICANT: Bacobed, Jaim
; APPLICANT: Bacobed, Jaim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: UNMERR: US/10/287, 949A
; CURRENT APPLICATION NUMBER: US/10/287, 949A
; CURRENT FILING DATE: 2003-04-11
; NOWBER OF SEQ ID NOS: 20822
; SEQ ID NO 8949
; LENGTH: 17
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Pred. No. 5.1e+02;
4; Mismatches 1; Indels
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US-10-287-949A-8954
Sequence 8954, Application US/10287949A
; Publication No. US/0040102389A1
; GENERAL INFORMATION:
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1 GUGUGUGUGGGGUGUG 17
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Best Local Similarity 70.6%;
Matches 12; Conservative
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US-10-287-949A-8949
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CORGANISM: Homo sapiens
US-10-287-949A-8510
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US-10-287-949A-8949
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679) A.
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/764,853
FRIOR APPLICATION NUMBER: US 09/764,853
FRIOR APPLICATION NUMBER: US 09/760,427
FRIOR FILING DATE: 2001-01-05
FRIOR FILING DATE: 2001-01-13
FRIOR APPLICATION NUMBER: US 09/855,768
FRIOR FILING DATE: 2001-01-13
FRIOR FILING DATE: 2001-05-15
FRIOR APPLICATION NUMBER: US 09/855,768
FRIOR FILING DATE: 2001-05-15
FRIOR PILING DATE: 2001-05-15
FRIOR OF SEQ ID NOS: 4593
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Sequence 2975, Application US/09969373
Fatent No. US2002013852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Scybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
FRIOR PFLING DATE: 2001-01-05
PRIOR PFLING DATE: 2001-01-05
PRIOR PRILING DATE: 2001-01-05
FRIOR PREING DATE: 2001-01-05
FRIOR PREING DATE: 2001-01-05
FRIOR PRILING DATE: 2001-01-05
FRIOR FILING DATE: 2001-01-05
FRIOR SPELIGATION NUMBER: US 09/760,427
FRIOR PRILING DATE: 2001-01-05
FRIOR SPELIGATION NUMBER: US 09/855,768
FRIOR SEQ ID NOS: 4593
FROUD NO 2975
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Pred. No. 5.5e+02;
0; Mismatches 1;
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4.1%; Pred. No. 5.5e+02;
ve 0; Mismatches 1;
                                                                                                                                               ; Sequence 1877, Application US/09969373
; Patent No. US20020133852A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2690 CITICCCACTICCCACC 2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2322 TGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 crarccacrrccacac
                18 CCTACACCCAAAGCTGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.13
Matches 16; Conservative
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Best Local Similarity 94.1-
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US-09-263-959-983/c
; Sequence 983, Application
; Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA

CORGANISM: Glycine max
US-09-969-373-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2975
                                                                                                                         US-09-969-373-1877/c
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APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Marcelino, Jose
TITLE ON INVERTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
CURRENT APPLICATION NUMBER: 09/619,175
PRIOR APPLICATION NUMBER: 09/619,175
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 15755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR PLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 7996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09802207
Publication No. US20020086824A1
GENERAL INFORMATION:
APPLICANT: Warman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1992 CACCTTCAAGCAGCTGG 2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCATCAAGCAGCTGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-723-361-7996
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Application US/09263959

2600 CCCACACCCAAAGCTGA 2616

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APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSES: Seed and Berry LLP
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                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/10773951
Publication No. US20040157255A1
GENERAL INFORMATION:
APPLICANT: Agus, David
APPLICANT: Shak, Steven
APPLICANT: Baker, Joffre
APPLICANT: Groin, Maureen
APPLICANT: Groin, Mair Expression Markers for Response to TITLE OF INVENTION: Gene Expression Drugs
FILE REFERENCE: 39740/0009
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIPICATION:
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                      Score 15.4; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 427, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                                          2337 GTGTGTGTGTGTGCA 2353
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TELEFAX: (206) 682-6031
INFORMATION FOR SEO ID NO. 427
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              17 Grardrererererete 1
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                                                                Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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ZIP: 98104-7092
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US-10-773-951-53/c
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US-09-263-959-427
US-10-321-039-716
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                                 APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: KOOD, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPBUTIC COMPOSITIONS AND METHODS WHICH UTI
WUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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us-lu-sar-vas-rub/c
sequence 716, Application US/10321039
publication No. US20040014067A1
sequence 716, Application No. US20040014067A1
septicant: Lukowiak, Andrew
APPLICANT: Usurensky, David
TITLE OF INVENTION: Amplification Methods and Compositions
TILLE OF INVENTION: UNMER: US/10/321,039
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-13
PRIOR FILING DATE: 2001-10-13
NUMBER OF EEQ ID NOS: 759
SOFTWARE: PatentIn version 3.2
SEQ ID NO 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 15.4; DB 1; Length 18; larity 94.1%; Pred. No. 5.5e+02; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

MEDIOM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

CLASSIFICATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

TELEPAN: (206) 682-6031

INFORMATION FOR SEQ ID NO: 983:

SEQUENCE CHARATERIESTICS:

LENGTH: 18 base pairs

TYPE: MUCLE, SINGLE

TYPE: MUCLE, SINGLE
                                                                                                                                                                                                                                   E: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2335 GTGTGTGTGTGTG 2351
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                         Washington
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-321-039-716/c
                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 63
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APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Usman, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
ITLE OF INVENTION: Gene Expression Using SHort Interfering Nucleic Acid (siNA)
FILE REPRENCE: 400/134 (02-742-H)
CURRENT FILING DATE: 2003-02-20
FRIOR PLILNG DATE: 2003-02-20
FRIOR FILING DATE: 2003-03-11
FRIOR FILING DATE: 2002-03-11
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-09-05
FRIOR FILING DATE: 2003-01-15
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Publication No. US20030087854A1
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
CURRENT APPLICATION NUMBER: US/09/953,047
CURRENT APPLICATION NUMBER: US/09/953,047
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 91
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
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                                                                                                                                                                                                                                                   Sequence 120, Application US/10683990
Publication No. US20040198682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2893 GGGGCACAGGAGGCAG 2909
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                                                               19 GGGGCACAGCAGCAG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.2
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Matches 16; Conservative
                                                                                                                                                                               RESULT 723
US-10-683-990-120
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US-09-953-047-91
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FDUBLication No. US20040198682A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SITAT Threateutics
APPLICANT: Usman, Nassin
APPLICANTON UNWERS: PCT/US03/0502
PRIOR APPLICATION UNWERS: PCT/US03/0502
PRIOR PLING DATE: 2002-00-10
PRIOR PLING DATE: 2002-00-10
PRIOR PLING DATE: 2002-00-10
PRIOR PLING DATE: 2002-00-10
PRIOR PLING DATE: 2002-00-20
PRIOR PLING DATE: 2002-00-20
PRIOR PLING DATE: 2002-00-20
PRIOR APPLICATION UNWERS: US 60/399, 348
PRIOR PLING DATE: 2002-00-20
PRIOR PLING DATE: 2002-00-30
PRIOR PLING DATE: 2003-00-15
PRIOR PLING DATE: 2003-00-15
PRIOR PLING DATE: 2003-00-15
PRIOR PLING D
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US-10-683-990-23
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CURRENT APPLICATION NUMBER: US/10/773,951
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/445,968
PRIOR FILING DATE: 2003-02-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PASLERQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: reverse primer US-10-773-951-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1747 GTGAAGTGGATGGCGCC 1763
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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TYPE: DNA

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                                                                                                                                                                                                           Sequence 89, Application US/08459455
Publication No. US20030124105A1
GENERAL INFORMATION:
APPLICANT: Vuan, Junying
APPLICANT: Miura, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 1; Length 20;
Pred. No. 6.1e+02;
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  Indels
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COMPOTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,455
FILING DATE: 2-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/368,704
FILING DATE: 4-JAN-1995
CLASSIFICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
FILING DATE: 10-JUN-1994
CLASSIFICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/080,850
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/080,850
FILING DATE: 10-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAMME: BUGGISKY, LAWYENCE B.
REGISTRATION NUMBER: 0609.3920003
TELECOMMUNICATION INFORMATION:
NAMME: BUGGISKY, LAWYENCE B.
REFERENCE/DOCKET NUMBER: 0609.3920003
TELECOMMUNICATION INFORMATION:
THE FORMATION INFORMATION:
     ;
                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 New York Avenue, Guldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 72, Application US/09976782; Publication No. US20030190715A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1353 GGAGATGATGAAGATGA 1369
                                                     3465 TATATATCTATATAT 3481
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TELEFAX: 48636 SSK
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 94.1
Matches 16; Conservative
     Matches 16; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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publication No. US20040116366A1

GENERAL INFORMATION:

APPLICANT: Isia Pharmaceuticals, Inc.

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT FILE REFERENCE: ISPH-0746

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: ISPH-0746

CURRENT APPLICATION NUMBER: US/10/467,008

CURRENT FILING DATE: 2002-01-31

PRIOR PILING DATE: 2002-01-31

PRIOR FILING DATE: 2002-01-31

PRIOR FILING DATE: 2001-02-09

WHORE POS EQ ID NOS: 135

BRO ID NO 110

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 91, Application US/10630401

Publication No. US20040048824A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

APPLICANT: Brett P. MONIA

TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
FILE REPERENCE: RTS-0157

CURRENT APPLICATION NUMBER: US/10/630,401

CURRENT FILING DATE: 2003-07-30

PRIOR PUBLICAND NUMBER: US/09/953,047

PRIOR FILING DATE: 2001-09-10

NUMBER OF SEQ 1D NOS: 95
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Pred. No. 6.1e+02;
                                                                                                                              Score 15.4; DB 1;
Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-630-401-91
                                                       ; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-91
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                              Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
       ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-630-401-91
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LENGTH: 20
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| APPLICANT: Slowa, Alan | APPLICANT: Slowa, Alan | APPLICANT: Slowa, Alan | APPLICANT: Behr, Regine | APPLICANT: Behr, Regine | APPLICANT: Behr, Regine | APPLICANT: Tang, Maria | APPLICANT: Tang, Maria | APPLICANT: Sternberg, David | APPLICANT: Sternberg, David | APPLICANT: Sternberg, David | APPLICANT: Brown, Stephen | TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell | TILE REPERENCE: 10241.200-US | CURRENT APPLICATION NUMBER: US/0/326,185 | CURRENT APPLICATION NUMBER: US 60/342,644 | RIOR APPLICATION NUMBER: US 60/342,644 | RIOR FILING DATE: 2001-12-21 | NUMBER OF SEQ ID NOS: 108 | SOFTWARE: PatentIn version 3.1 | SEQ ID NO 18 | LENGTH: 20
                                                                                                                                                                  APPLICANT: Slome, Alan
APPLICANT: Behr, Regine
APPLICANT: Behr, Regine
APPLICANT: William
APPLICANT: William
APPLICANT: Tang, Maria
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell
FILE REFERENCE: 10241.200-US
CURRENT FILING DATE: 2002-12-20
FRIOR APPLICATION NUMBER: US 60/342,644
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
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Pred. No. 6.1e+02;
0; Mismatches 1;
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; Publication No. US20030185829A1
; GENERAL INFORMATION:
                                                                                 Sequence 15, Application US/10326185
Publication No. US20030175902A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 18, Application US/10326185; Publication No. US20030175902A1; GENERAL INFORMATION;
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; ORGANISM: Bacillus subtilis
US-10-326-185-15
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; ORGANISM: Bacillus subtilis
US-10-326-185-18
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Best Local Similarity 94.1
Matches 16; Conservative
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### APPLICANT: Grosse et al
TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFREENCE: 12402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT PILING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-12
PRIOR PELING DATE: 2000-10-16
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2000-10-16
PRIOR PELING DATE: 2.1
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US-09-976-782-72
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-091-625-51
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 16; Conserva
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Gaps

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Length 20; Indels

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Sequence 21, Application US/10199199

Sequence 21, Application US/10199199

Publication No. US20040014047A1

GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
FILE REPERBENCE: RIS-0375
CURRENT APPLICATION NUMBER: US/10/199,199
CURRENT FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 21
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 15.4; DB 1; ilarity 94.1%; Pred. No. 6.1e+02; Conservative 0; Mismatches 1;
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ilarity 94.1%; Pred. No. 6.1e+02;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                  0.4%; Score 15.4; DB 1;
94.1%; Pred. No. 6.1e+02;
:ive 0; Mismatches 1;
                                                                                                                                                                                             , OTHER INFORMATION: Antisense Oligonucleotide US-10-388-263-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Antisense Oligonucleotide
FILE REFERENCE: ISIS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
LENGTH: 20
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ORGANISM: Artificial Sequence
                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    Query Match 0.4
Best Local Similarity 94.1
Matches 16; Conservative
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ORGANISM: H. sapiens
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Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
TITLE OP INVENTION: GENERATION OF OLIGONUCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
FILE REFERENCE: RTS-0244
CURRENT APPLICATION NUMBER: US/10/461,668
CURRENT PILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/10/091,625
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 51
LENGTH: 20
                       APPLICANT: Shepard, Peter J.
TITLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS
FILE REPERENCE: ISPH-0660
CURRENT APPLICATION NUMBER: US/10/096,399A
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                    Query Match 0.4%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 6.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 6.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-461-668-51
                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense oligonucleotide US-10-096-399A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 421, Application US/10388263
Publication No. US20030228597A1
GENERAL INFORMATION:
APPLICANT: Cowsert, Lex M.
APPLICANT: Baker, Brenda F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/10461668 Publication No. US20030207839A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       1542 CACCTTCAAGGACCTGG 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1542 CACCTTCAAGGACCTGG 1558
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Borchers, Alexander
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Freier, Susan M.
Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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        APPLICANT: Koller, Erich
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APPLICANT:
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APPLICANT:
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Publication No. US20040023383A1
Publication No. US20040023383A1
SEGUENCE INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: REFERENCE: RTS-0396
CURRENT APPLICATION UNMBER: US/10/210,833
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 149
LENGTH: 20
                                                                                                                                                                                                                                             APPLICANT: Sugan M. Freier
APPLICANT: Sugan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION
FILE REFERENCE: RTS-0396
CURRENT APPLICATION NUMBER: US/10/210,833
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 165
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 6.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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Pred. No. 6.1e+02;
0; Mismatches 1; Indels
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TITLE OF INVENTION: MODULATION OF MAD2-LIKE 1 EXPRESSION
FILE REPERENCE: FTS-037-C
CURRENT APPLICATION NUMBER: US/10/304,109
CURRENT FILING DATE: 2002-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-833-50
                                                                                                                                                        Sequence 50, Application US/10210833 Publication No. US20040023383A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/10304109
Publication No. US20040101856A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1352 TGGAGATGATGAAGATG 1368
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      19 TACCTGGAGATGGGAGC 3
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ORGANISM: H. sapiens
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Best Local Similarity
                                                                                                                              US-10-210-833-50/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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FILLE NETERRENGE: 21402-462D
CURRENT APPLICATION NUMBER: 60/327,454
FRIOR PAPLICATION NUMBER: 60/327,454
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-09
FRIOR APPLICATION NUMBER: 60/328,029
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-12
FRIOR PELING DATE: 2001-10-12
FRIOR PELING DATE: 2001-10-12
FRIOR APPLICATION NUMBER: 60/329,414
FRIOR PELING DATE: 2001-10-15
FRIOR PELING DATE: 2001-10-25
FRIOR PELING DATE: 2001-10-22
FRIOR PELING DATE: 2001-10-22
FRIOR PELING DATE: 2001-10-22
FRIOR PELING DATE: 2001-10-22
FRIOR PELING DATE: 2001-10-24
FRIOR PELING DATE: 2001-10-24
FRIOR PELING DATE: 2001-10-24
FRIOR PELING DATE: 2001-10-24
FRIOR PELING DATE: 2001-10-29
FRIOR FILING DATE: 2001-10-29
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Patturajan, Mera
Rieger, Daniel
Spytek, Kimberly
Taupier, Jr., Raymond J.
Zerhueen, Bryan
Zhong, Haihong
                                                                                                                                                                                                                   Sequence 72, Application US/10262445
Publication No. US20040014058A1
2382 TCTTGCCTCCAGGTGCA 2398
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Chant, John
Chaudhuri, Amitabha
Edinger, Shlomit
Gerlach, Valerie
                                                             19 rcrrccrccaddraca 3
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ORGANISM: Artificial Sequence
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Guo, Xiaojia
Kekuda, Ramesh
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Best Local Similarity
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CURKENT FILING DATE: 2002-11-23 NUMBER OF SEQ ID NOS: 151

2734 TACCTGAAGATGGGAGC 2750

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Score 15.4; DB 1;
Pred. No. 6.1e+02;
                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1204
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                   Query Match 0.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative (
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Best Local Similarity 94.15
Matches 16; Conservative
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; Sequence 1171, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REPRENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT PILING DATE: 2003-09-25
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1171
LENGIN: 20
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GENERAL INFORMATION:

APPLICANT: Glerse, James K

APPLICANT: Glerse, James K

TITLE OF INVENTION: ANTIEBNSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT APPLICATION NUMBER: 60/413,549

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SEQ ID NO 1187

LENGTH: 20

LENGTH: 20
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                                                                                                                                                                                0.4%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; tive 0; Mismatches 1; Indels
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                                                                                                                OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1187, Application US/10671395; Publication No. US20040132063A1
                                                                                                                                                                                                                                                                               1281 TGTCACCGTAGCCGTGA 1297
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                                                                                                                                                                                                                                                                                                            2 TGTCACCGTAGCTGTGA 18
SEQ ID NO 45
LENGTH: 20
TYBE: DNA
ORGANISM: Artificial Sequence
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Matches 16; Conservative
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ORGANISM: artificial
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US-10-671-395-1171/c
                                                                                                                                       US-10-304-109-45
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Sequence 1204, Application US/10671395

| Sequence 1204, Application US/10671395
| Publication No. US20040132063A1
| GENERAL INFORMATION:
| APPLICANT: Pharmacia Corp.
| APPLICANT: Giers, James K
| TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
| TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
| TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
| TITLE OF INVENTION: ANTISENSE (60/413, 49)
| FILE REPERENCE: 1179/1/US
| CURRENT APPLICATION NUMBER: 60/413, 549
| PRIOR FILING DATE: 2002-09-25
| NUMBER OF SEQ ID NOS: 1809
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 1204
| LENGTH: 20
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; Sequence 1333, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TUTLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PALENTIN Version 3.2
; SEQ ID NO 1333
; LENGTH: 20
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0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
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US-10-466-347-17

Sequence 17, Application US/10466347

Sequence 17, Application US/10466347

Sequence 17, Application US/10466347

Sequence 17, Vico W.

APPLICANT: Fazio, Vito M.

APPLICANT Fazio, Vito M.

TITLE OF INVENTION: DAN AACCINES EXPRESSING HYPERVARIABLE VH-CDR3 IDIOTYPIC DETERMIN/
FILE REPERBNCE: 02901/0000028-USO

CURRENT APPLICATION NUMBER: US/10/466,347

CURRENT APPLICATION NUMBER: PCT/IT01/00014

PRIOR APPLICANTION DATE: 2003-07-18

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 17

LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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APPLICANT: MORNHINWEG, ESTHER
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THELI
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
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                                                    Sequence 26, Application US/10151320
; Sequence 26, Application US/20030092114A1
; GENERAL INPORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE;
; FILE REFERENCE: 200125.436
; CURRENT APPLICANTON NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Oligonucleotide primer used for PCR US-10-151-320-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 351, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      853 GAGGAGGAGCTGGTGGAGGCT 873
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: PCR primer
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Best Local Similarity 76.4.
Best Local Similarity 76.4.
                                          US-10-151-320-26/c
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                                                                                                                                                                                                                                                                                                          LENGTH: 21
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                                                                                                                                                      APPLICANT: Pharmacia Corp.
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTIERNSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2002-09-25
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1595
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: synthetic construct US-10-000-864-28
                                                                                             Sequence 1595, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2334 CGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001 GCAGCTGGTGGAGGACC 2017
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ORGANISM: Artificial Sequence
  CGTGTGTGTATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Best Local Similarity
                                                                                US-10-671-395-1595/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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US-09-918-186A-235/c

Sequence 235, Application US/09918186A

Patence 235, Application US/09918186A

Patence No. US20020137708A1

GENERAL INFORMATION:
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Est E Swayze

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: 126PH-0585

CURRENT APPLICATION NUMBER: US/09/918,186A

CURRENT FILING DATE: 2000-02-02

PRIOR FILING DATE: 1999-04-05

PRIOR PRILING DATE: 1998-04-05

PRIOR FILING DATE: 1998-04-05

PRIOR FILING DATE: 1998-04-05

PRIOR FILING DATE: 1998-04-05

SEQ ID NO 235

LENGTH: 20
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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Sequence 235, Application US/10181316
Publication No. US20030211607A1
GENERAL INFORMATION:
APPLICANT: Elizabeth 3. Ackermann
APPLICANT: Elizabeth 3. Ackermann
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
TILLE OF INVENTION ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0650
CURRENT APPLICATION NUMBER: US/10/181,316
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30;
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0.4%; Score 15.4; DB 1;
Best Local Similarity 76.0%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 6;
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CURRENT APPLICATION NUMBER: US/09/874,991C CURRENT FILING DATE: 2001-06-07 PRIOR APPLICATION NUMBER: 60/209,797 PRIOR FILING DATE: 2000-06-07 NUMBER OF SEQ ID NOS: 620 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 11 LENGTH: 30
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                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: BRINKMANN, ULRICH
APPLICANT: BRINKMANN, ULRICH
APPLICANT: HOFFWEYER, SVENN
APPLICANT: HOFFWEYER, SYENN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: PLACEMENT ASSOCIATED PROTEIN 1 (WRP-1)
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
FILE REPERBENCE: VOS-42 CON
CURRENT FILING DATE: 2003-07-24
PRIOR PLILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: PCT/EP02/00796
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SSCP THE NOS: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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| Sequence 11, Application US/08874991C
| Sequence 11, Application US/08874991C
| Sequence 11, Application US/08074991C
| GENERAL INFORMATION:
| APPLICANT: FLORA, MICHAEL
| APPLICANT: FLORA, MICHAEL
| APPLICANT: FLINMAN, DENNIS M.
| TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
| FILE REFERENCE: 07787.0042-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 15.4; DB 1; Length 21; 84.2%; Pred. No. 6.5e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 15.4; DB 1; Length 21;
84.2%; Pred. No. 6.5e+02;
tive 1; Mismatches 2; Indels
           FILE REFERENCE: VOS-42 CON
CURRENT APPLICATION NUMBER: US/10/627,253A
CURRENT FILING DATE: 2003-07-24
FRIOR APPLICATION NUMBER: PCT/FP02/00796
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOFTWARE: Patentin version 3.2
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 352, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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US-10-627-253A-352/c
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Pred. No. 6.6e+02;
0; Mismatches 3; Indels
                                    APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J. APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
               : Loren J. Miraglia, Pamela Nero, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                         ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
FILING DATE: 02-Jan-2001
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
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Patent No. US20010016575A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRELICATION NUMBER: 09/280,805
FILING DATE: «UNKNOWN-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
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INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 08053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-752-983-209/c
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          APPLICANT
                                                                                                                                                                                                                                     STATE:
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APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: YANADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: NETHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US 09/556,127
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-04-20
FRIOR PILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SSOFTWARE: PALENTIN VERSION 3.1
SSOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-316-235
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02939
PRIOR FILING DATE: 2001-0.30
PRIOR PILING DATE: 2000-0.2-02
PRIOR PILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR PILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
LENGTH: 20
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Patent No. US20010016575A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3458 AAGTITATATATATCTATAT 3477
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Publication No. US20010000175A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATATATATTTTTTGGG 20
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.0%
Matches 17; Conservative
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US-09-752-983-147/c
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Gaps

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Frank van de Loo
                                                                                 NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                       COUNTRY: USA
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nes 17; Conserv
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Matches
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APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Robert MCKAY
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION OF ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION DATE: 2001-05-14
PRIOR PELICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 15.2; DB 1; Length 20;
ilarity 85.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonuclectide US-09-854-883-305
                                                                                                                                 NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION:
TELEPHONE: 609-810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 305, Application US/09854883 Patent No. US20020055479A1
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Patent No. US20020104125A1
GENERAL INFORMATION:
                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 TCATGGAAAGCGTGGTGCCC 435
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
02-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
HANTI-SENSE: Yes
US-09-752-983-209
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Matches 17; Conserv
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APPLICANT: Chris Somerville

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GENERAL INFORMATION:
APPLICANT: KURANE, RYLICHIRO
APPLICANT: KRANGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: TORIMURA, MASAKI
APPLICANT: TORIMURA, KAZUTAKA
APPLICANT: YAWADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, RAZUTAKA
APPLICANT: WOKOMAKU, RAZUTAKA
APPLICANT: WOKOMAKU, RAZUTAKA
APPLICANT: WOKOMAKU, RAZUTAKA
APPLICANT: WOKOMAKU, RAZUTAKA
APPLICANTON: WOETHOD BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: WORTHOD
TITLE OF INVENTION: WORTHOD
TITLE OF DATE: 210352US-1994-163-0-X
CURRENT APPLICATION NUMBER: US/09/891,517
CURRENT PILLING DATE: 2001-06-27
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TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in
Genetically Modified Plants
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3;
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APPLICATION NUMBER: US/08/530,862B
FILING DATE: 06-Feb-1996
APPLICATION NUMBER: PCT/US95/11855
FILING DATE: September 25, 1995
APPLICATION NUMBER: US 08/330,862
FILING DATE: September 20, 1995
APPLICATION NUMBER: US 08/320,982
FILING DATE: October 11, 1994
APPLICATION NUMBER: US 08/314,596
FILING DATE: September 26, 1994
INFORMATION FOR SEQ 1D NO: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC-compatible
COMPATING SYSTEM: MS-DOS
SOFTWARE: MS WOACH
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
CLASSIPICATION:
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                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop,
STREET: 1600 Tysons Boulevard
CITY: McLean
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP2000-193133
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2982 CAGGGCTTTTTCTGGCACCG 3001
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Patent No. US20020106653A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 caagecerrrrrragenaced 1
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APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Lusis, Aldons J.
APPLICANT: Ohmen, Jeff
APPLICANT: Tafuri, Sherrie
APPLICANT: Tafuri, Sherrie
APPLICANT: Tafuri, Sherrie
APPLICANT: Wu, Chenyan
TITLE ROF INVENTION: Gene and Sequence Variation Associated with Cancer;
FILE REFERENCE: 02810.0014.NPUSO2
CURRENT APPLICATION NUMBER: US/09/949,427
CURRENT FILING DATE: 2000.09-07
PRIOR PILING DATE: 2000.09-08
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         TITLE OF INVENTION: Genetically Modified Plants
                                                                                                  ADDRESSEE: PILLSBURY MADISON & SUTRO, LLP STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-June-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/597,313D
FILING DATE: February 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520, 1995
FILING DATE: September 20, 1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: October 11, 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: September 26, 1994
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: WGOAT Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/885,189
PILING DATE: 21-June-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 252, Application US/09949427
Publication No. US20030054418A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 252
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleotide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-885-189-13
                                                                                                                                                                WASHINGTON
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APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: YOKINYA, WASAII
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: WETHOD
TITLE OF INVENTION: WETHOD
TITLE OF INVENTION: WETHOD
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TITLE OF INVENTION: METHOD
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APPLICANT: Pierre BROUN
APPLICANT: Frank VAN DS
TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 2001-06-27
PRIOR PELING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: JP2000-193133
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR APPLICATION NUMBER: JP2000-292483
PRIOR PILING DATE: 2000-09-26
NUMBER OP SEQ ID NOS: 108
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 34
LENGTH: 20
PRIOR APPLICATION NUMBER: JP2000-292483
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 20
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; Sequence 13, Application US/09885189
; Patent No. US20020151699A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/09891517
Patent No. US20020106653A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rararararrrrrrrccc 20
                                                                                                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-23
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                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 85.03
Matches 17; Conservative
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US-09-953-318-72/C

US-09-953-318-72/C

Sequence 72, Application US/09953318

Publication No. US20030105036A1

GENERAL INFORMATION:

APPLICAWT: C. Frank Bennett

APPLICAWT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT

TITLE OF INVENTION: ANTISENSE WODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT

TITLE REFERENCE: RTS-0232

CURRENT APPLICATION NUMBER: US/09/953,318

CURRENT FILING DATE: 2001-09-13

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 72

LENGTH: 20
                                                                                                                                                                                                                                              US-09-919-197-76/c
US-09-919-197-76/c
US-09-919-197-76/c
US-09-919-197-76/c
US-09-919-197-76/c
Sequence 76, Application US/09919197
Publication No. US20030083484A1
GENERAL INFORMATION:
APPLICANT: Rosame M. Crooke
APPLICANT: Mark J. Graham
APPLICANTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
TITLE OP INVENTION: ANTISENSE: US/09/919,197
CURRENT APPLICATION NUMBER: US/09/919,197
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 89
SSOTIMARE: FastSEQ for Windows Version 4.0
SSOTIMARE: 20
LENGTH: 20
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Query Match
0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Antisense Oligonucleotide US-09-953-318-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Antisense Oligonucleotide US-09-919-197-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2396 GCAGAGGTACCCTGGGTGTC 2415
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                                                                                                     1945 TACATGATCATGCGGGAGTG 1964
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; Sequence 74, Application US/09953318
; Publication No. US20030105036A1
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                                                                                                                                      20 TACATGATGATGAGGGACTG 1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Publication No. US20030078219A1
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
APPLICANT: Susan M. Freier
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTIENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
FILE REPRENCE: RTS-0250
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 98
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Chatterjee, Aurobindo
APPLICANT: de Jong, Pieter
APPLICANT: Dense, Aldons J.
APPLICANT: Nose, David
APPLICANT: Tafuri, Sherrie
APPLICANT: Tafuri, Sherrie
APPLICANT: Wu, Chenyan
TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
FILE REFERENCE: 02810.0014.NPUS01
CURRENT APPLICATION NUMBER: US/09/949,428
CURRENT FILING DATE: 2000-09-08
FRIOR RILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PatentIn version 3.1
SEQ ID NO 252
LENGTH: 20
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                                                                                                            Length 20;
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                                                                                                                                                             3; Indels
                                                                                                       Query Match

0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-252
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               ; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-252
                                                                                                                                                                                                                                                                                                                                                                               Sequence 252, Application US/09949428 Publication No. US20030064372A1 GENERAL INFORMATION:
                                                                                                                                                                                                             3651 CTTGCTTGCCTGCAGGGCCA 3670
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US-09-954-556-98/c
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          APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
FILE REPERENCE: ISPH-0617
CURRENT APPLICATION NUMBER: US/10/001,844
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 33
LENGTH: 20
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APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANYISENSE MODULATION OF HCK EXPRESSION
FILE REFERENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT APPLICATION NUMBER: 2001-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 56
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llarity 85.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WS-10-229-346-34/C

| Sequence 34, Application US/10229346 |
| Sequence 34, Application US/10229346 |
| Publication No. US20030120054A1 |
| GENERAL INFORMATION: |
| APPLICANT: Chen, Bric |
| APPLICANT: Chen, Bric |
| TITLE OF INVENTION: Modified Cry3A Toxins |
| TITLE OF INVENTION: Modified Cry3A Toxins |
| TITLE OF INVENTION: WOMBER: US/10/229,346 |
| CURRENT APPLICATION NUMBER: US/10/229,346 |
| CURRENT FILING DATE: 2002-08-27 |
| PRIOR PRILICATION NUMBER: 60/316,421 |
| RINDRER OF SEQ ID NOS: 38 |
| SOFTWARE: Patentin version 3.0 |
| LENGTH: 20
                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-001-844-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004 GCTGGTGGAGGACCTGGACC 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1995 CTTCAAGCAGCTGGTGGAGG 2014
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; OTHER INFORMATION: CMS16 Primer US-10-229-346-34
                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserv
GENERAL INFORMATION:
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  APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT PILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGATA, YOLCHI
APPLICANT: KANAGATA, YOLCHI
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, OSAMU
APPLICANT: FUBUSHO, KENTA
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI TITLE OF INVENTION: THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 19995JUSOXIV
CURRENT APPLICATION NUMBER: US/10/209,608
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/725,265
PRIOR PILING DATE: 2000-11-29
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 1999-04-20
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Publication No. US20030082592A1
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; Sequence 33, Application US/10001844
; Publication No. US20030105041A1
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                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 20
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GENERAL INFORMATION:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ.ID NO: 75:
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REFERENCE/DOCKET NUMBER: 620-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 147, Application US/10005344 Publication No. US20030203862A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 GCTCCATCCTCGGGAGATGA 176
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Loren J. Miraglia APPLICANT: Pamela Nero
            STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-005-344-147/c
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STREET: 1100 No. US20030181660Alth Glebe Road, Eighth Floor
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                  Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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Rezriman, Tony R
Merziman, Tony R
Mezker, Michael L
TITLE OF INVENTION: No. US20030181660A1el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide US-10-007-010-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
COTHER INFORMATION: antisense sequence US-10-238-442-22
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Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John A
Hess, John W
                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/10238442; Publication No. US20030176383A1
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Gerhold, David
Hammond, Holly
Hey, Patricia
              TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 17; Conserv
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US-10-331-907-75/c
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LENGTH: 20
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                                                     FEATURE:
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APPLICANT: Pamela Nero
APPLICANT: Pamela Nero
APPLICANT: Bract P. Monia
APPLICANT: Erich Koller
APPLICANT: Erich Koller
APPLICANT: MingYi Chiang
APPLICANT: MingYi Chiang
TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
FILE REFERENCE: ISPH-6622
CURRENT APPLICATION NUMBER: US/10/005,344
CURRENT FILING DATE: 1990-03-26
PRIOR APPLICATION NUMBER: US 09/048,810
PRIOR APPLICATION NUMBER: US 09/048,805
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 147

"ERGTH: 20
                                                                                                                                                      Version #1.25 (EPO)
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
APPLICATION NUMBER: ECT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/31,907
FILING DATE: 31-DEC-2002
PRIOR APPLICATION DATA:
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Sequence 74, April cation US/10446373

Publication No. US20030204076A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Wat.
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: BXPRESSION
FILE REPERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/10/446,373
CURRENT PILING DATE: 2003-05-28
FRIOR APPLICATION NUMBER: US/09/953,318
FRIOR PILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 74
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Sequence 60, Application US/10380931

Publication No. US20030215944A1

GENERAL INFORMATION:

APPLICANT: ISIE Pharmaccuticals, Inc.

APPLICANT: Grank Bennett

APPLICANT: Jacqueline Wyatt

APPLICANT: Jacqueline Wyatt

APPLICANT: Basan M. Preier

TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION

FILE REFERENCE: RTSP-0187

CURRENT APPLICATION WUMBER: US/10/380, 931

CURRENT FILING DATE: 2003-03-18

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 182

LENGTH: 20
                                                                  Gaps
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                      Length 20;
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                                                               Indels
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                  Score 15.2; DB 1;
Pred. No. 6.6e+02;
0; Mismatches 3;
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Fred. No. 6.6e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-931-60
                                                                                                           1573 CAGGTGGCCCGGGGCATGGA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1610 AGTGCATCCACAGGGACCTG 1629
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                    Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
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ORGANISM: Artificial Sequence
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US-10-446-373-72/C

US-10-446-373-72/C

US-10-446-373-72/C

SQUENCE 72, Application US/10446373

Publication No. US20030204076A1

Publication No. US20030204076A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: EXPRESSION
FILE OF INVENTION: EXPRESSION
FILE REPERENCE: RTS-023

CURRENT APPLICATION NUMBER: US/10/446,373

CURRENT FILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-09-13

NUMBER OF SQ ID NOS: 154

SEQ ID NO 72

LENGTH: 20
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FILE REFERENCE: ISPH-0622
CURRENT APPLICATION NUMBER: US/10/005,344
CURRENT FILING DATE: 2001-12-04
FRIOR APPLICATION NUMBER: US 09/048,810
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 379
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 209
LENGTH: 20
                                                             Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
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OTHER INFORMATION: Antisense Oligonucleotide
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                                                                                                                                                                                                                                                                                                        Sequence 209, Application US/10005344
Publication No. US20030203862A1
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia
                                                                                                                                                    1346 CTGAGATGGAGATGAAG 1365
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ORGANISM: Artificial Sequence
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Mark J. Graham
Brett P. Monia
Erich Koller
MingYi Chiang
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Matches 17; Conservative
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    ; OTHER INFORMA
US-10-005-344-147
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APPLICANT:
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APPLICANT:
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US-10-160-497-22/c
US-10-160-497-22/c
US-10-160-497-22/c
Sequence 22, Application US/10160497
Publication No. US20030224513A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Erich Koller
APPLICANT: Erich Koller
TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
FILE REFERENCE: RTS-0386
CURRENT APPLICATION NUMBER: US/10/160,497
CURRENT PILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 145
SEQ ID NO 22
LENGTH: 20
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
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RESULT 781 US-10-348-750-22/c

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Sequence 15, Application US/10372909

Sequence 15, Application US/10372909

Publication No. US20030237109A1

GENERAL INFORMATION:
APPLICANT: KOTODA, NOBURIRO

APPLICANT: WADA, MASATO

APPLICANT: SOCJINA, UUNICHI

TITLE OF INVENTION: FLOWER-BUD FORMATION SUPPRESSOR GENE AND EARLY FLOWERING PLANT

TITLE OF INVENTION: FLOWER: US/10/372,909

CURRENT FILING DATE: 2003-02-26

PRIOR PAPLICATION NUMBER: US/10/372,909

CURRENT FILING DATE: 2003-06-20

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 15

LENGTH: 20

LENGTH: 20

LENGTH: 20
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Sequence 74, Application US/10210290

Sequence 74, Application US/10210290

Sequence 74, Application US/10210290

GENERAL INFORMATION:
APPLICANT: Ming-Yi Chiang

APPLICANT: Exic G. Marcusson

APPLICANT: Exic G. Marcusson

TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

FILE REFERENCE: RIS-0367
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; Sequence 22, Application US/10348750;
; Publication No. US20030225019A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: NOTCHI INHIBITORS FOR INDUCING APOPTOSIS; FILE REFERENCE: ISPH-0729
; CURRENT APPLICATION NUMBER: US/10/348,750
; CURRENT APPLICATION NUMBER: 10/160,497
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 22
; LENGTH: 20
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85.0%; Pred. No. 6.6e+02;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.0%
Matches 17; Conservative
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TYPE: DNA ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 128, Application US/10210290
| Bublication No. US20040023378A1
| GENERAL INFORMATION:
| APPLICANT: Ming-Yi Chiang
| APPLICANT: Eric G. Marcusson
| APPLICANT: Kenneth W. Dobie
| TILLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
| TILLE OF INVENTION: ANTISENSE US/10/210,290
| CURRENT APPLICATION NUMBER: US/10/210,290
| CURRENT PILING DATE: 2002-07-31
| WUMBER OF SEQ ID NOS: 134
| SEQ ID NO 128
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; Sequence 39, Application US/10380124
; Publication No. 200040053874A1
; GENERAL INFORMATION:
    APPLICANT: Isis Pharmaceuticals, Inc.
    APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
    TILE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE RPERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT PILING DATE: 2003-03-10
; SEQ ID NOS: 90
; SEQ ID NOS: 90
; SEQ ID NOS: 90
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-74
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US-10-380-124-39
CURRENT APPLICATION NUMBER: US/10/210,290 CURRENT FILING DATE: 2002-07-31 NUMBER OF SEQ ID NOS: 134 SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                      1610 AGTGCATCCACAGGGACCTG 1629
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                                                                                   LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 85.01
Matches 17; Conservative
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JOHNSTON TRY KURANE, RYUCHIRO
JAPPLICANT: KUNAGAWA, TAKAHIRO
JAPPLICANT: KUNAGAWA, TAKAHIRO
JAPPLICANT: KANAGAWA, TAKAHIRO
JAPPLICANT: KANAGAWA, TAKAHIRO
JAPPLICANT: YOKOMAKU, TOYOKAZU
JAPPLICANT: WOYONAM: WINCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT
JITLE OF INVENTION: THE METHOD
JAPPLICANT: WOWHER: US/10/683,386
JUNEMENT APPLICATION NUMBER: US/09/556,127
JERICR APPLICATION NUMBER: US/09/556,127
JERICR APPLICATION NUMBER: UP 1999-111601
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Publication No. US20040077099A1

JERERAL INFORMATION:
APPLICANT: Argome National Laboratory
APPLICANT: Argome National Laboratory
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APPLICANT: Alexander
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APPLICANT: Alexander
APPLICANT: Alexander
APPLICANT: ALIVENTION: BOOSITIONING
FILE OF INVENTION: BOSSITIONING
FILE REFERENCE: ANL-IN-01-052
CURRENT APPLICATION NUMBER: US/10/619,284A
FILE REPERENCE: ANL-IN-01-052
CURRENT FILING DATE: 2003-07-14
FRIOR APPLICATION NUMBER: US/10/139842
FRIOR APPLICATION NUMBER: US/10/139842
FRIOR APPLICATION NUMBER: US/10/139842
FRIOR PROPER APPLICATION NUMBER: US/10/139842
FRIOR PERIOR APPLICATION NUMBER: US/10/139842
FRIOR PERIOR APPLICATION NUMBER: US/10/139842
FRIOR PERIOR APPLICATION NUMBER: US/10/139842
FRIOR APPLICATION NUMBER: US/10/139842
FRIOR FILING DATE: 2003-05-06
FRIOR APPLICATION NUMBER: US/10/139842
FRIOR FILING DATE: 2003-05-06
FRIOR FILING DATE: 2003-07-05-06
FRIOR FILING DATE: 2003-05-06
FRIOR FILING DATE:
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3473 TATATATATATTATTGAG 3492
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Publication No. US20040063137A1
489 GCAGACGTACACGCTGGACG 508
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                                                                                                                         20 GCAGACGCACATGCTGGATG 1
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Wis-lot-145
(Wis-lot-145)
Sequence 145, Application US/10274085
Sequence 145, Application US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Sanjay Bhanot
TITLE OF INVENTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
FILE REFERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PILING DATE: 2002-10-17
SEQ ID NO 145
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Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Susan M W. Dobie
APPLICANT: Kenneth W. Dobie
APPLICANT: Sanjay Bhanot
TITLE OF INVENTION ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
FILE REPERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PEING DATE: 2002-10-17
SEQ ID NO 172
                                                      Sequence 64, Application US/10274085
; Sequence 64, Application US/20040077570A1
; Sequence 64, Application NO. US20040077570A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Seneth W. Dobie
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
; TITLE REPERENCE: ISPH-0714
; CURRENT PILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 225
; SEQ ID NO 64
LENGTH: 20
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Pred. No. 6.6e+02;
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: H. sapiens
US-10-274-085-145
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## APPLICANT: Argenne National
## APPLICANT: Argenne National
## TITLE OF INVENTION: BIOCHIP READER WITH ENHANCED ILLUMINATION AND BIOARRAY
## TITLE OF INVENTION: BOSTIONING
## CURRENT APPLICATION NUMBER: US/10/619,284A
## CURRENT APPLICATION NUMBER: US/10/619,284A
## CURRENT FILING DATE: 2003-07-14
## PRIOR FILING DATE: 2002-05-06
## SEQ ID NO 74
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| Sequence 33, Application No. US20040077570A1
| GENERAL INFORMATION:
| APPLICANT: Susan M. Freier
| APPLICANT: Kenneth W. Dobie
| APPLICANT: Sanjay Bhanot
| TITLE OF INVENTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION TITLE OF INVENTION NUMBER: US/10/274,085
| CURRENT APPLICATION NUMBER: US/10/274,085
| CURRENT PILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 225
| LENGTH: 20
| LENGTH: 20
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Score 15.2; DB 1; Length 20;
Pred. No. 6.6e+02;
0; Mismatches 3; Indels
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                              Sequence 74, Application US/10619284A Publication No. US20040077099A1 GENERAL INFORMATION:
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             Query Match 0.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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US-10-300-642-65
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Publication No. US20040087523A1
Publication No. US20040087523A1
Sequence 77, Application US.
Publication No. US20040087523A1
APPLICANT: Ming-Yi Chiang
APPLICANT: Memeth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION FILE REPERENCE: RTS-0367
CURRENT APPLICATION NUMBER: US/10/210,802
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 74
LENGTH: 20
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; Sequence 118, Application US/10210802
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
APPLICANT: Ming-Yi Chiang
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
FILE REFERENCE: FIS-036
CURRENT APPLICATION NUMBER: US/10/210,802
CURRENT FILING DAIE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
ENGIH: 20
LENGTH: 20
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                                                                                                           Query Match
0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-802-74
                                                                                                                                                                                                  1891 CTGCTGAAGGAGGCCACCG 1910
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                                                                                                                                                                                                                             1 CTGCTGGAGCAGGCCTCCG 20
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Best Local Similarity 85.0
Matches 17; Conservative
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-274-085-172
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US-10-210-802-128/c
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                                                                                                                                                                                                                                                                                                         RESULT 793
US-10-210-802-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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RESULT 795 US-10-300-642-33/c

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Sequence 33, Application US/10300642
Publication No. US20040096836A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 13 EXPRESSION
FILE REFERENCE: HTS-0045
CURRENT APPLICATION NUMBER: US/10/300,642
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ 1D NOS: 78
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Dobie
TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 13 EXPRESSION
FILE REFERENCE: HTS-0045
CURRENT APPLICATION NUMBER: US/10/300,642
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 65
LENGTH: 20
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Publication No. US20040102412A1

GENERAL INPORMATION:

APPLICANT: Pharmacia Corp.

TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

TITLE OF INVENTION: ANTISENSE: US/10/688,706

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT FILING DATE: 2003-10-17

PRIOR FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: PATENTIN version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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Pred. No. 6.6e+02;
0; Mismatches 3;
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-642-33
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Best Local Similarity 85.0%;
Matches 17; Conservative C
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ORGANISM: H. sapiens
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LENGTH: 20
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RESULT 802
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i Sequence 102, Application US/10688706

i Sequence 102, Application US/10688706

i Publication No. US20040102412A1

i GENERAL INFORMATION:

i APPLICANT: Pharmacia Corp.

APPLICANT: Broschat, Kay

i TILLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

FILE REFERENCE: 01393/1

CURRENT PLING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR PILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: Patentin version 3.2

LENGTH: 20
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US-10-319-915-120/c
s Gequence 120, Application US/10319915
; Fadulation No. US20040115653A1
; GENERAL INFORMATION:
   APPLICANT: Kenneth W. Dobie
; FILLE REFERENCE: RTS-0447
; CURRENT FILLING DATE: 2002-12-12
; SEQ ID NO 120
; SEQ ID NO 120
; LENGTH: 20
                                                                                                     Length 20;
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                              3; Indels
                                                                                                Query Match

0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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               FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-88
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; OTHER INFORMATION: human GFAT antisense
US-10-688-706-102
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Best Local Similarity 85.0°
Matches 17; Conservative
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ORGANISM: artificial
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Sequence 1138, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT FILING DATE: 2003-09-25
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   Sequence 247, Application US/10319915
Publication No. US20040115653A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION FILE REFERENCE: RTS-0447
CURRENT APPLICATION NUMBER: US/10/319,915
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 279
SEQ ID NO 247
LIENGTH: 20
                                                                                                                                                                                                                                                                                                           Score 15.2; DB 1; Length 20; Pred. No. 6.6e+02;
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: M. musculus
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JS-10-319-915-247
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SOFWARE: Patentin version 3.2
SEQ ID NO 1312
LENCTH: 20
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SOFWHARE: Patentin version 3.2
SEQ ID NO 1350
LENGTH: 20
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Best Local Similarity 85.0%
Matches 17; Conservative
  ORGANISM: artificial
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Best Local Similarity
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Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Glarse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
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APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
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Pred. No. 6.
                                                                                                                                                                                               ; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1138
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US-10-671-395-1175
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Publication No. US20040132063A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
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                                         NUMBER OF SEQ ID NOS: 1809
SOFWARE: Patentin version 3.2
SEQ ID NO 1138
LENGTH: 20
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1175
LENGTH: 20
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Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                      ORGANISM: artificial
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                                                                                                                                 TYPE: DNA
                                                                                                                                                                               FEATURE:
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Sequence 1312, Application US/10671395
Sequence 1312, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
PRIOR FILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-09-25
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Sequence 1350, Application US/10671395
Fublication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Clerke, James K
TITLE OF INVENTION: ANTIENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTIENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTIENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-09-25
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                                                                                                                   2; DB 1;
6.6e+02;
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85.0%; Pred. No. 6.6e+02;
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                                                                                                                   Score 15.2; D
Pred. No. 6.6e
0; Mismatches
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1279
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US-10-671-395-1312
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US-10-671-395-1423/c

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Sequence 1423, Application US/10671395

Publication No. US20040132063A1

Publication No. US20040132063A1

Publication No. US20040132063A1

Publication No. US20040132063A1

PREDICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN EZ SYNTHASE

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT FILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin Version 3.2

SEQ ID NO 1423

LENGTH: 20

TENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Giere, James K
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 60/413,549
FRIOR APPLICATION NUMBER: 60/413,549
FRIOR APPLICATION NUMBER: 60/413,549
FRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
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Pred. No. 6.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1423
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US-10-671-395-1431
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT FILING DATE: 2003-09-25
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SSOFTWARE: Patentin version 3.2
SEQ ID NO 1399
LENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-09-25
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                    3; Indels
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US-10-671-395-1406
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US-10-671-395-1399
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Publication No. US20040132063A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1406
LENGTH: 20
                       Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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NUMBER OF SEQ ID NOS: 1809
SOFWARE: Patentin version 3.2
SEQ ID NO 1627
LENGTH: 20
                                                                                           TYPE: DNA
ORGANISM: artificial
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ORGANISM: artificial
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APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NOS: 1809
SEQ ID NO 1566
LENGTH: 20
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE TITLE OF INVENTION: EXPRESSION FILE REFERENCE: 1179/1/US CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILLING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
LENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT PILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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Pred. No. 6.6e+02;
0; Mismatches 3;
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US-10-671-395-1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1566
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; Sequence 1566, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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ORGANISM: artificial
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: artificial
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Sequence 1628, Application US/10671395
; Sequence 1628, Application US/10671395
; Publication No. US2004013206341
; GENERAL INFORMATION:
    APPLICANT: Diames K
    TITLE OF INVENTION: EXPRESSION
    TILE OF INVENTION: EXPRESSION
    FILE REFERENCE: 1179/1/US
    CURRENT APPLICATION NUMBER: US/10/671,395
    CURRENT APPLICATION NUMBER: 60/413,549
    PRIOR RILING DATE: 2002-09-25
    NUMBER OF SEQ ID NOS: 1809
    SEQ ID NO 1628
    LENGTH: 20
    LENGTH: 20
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## Sequence 1640, Application US/10671395

## Publication No. US20040132063A1

## Publication No. US20040132063A1

## SPELICANT: Pharmacia Corp.

## APPLICANT: Gierse, James K

## TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

## TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

## TITLE OF INVENTION: ANTISENSE NON

## TITLE OF INVENTION NUMBER: 60/413,549

## PRIOR APPLICATION NUMBER: 60/413,549

## PRIOR PILING DATE: 2002-09-25

## NUMBER OF SEQ ID NOS: 1809

## SEQ ID NO 1640

## LENGTH: 20

## LENGTH
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85.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 3; Indels
                                                                                                                                                                            Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1627
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Matches 17; Conservative
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US-10-671-395-1670/c

i Sequence 1670, Application US/10671395

i Publication No. US20040132063A1

i Publication No. US20040132063A1

i Publication No. US20040132063A1

i APPLICANT: Pharmacia Corp.

i APPLICANT: Gierse, James K

i TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

I TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT APPLICATION NUMBER: 60/413,549

PRIOR FILING DATE: 2003-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin version 3.2

SEQ ID NO 1670

"DENGTH: 20

"DENGTH: 20
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; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Pharmacia Corp.
; APPLICANT: PLANCE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT PILING DATE: 2003-09-25
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1685

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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2326 IGIGIGIGIGIGIGIGIGI 2345
2319 GTGTGTGTGTGTGCGTGT 2338
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Best Local Similarity 85.0°
Matches 17; Conservative
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Matches 17; Conservative
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US-10-671-395-1685/c
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US-10-654-102-126/c
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US-10-671-395-1641/c

is Sequence 1641, Application US/10671395

sequence 1641, Application US/10671395

publication No. US20040132063A1

ceneral information:

APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: EXPRESSION

TITLE OF INVENTION: APPLICANTION: LARRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT APPLICATION NUMBER: 60/413,549

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin version 3.2

LENGTH: 20
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; Sequence 1665, Application US/10671395
; Sequence 1665, Application No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: EXPRESSION
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/L/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2002-09-25
; PRIOR PAPLICATION NUMBER: 60/413,549
PRIOR PLING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1665
: LENGTH: 20
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                                                                  Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1641
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1640
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-671-395-1665/c
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GENERAL INFORMATION:
APPLICANT: Rosanne M. Crooke
APPLICANT: MATK J. Graham
TITLE OF INVENTION: ANTIESENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
FILE REFERENCE: ISPH-0593
CURRENT APPLICATION NUMBER: US/10/835,208
CURRENT FILING DATE: 2004-04-29
PRIOR APPLICATION NUMBER: US/09/919,197
PRIOR APPLICATION NUMBER: US/09/919,197
                                                                                                                                                                                                                                                                                                                                                                                                          ), OTHER INFORMATION: Antisense Oligonucleotide US-10-835-208-76
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
       US20040192633A1
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US-09-771-730-103
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APPLICANT: Gaarde, William A.
APPLICANT: Nerco, Pamela S.
APPLICANT: Morky, Robert
APPLICANT: Popoff, Ian
APPLICANT: Wong, Wai Shiu Fred
APPLICANT: Wong, Wai Shiu Fred
TITLE OF INVENTION: Artisense Oligonucleotide Modulation of p38 Mitogen
TITLE OF INVENTION: Activated Protein Kinase Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Primer US-10-654-102-126
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                      APPLICANT: KOJIMA, HIDETO
TITLE OF INVENTION: INDUCTION OF PANCREATIC ISLET FORMATION
FILE REFERENCE: PO2409US1
CURRENT APPLICATION NUMBER: US/10/654,102
CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 126
LENGTH: 20
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CURRENT APPLICATION NUMBER: US/10/641,455A
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 10/238,442
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2000-08-15
PRIOR PILING DATE: 2000-08-15
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 22
LENGTH: 20
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Sequence 126, Application US/10654102
Publication No. US20040132679A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                       APPLICANT: CHAN, LAWRENCE
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APPLICANT: Syngenta Participations AG
TITLE OF INVENTION: Additied Cry3A Toxins and Nucleic Acid Sequences Coding Therefor FILE REFERENCE: 60065/PCT
CURRENT APPLICATION NUMBER: US/10/487,846
CURRENT APPLICATION NUMBER: US 60/316421
PRIOR APPLICATION NUMBER: US 60/316421
PRIOR PILING DATE: 2001-08-31
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 34
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     Length 20;
                                                     3; Indels
Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
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Patent No. US20020146807A1
GENERAL INFORMATION:
APPLICANT: Prayage, Sudhirdas K.
APPLICANT: Li, Li
                                                                                                        2396 GCAGAGGTACCCTGGGTGTC 2415
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Publication No. US20040199939A1
GENERAL INFORMATION:
                                                                                                                                                          20 GCAGCGGTACCCAGGGTGCC 1
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MacDougall, John R.
Spytek, Kimberly Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

// DCCATION: (1)...(20)

// OTHER INFORMATION: CMS16 Primer

US-10-487-846-34
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APPLICANT:
APPLICANT:
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; Sequence 76, Application US/10835208

RESULT 822 US-10-835-208-76/c

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Gaps
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APPLICANT: Majumder, Kumud

APPLICANT: Maina, Vishna

APPLICANT: Mezes, Peter S

APPLICANT: Reacelll, Luca

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REPRENCE: 15966-697

CURRENT APPLICATION NUMBER: US/09/800,198

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: 60/186,596

PRIOR APPLICATION NUMBER: 60/186,596

PRIOR PRILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 98

SOFTWARE PATENTING VET: 2.1

SEQ ID NO 33

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                           TYPE: DNA;
; ORGANISM: Artificial Sequence;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ag427 Probe US-09-808-602-35
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APPLICANT: Echt, Craig. S
APPLICANT: Nelson, C. Dana
TITLE OF INVENTION: MICROSATELITE DNA MARKERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 4481/1E188US1
                                                                                                                                                                                                                                                                                     Query Match

0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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; Sequence 390, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 21
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Best Local Similarity 85.0
Matches 17; Conservative
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; ORGANISM: Pinus taeda L.
US-09-232-785-390
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFREENCE: 15566-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
                                        OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: NOV 12 Probe; OTHER INFORMATION: Primer Sequence
US-09-771-730-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 15.2; DB 1; Length 21; 85.0%; Pred. No. 6.9e+02; tive 0; Mismatches 3; Indels
                              TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUTILE OF INVENTION: NOVEL POLYPEPTIDES AND NUTILE OF INVENTION: NOVEL POLYPEPTIDES AND NUTILE OF INVENTION NUMBER: US/09/771,730 CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/178,413
PRIOR APPLICATION NUMBER: 60/178,371
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,406
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,409
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,409
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,409
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/120,634
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/220,516
PRIOR APPLICATION NUMBER: 60/221,408
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/221,943
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/221,943
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/220,516
PRIOR APPLICATION NUMBER: 60/221,943
PRIOR FILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/220,516
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/220,516
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PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
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ORGANISM: Artificial Sequence
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Matches 17; Conservative
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APPLICANT: Borchers, Alexander
APPLICANT: Borchers, Timothy A.
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: DENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR
TITLE REFERENCE: ISS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
NUMBER OF SEQ ID NOS: 947
SOUTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 21
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Publication No. US20030228302A1

GENERAL INFORMATION:

TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS

TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS

FILE REPRENCE: 1551.2001-001

CURRENT APPLICATION NUMBER: US/10/418,182

CURRENT FILING DATE: 2003-04-16

PRIOR FILING DATE: 2002-04-17

NUMBER OF SEQ ID NOS: 423

SOFTWARE: FastSEQ for Mindows Version 4.0

SEQ ID NO 112

LENGTH: 21
                                                                                                                                               Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
                        ; FEATURE:
; NAME/KRY: misc_feature
; OTHER INFORMATION: Allele DQB1*06011
US-10-253-967-36
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Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cowsert, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-388-263-203/c
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LOCATION: (16) ...(16)
OTHER INFORMATION: Glen research spacer 9 (cat # 10-1909-90) between c 15 and c 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/10142566
Publication No. US20030119016A1
GENERAL INFORMATION:
APPLICANT: Riley, Timothy A.
APPLICANT: Brown, Bob D.
APPLICANT: Arnold, Lyle J.
APPLICANT: Arnold, Lyle J.
TITLE OF INVENTION: ANTIERNSE OLIGONUCLEOTIDES WITH INCREASED RNASE SENSITIVITY
CHRENT APPLICATION NUMBER: US/10/142,566
FRICK PRING DATE: 2002-08-06
PRIOR FILING DATE: 2002-08-06
PRIOR FILING DATE: 1996-08-18
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                      ) OTHER INFORMATION: Description of Artificial Sequence:Ag427 Probe; OTHER INFORMATION: Primer
US-09-800-198-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 70.0%; Pred. No. 6.9e+02; Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                          Query Match
0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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Sequence 36, Application US/10253967

Publication No. US20030165925A1

GENERAL INFORMATION:

APPLICANT: SAITO et al.

TITLE OF INVENTY DATE: 27978/37504A

CURRENT APPLICATION NUMBER: US/10/253,967

CURRENT FILING DATE: 2002-09-24

PRIOR FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.1

SEQ ID NO 36

LENGTH: 21
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; OTHER INFORMATION: propyl linker attached to t 21
US-10-142-566-49
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                     ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 828
US-10-142-566-49
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LENGTH: 21
                                                   FEATURE
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US-10-380-195A-44/C

US-10-380-195A-44/C

Sequence 44, Application US/10380195A

Publication No. US20040072776A1

Publication No. US20040072776A1

Publication No. US20040072776A1

APPLICANT: Gleave, Martin

APPLICANT: Gleave, Martin

APPLICANT: Rennie, Paul

TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2

TITLE OF INVENTION: Oligodeoxymucleotides for Prostate and Endocrine Tumor Therapy

FILE REFERENCE: UBC.P-02

TITLE OF INVENTION: UNMBER: PCT/US01/28748

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 44

LENGTH: 21
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                   PRIOR FILING ATELIAN NUMBER: 60/310, 291
PRIOR PELICATION NUMBER: 60/310, 291
PRIOR FILING DATE: 2001-08-03
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-17
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
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2001-08-02
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APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Taupier, Stacie
APPLICANT: Caeman, Stacie
APPLICANT: Rothenberg, Mark E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
TITLE OF INVENTION: THE SAME
FILE OF INVENTION: THE SAME
FILE REFERENCE: 21402-416D
CURRENT APPLICATION UNMBER: US/10/210,281
PRIOR APPLICATION NUMBER: 60/309,501
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VESULT 832

SEQUENCE 82, Application US/10377079

SEQUENCE 82, Application US/10377079

PUBLICATION NO. US2030236395A1

SERVERAL INFORMATION:

TITLE OF INVENTION: PR-Domain Containing Nucleic Acids, Polypeptides,

TITLE OF INVENTION: Antibodies and Methods

TITLE OF INVENTION: Antibodies and Methods

FILE REFERENCE: P-LJ 3611

CURRENT APPLICATION NUMBER: US/10/377,079

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 93

SEQ ID NO 82

LENGTH: 21
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                                                                                                                     Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1722 GAAGACAACCAACGGCGGC 1741
                                                                                                                                                                                                                                                     860 AGCTGGTGGAGGCTGACGAG 879
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Burgess, Catherine E.
Sciore, Paul
Stone, David J.
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APPLICANT: Zerhusen, Bryan D.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                              20 AGCTGGTGGATGCAGAGGAG 1
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Miller, Charles E.
Ji, Weizhen
                            ) OTHER INFORMATION: PCR Primer US-10-388-263-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-079-82
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   FEATURE:
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TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN TITLE OF INVENTION: KINASE FILE REPERENCE: AM101071 CURRENT APPLICATION NUMBER: US/10/702,496 CURRENT FILING DATE: 2003-11-07 PRIOR APPLICATION NUMBER: 60/429,381 PRIOR PELLING DATE: 2002-11-27 NUMBER OF SEQ ID NOS: 306 SOFTWARE: PATEURIN OF SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: My, wei
APPLICANT: My, Leeying
APPLICANT: Wu, Leeying
TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
TITLE OF INVENTION: KINASE
FILE OF INVENTION: KINASE
FILE OF INVENTION: WUMBER: US/10/702,496
CURRENT APPLICATION NUMBER: L05/11-07
PRIOR PILING DATE: 2003-11-27
NUMBER OF SEQ ID NOS: 306
SOFTWARE PACENTIN VERSION 3.2
SEQ ID NO 289
LENGTH: 21
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Publication No. US20040142896A1
GENERAL INFORMATION:
APPLICANT: Wang, Jui, H
APPLICANT: Wang, Jui, H
TITLE OF INVENTION: High Efficacy Antisense RI alpha PKA Poly-DNP Oligoribonucleotide
FILE REFERENCE: 11520.0338
CURRENT APPLICATION NUMBER: US/10/728,491
CURRENT APPLICATION NUMBER: US 60/431,694
PRIOR APPLICATION NUMBER: US 60/431,694
PRIOR FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 27
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Pred. No. 6.9e+02;
4; Mismatches 3; Indels
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Pred. No. 6.9e+02;
0; Mismatches 3; Indels
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GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2046 CGACGAGTACCTGGACCTGT 2065
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Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.0°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-702-496-161
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US-10-702-496-289
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                                                                                                                              US-10-432-364-35/c

US-10-432-364-35/c

Sequence 35, Application US/10432364

Publication No. US20040091996A1

Publication No. US20040091996A1

GENERAL INFORMATION:

APPLICANT: VIRGENE BIOTECHNOLOGY LIMITED

TITLE OF INVENTION: SPECIFIC TUMOR CELLS AND THE USE OF IT

TITLE OF INVENTION: SPECIFIC TUMOR CELLS AND THE USE OF IT

TITLE REPERENCE: icc010042pct

CURRENT APPLICATION NUMBER: US/10/432,364

CURRENT FILING DATE: 2003-11-06

NUMBER OF SEQ ID NOS: 36

SOOFWARE: Patentin version 3.1

SEQ ID NO 3:

LENGTH: 21
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APPLICANT: Mu, Leeying
APPLICANT: Wu, Leeying
TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
TITLE OF INVENTION: KINASE
FILE REFERENCE: AM101071
CURRENT APPLICATION NUMBER: US/10/702,496
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 60/429,381
PRIOR FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 306
SOFTWARE: Patentin version 3.2
SEQ ID NO 154
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Primer 31: 3'-primer (containing a Kpal site)
US-10-432-364-35
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US-10-702-496-154
; Sequence 154, Application US/10702496
; Publication No. US20040121383A1
; GENERAL INFORMATION:
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o. US20040121383A1
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                  20 CCATCCGGGGGGACCCCGAG 1
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ORGANISM: Homo sapiens
US-10-702-496-154
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APPLICANT: Liu, Wei
APPLICANT: Wu, Leeying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 161, Applic
Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Sequence 11538, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'TOOLE, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION: DISEASES
FILE REFERENCE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOGTWARR: Patentin version 3.2
SEQ ID NO 11538
LENGTH: 21
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Publication No. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: With

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES

FILE REFERENCE: 031896-023000 (AAA101331L)

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT PILING DATE: 2004-02-26

NUMBER: OF SEQ ID NOS: 21135

SOFTWARE: Patentin version 3.2

SEQ ID NO 12987

LENGTH: APPLICANT APP
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Sequence 17100, Application US/10786720

Sequence 17100, Application US/10786720

Publication No. US20040191818A1

GREATICANT: Wyeth

APPLICANT: Wyeth

APPLICANT: Liu, Weith

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT FILING DATE: 2004-02-26
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US-10-786-720-12987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: RNAi-antisense strand US-10-786-720-11538
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11203, Application US/10786720
Fublication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 11203
LENGTH: 21
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                                                                                                                                     Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.9e+02;
iive 0; Mismatches 3; Indels
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APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR:
TITLE OF INVENTION: DISEAGES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARES PATENTIN VERSION 3.2
LENGTH: 21
       ; FEATURE:
; OTHER INFORMATION: 5-base mismatched strand
US-10-728-491-9
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US-10-786-720-11219/c
; Sequence 11219, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2234 CAGCCCACCCTGCTGGT 2253
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                                                                                                                                                                                                                                                                               885 CAGTGTGTATGCAGGCATCC 904
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Best Local Similarity 85.0
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-786-720-11203
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Best Local Similarity
Matches 17; Conserv
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FEATURE:
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Weit
APPLICATION WUMBER: 18/10/786,720
CURRENT APPLICATION WUMBER: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 12255
LENGTH: 21
                                                                                                                               Sequence 17110, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Usu, Weth
APPLICANT: Liu, Weth
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 17110
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40.0%; Pred. No. 6.9e+02;
tive 9; Mismatches 3;
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Publication No. US20040191818A1
GENERAL INFORMATION:
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; Sequence 18288, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
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; ORGANISM: RNAi-antisense strand
US-10-786-720-18285
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Best Local Similarity 40.0°
Matches 8; Conservative
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US-10-786-720-17110
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Publication No. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: DOEBASES:

FILE REFERENCE: 031896-023000 (AM101331L)

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SOFTWARE: Patentin version 3.2

SEQ ID NO 17103
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Sequence 17106, Application US/10786720
Sublication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOGTWARE: Patentin version 3.2
SEQ ID NO 17106
LENGTH: 21
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40.0%; Pred. No. 6.9e+02;
tive 9; Mismatches 3; Indel8
                                                                                                                                                                                      Length 21;
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Pred. No. 6.9e+02;
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Best Local Similarity 40.0%; Pred. No. 6.9e
Matches 8; Conservative 9; Mismatches
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                                                                                                                                                                                                                                                                                                     TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-786-720-17100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA ORGANISM: RNAi-antisense strand
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; ORGANISM: RNAi-antisense strand
US-10-786-720-17106
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 17100
LENGTH: 21
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Best Local Similarity 40.0°
Matches 8; Conservative
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Sequence 16, Application US/0973533A
; Sequence 16, Application US/0973533A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
APPLICANT: Fillon, Mario
; APPLICANT: Fillon, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFREENCE: 02811-018
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT PILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 2000-08-29
; PRIOR FILING DATE: 2000-08-29
; RIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.2; DB 1; Length 38;
Pred. No. 1.2e+03;
0; Mismatches 13; Indels
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                                           Indels
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85.0%; Pred. No. 6.9e+02;
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100.0%; Pred. No. 5.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                      Sequence 10176, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Best Local Similarity 63.9%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
               Best Local Similarity 85.09
Matches 17; Conservative
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ORGANISM: Homo Bapiens
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Best Local Similarity
Matches 15; Conserv
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US-09-263-959-543/C
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US-10-786-720-18291
US-10-786-720-18291
Sequence 18291, Application US/10786720
Sublication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 18291
LENGTH: 21
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Pred. No. 6.9e+02;
9; Mismatches 3; Indels
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Pred. No. 6.9e+02;
9; Mismatches 3;
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US-10-786-720-18295/C

Sequence 18295, Application US/10786720

Publication No. US20040191818A1

GENERAL INFORMATION:
APPLICANT: Weth
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SEQ ID NO 18295
LENGTH: 21
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                           TITLE OF INVENTION: DISEASES FILE REFERENCE: 031896-023000 (AM101331L) CURRENT APPLICATION NUMBER: US/10/786,720 CURRENT FILING DATE: 2004-02-26 NUMBER OF SEQ ID NOS: 21135 SOFTWARE: Patentin version 3.2 SEQ ID NO 18288 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2325 GTGTGTGCGTGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                 2327 GTGTGTGTGTGTGTGTGT 2346
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| GUGUCUGCUUGUGUGUCUGU 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-786-720-18291
                                                                                                                                                                                                           TYPE: RNA · ORGANISM: RNAi-antisense strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%;
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Local Similarity 40.0%;
les 8; Conservative (
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Best Local Similarity 40.0
Matches 8; Conservative
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US-10-786-720-18295
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US-10-138-674-6070
US-10-138-674-6070
Sequence 6070, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Ravco, Pan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
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Sequence 222, Application World US/20030054371A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Wu, Paul
APPLICANT: Wu, Paul
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION WOMBER: US/10/085,906
CURRENT APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 69/534,061
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
PRIOR SEQ ID NOS: 545
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 222
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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. 5.1e+02;
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Pred. No. 5.1e+02;
                      NAME: MCMGatters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 545:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 5.1 Matches 15; Conservative 0; Mismatches
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Mismatches
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100.0%; Pre
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         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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Patent No. US20020150891A1
GENERAL INFORMATION
APPLICANT: Hood, Lerry E.
APPLICANT: Rowen, Lee
APPLICANT: KOOP, Ben P.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APENICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2823 TATATATACATATAT 2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEO ID NO: 543
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TATATATACATATAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
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US-09-263-959-545/c
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Sequence 8256, Application US/10138674

Publication No. US20040077565A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bloozyme Pharmaceuticals, Inc.
APPLICANT: Barcobed, Jam
APPLICANT: Broched, Jam
APPLICANT: Broched, Jame
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674

FURENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

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0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 53.3%; Pred. No. 5.9e+02;
Matches 8; Conservative 7; Mismatches 0; Indels
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                          Length 17;
                                                                                0; Indels
                          DB 1; Le
5.9e+02;
                       Query Match 0.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 5.5 Matches 15; Conservative 0; Mismatches
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                                                                                                                                               1197 GGGCAAGCCCCTTGG 1211
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US-10-287-949A-8256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-10-138-674-8256
                                                                                                                                                                                                                                                                                                                   US-10-138-674-8256
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Sequence 6070, Application US/10287949A

Publication No. US20040102389A1

Sequence 6070, Application US/10287949A

Publication No. US20040102389A1

APPLICANT: Rabozyme Pharmaceuticals, Inc.

APPLICANT: Raviggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinch
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US-10-238-700-3390/c

Sequence 3390, Application US/10238700

Sequence 3390, Application US/10238700

Publication No. US20030153521A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION NUCLEIC Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/057 (MEHBOL-1158-A)

CURRENT APPLICATION NUMBER: US/10/238,700

CURRENT APPLICATION NUMBER: US 60/318,471

PRIOR FILING DATE: 2001-05-10

NUMBER OF SEQ ID NOS: 4666

SOFTWARE: PatentIn version 3.0

SEQ ID NOS: 4666

SEQ ID NOS: 4666
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53.3%; Pred. No. 5.5e+02;
tive 7; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6070
LENGTH: 16
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1 GUGUGUGUGUGUGUG 15
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-238-700-3390
                                                                                                                                                                                TYPE: RNA
CORGANISM: Homo sapiens
US-10-138-674-6070
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Gaps
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Fublication No. US20030219772A1

GENERAL INFORMATION:

APPLICANT: KUJ v.d., Antoinette C.

APPLICANT: KUJ v.d., Antoinette C.

APPLICANT: Cornelissen, Marion

TITLE OF INTURNION Means and methods for treatment evaluation

FILE REPERENCE: P55190US10

CURRENT APPLICATION NUMBER: US/10/310,677

CURRENT PILING DATE: 2002-12-05

FRIOR APPLICATION NUMBER: EP 01200228.3

PRIOR PILING DATE: 2001-01-23

PRIOR FILING DATE: 2001-09-28

FRIOR PILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 45

LENGTH: 20
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TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION FILE REFERENCE: 5244US (REN/PS5190USOO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: TAG019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7e+02;
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US-10-310-677-45
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                          FILE REFERENCE: 5244US (REN/P55190USO)
CURRENT APPLICATION NUMBER: US/10/055,728
CURRENT FILING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: EP 0120373.2
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-01-3
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: modified base
; LOCATION: (1)..(5)
; OTHER INFORMATION: a stands for inosine
US-10-055-728-45
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Matches 15; Conservative
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                                              WENDUR 862
US-10-464-158-21/C
; Sequence 21, Application US/10464158
; Publication No. US20040009593A1
; GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
    APPLICANT: SIJON-64-18
    PRIOR PILING DATE: 2001-09-24
    PRIOR PILING DATE: 1999-61-6
    PRIOR PILING DATE: 1999-61-6
    PRIOR PILING DATE: 1998-12-03
    NUMBER: OF SEQ ID NOS: 48
    SEQ ID NO 21
    LENGTH: 18
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Publication No. US20040072769A1

GENERAL INFORMATION:

APPLICANT: Yin, James Q.

TITLE OF INVENTION: Methods for design and selection of short double-stranded

TITLE OF INVENTION: oligonucleotides, and compounds of gene drugs

TITLE OF INVENTION: oligonucleotides, and compounds of gene drugs

TITLE OF INVENTION: 01900ucleotides, and compounds of gene drugs

TITLE OF INVENTION: 01900ucleotides, and compounds of gene drugs

CURRENT APPLICATION NUMBER: US/10/016,490C

CURRENT FILING DATE: 2002-11-22

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 19
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100.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 0; Indels
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Sequence 45, Application US/10055728;
Publication No. US20030170720A1;
Publicant INFORWATION:
APPLICANT: van der Kuyl, Antoinette C.;
APPLICANT: Cornelissen, Marion
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Matches 15; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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CURRENT FILING DATE:
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APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
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                                ; Sequence 47, Application US/10380124; Sequence 47, Application US/10380124; Publication No. US20040053874A1; GENERAL INFORMATION:
; APPLICANT: Breis Pranaceuticals, Inc.; APPLICANT: Breis P. Monia; APPLICANT: Susan M. Freier; TILE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION; FILE REFERENCE: RTS-0156; CURRENT APPLICATION NUMBER: US/10/380,124; CURRENT FILING DATE: 2003-03-10; SEQ ID NO 47; LENGTH: 20
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APPLICANT: Taylor, Kent D.
APPLICANT: Rotter, Jerome I.
APPLICANT: Sugiamura, Kazuhito
APPLICANT: Sugiamura, Kazuhito
APPLICANT: Targan, Stephan
TITLE OF INVENTION: Methods of Using a NOD2/CARD 15
TITLE OF INVENTION: Haplotype to Diagnose Crohn's Disease
FILE REFERRNCE: P-CE 5451
CURRENT APPLICATION NUMBER: US/10/274,300
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 89
SOFTWARS: FastSEQ for Windows Version 4.0
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 7e+02;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-47
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Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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                         US-10-380-124-47
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Sequence 31, Application US/09971353
Sequence 31, Application US/09971353
Sequence 31, Application No. US20030113723A1
GENERAL INFORMATION:
AFPLICANT: BABL, Bharati
AFPLICANT: BOSE, Melanie Anne
TITLE OF INVENTION: METHOD FOR EVALUATING MICROSATELLITE INSTABILITY IN A TUMOR SAMPL!
FILE REFRENCE: 11757-54USU1
CURRENT APPLICATION NUMBER: US/09/971,353
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTING DATE: 3000-10-04
NUMBER OF SEQ ID NOS: 35
LENGTH: 38
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; Sequence 37, Application No. US2003165917A1
; Publication No. US2003165917A1
; GENERAL INFORMATION:
; APPLICANT: ULLMAN, EDWIN
; APPLICANT: ULLMAN, EDWIN
; APPLICANT: ULLMAN, EDWIN
; TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
; TILE REFERENCE: 3817.05-1
; CURRENT APPLICATION NUMBER: US/10/219,195
; CURRENT APPLICATION NUMBER: 60/312,505
; PRIOR PLING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PALENTIN Ver. 2.1
; SEQ ID NO 37
: LENGTH: 39
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78.3%; Pred. No. 1.2e+03;
iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                            DB 1;
7e+02;
                                                                                                                                                                                                                                                                                                          0.4%; Score 15; DB 100.0%; Pred. No. 7e+tive 0; Mismatches
                                                                                                                                                                                                           FEATURE:
COTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1491
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                 PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1491
LENGTH: 20
2003-09-25
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Best Local Similarity 100.03
Matches 15; Conservative
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Matches 18; Conservative
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ORGANISM: Homo sapiens
US-09-971-353-31
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Fublication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, EDWIN
APPLICANT: WU, MING
APPLICANT: LIU, YEN PING
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
CURRENT APPLICATION NUMBER: 60/312,505
FRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 33
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ULLMAN, EDWIN
APPLICANT: WI, WING
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REPERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: 0/312,505
PRIOR PILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE PACENTIN Ver. 2.1
IENGTH: 42
                                                                                                                                            Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: oligonucleotide US-10-219-195-37
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                                                                                        Query Match 0.4%; Score 15; DB 1; Length 39; Best Local Similarity 67.7%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3262 TATTTTATTTGCTTTGTCCTTTTTCAGGAGAATTAGATT 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3310 TITITCTTTAGGAGATTTATTTTTGGACTT 3340
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Publication No. US20030165917A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 61.5
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                             US-10-219-195-32
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0.4%; Score 15; DB 1; Length 42;

Query Match

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APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Lee
APPLICANT: ROSOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Publication No. US20040014036A1
GENERAL INFORMATION:
APPLICANT: Ptashne, et al.,
TITLE OF INVENTION: Therefor
FILE REPREMENCE: 04241-0065
CURRENT APPLICATION NUMBER: US/09/943,944E
CURRENT FLING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 119
LENGTH: 18
                           Gaps
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  Pred. No. 1.3e+03;
): Mismatches 15; Indels
                                                                          3262 TATITIATITICCTITICTCCTITITICAGGAGAATIAGAIT 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PREMP PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                          4 TITITITITITITITITITITITITITICACTGGTCATGGTTT
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NAMME: MCMARters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID No: 971:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        Sequence 911, Application US/09263959; Patent No. US20020150891A1; GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 24; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Seattle
STATE: Washington
COUNTRY: US
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Best Local Similarity
Matches 16; Conserv
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                             Gaps
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US-10-327-805-42
$$is Sequence 42, Application US/10327805
$$is Publication No. US20031014241A1$
$$is Publication No. US20031014241A1$
$$is Publication No. US20031014241A1$
$$is PPPLICANT: Brett P. Monia
$$is APPLICANT: Brett P. Cowsert
$$is TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6 EXPRESSION
$$is FILE REFERENCE: RTS-0045
$$is CURRENT FILING DATE: 2002-12-20
$$is FILING DATE: 2002-12-20
$$is FILING DATE: 2001-03-05
$$is NUMBER OF SEQ ID NOS: 47
$$is ENGRETIES TO NOS: 47
$$is ENGRETIES TO NOS: 47
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APPLICANT: Linnen, Jeffery M.
APPLICANT: Kolk, Daniel P.
APPLICANT: Cockter, Jamel M.
APPLICANT: Getman. Damon K.
APPLICANT: Getman. Damon K.
APPLICANT: String-Loy, Marcy, Marcy, APPLICANT: String-Lloy, Marcy, APPLICANT: String-Llow, MUMBER: 60,389,393
PRIOR APPLICATION NUMBER: 60,389,393
PRIOR PLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 18
                                                     FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Random
OTHER INFORMATION: nucleotide sequences.
US-09-943-944E-119
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                                                                                                                                                                                                 Query Match
0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-10-327-805-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 129, Application US/10461790
                                                                                                                                                                                                                                                                                                                     2698 CTTCCCACCTGCCCTC 2715
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                                                                                                                                                                                                                                                                                                                                                      1 CTCCCCACCATGCCCCTC 18
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                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20040029111A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA ORGANISM: Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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APPLICANT: MCSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Eacobe Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stindscomb, Dan
APPLICANT: Stindscomb, Dan
APPLICANT: Scobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re-
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHBOO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1449
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Riboryme Pharmaceuticals, Inc.
APPLICANT: Strinchcomb, Dan
APPLICANT: Strin
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels
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                                                                                                                                                                                  Query Match 0.4%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.7e+02; Matches 16; Conservative 0; Mismatches 2; Indels
; LOCATION: (1)...(18)
; OTHER INFORMATION: 2'-OMe nucleotide analogs
US-10-461-790-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1449, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-1449
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; ORGANISM: Mus musculus
US-10-138-674-3004
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APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 3004
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Sequence 22, Application US/09813289

Sequence 22, Application US/09813289

GENERAL INFORMATION:
APPLICANT: Mahadevan, M.S.
APPLICANT: Tiscornia, G

TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: UNMBER: US/09/813,289

CURRENT APPLICATION NUMBER: US 60/190,590

PRIOR APPLICATION NUMBER: US 60/190,590

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 118, Application US/08983605A
; Sequence 118, Application US/08983605A
; Publication No. USZ0020066118A1
; GENERAL INFORMATION:
; AFPLICART: ROGEr, MATION:
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: 1996-1040
; TITLE OF INVENTION UNMER: US/08/983,605A
; CURRENT APPLICATION NUMBER: US 1995-25 284.5
; EARLIER PILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 118
LENTIN: 19
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Pred. No. 7.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1678 GACTICGGGCTGGCCCGG 1695
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; ORGANISM: Triticum aestivum
US-08-983-605-118
                           McSwiggen, Jim
Stinchcomb, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.49
Best Local Similarity 72.23
Matches 13; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
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                                                                                                                                                                                                                                                             APPLICANT: Karin, Nathan
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS FOR TREATING RHEUMATOID
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS FOR TREATING RHEUMATOID
TITLE OF INVENTION OF 202/2310
CURRENT APPLICATION NUMBER: US/10/203,102A
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
LENGTH: 18
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.8; DB 1; Length 18;
Pred. No. 6.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Single strand DNA oligonucleotide US-10-203-102A-12
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                            ; Sequence 12, Application US/10203102A; Publication No. US20040086483A1; GENERAL INFORMATION:
1678 GACTTCGGGCTGGCCCGG 1695
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1 UNAACCUGCUGGGAGCCU 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 88.9
Matches 16, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-287-949A-1449
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LOCATION: (1). 7(19) CTHER INFORMATION: potential microsequencing oligo for 99-128-202.mis2 US-09-901-484A-546
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NAMEKEY: misc feature
LOCATION: 1..15
COTHER INFORMATION: potential microsequencing oligo for 99-148-129.misl US-09-853-526-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2;
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; Sequence 483, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
    APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1998-09-09
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PATENT. PM
; SEQ ID NO 483
; LEMENT. 198
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SSQF TWO SEQ ID NOS: 578
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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ORGANISM: Homo Sapiens
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CTHER INFORMATION: potential microsequencing oligo for 99-148-129.misl US-09-901-484A-483
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                                                                                                                                                                                                                                             0.4%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 7.16+02; tive 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                              ; FEATURE:
; OTHER INFORMATION: A mutated DMPK 3'UTR fragment
US-09-813-289-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 483, Application US/09901484A; Sequence 483, Application US/09901484A; Patent No. US20020119460A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfedd, Marta
APPLICANT: Bugueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
TITLE OF INVENTION: ENGLOSOPO 191,484A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR APPLICATION NUMBER: US 09/996,58
PRIOR PRILING DATE: 1998-09-09
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/318,207
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/318,207
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/318,307
PRIOR APPLICATION NUMBER: US 09/318,207
PRIOR APPLICATION NUMBER: US 09/318,207
PRIOR APPLICATION NUMBER: US 09/33,526
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US-09-901-484A-546
; Sequence 546, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumenfeld, Marta
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T111XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
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                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
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               SEQ ID NO 22
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Length 19; Indels ö

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Length 19;

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, OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense {
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US-10-251-117-180

US-10-251-117-180

Sequence 180, Application US/10251117

Publication No. US20030170891A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: NGSWIGHOUS Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REPERENCE: 900/042 (MBHB02-466-A)

CURRENT APPLICATION NUMBER: US 60/393,924

PRIOR PLILNG DATE: 2002-06-06

PRIOR PLILNG DATE: 2002-06-06

PRIOR PLILNG DATE: 2002-06-06

PRIOR PLILNG DATE: 2001-07-25

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR PLILNG DATE: 2001-07-25

SEQ ID NO 180

SEQ ID NO 180

LENGTH: 19

TVDR: DATE

TVDR
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0.4%; Score 14.8; DB 1;
Best Local Similarity 72.2%; Pred. No. 7.1e+02;
Matches 13; Conservative 3; Mismatches 2;
2323 GTGTGTGTGTGCGTGTGT 2340
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ORGANISM: Artificial Sequence
PEATURE:
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; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 99-128-202.mis2
US-09-853-526-546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48, Application US/09766450
; Sequence 48, Application US/09766450
; Publication No. US20030022166A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Colin
; APPLICANT: Gray, Joe W.
; APPLICANT: Pinkel, Daniel
; APPLICANT: Pinkel, Daniel
; APPLICANT: Pinkel, Daniel
; APPLICANT: Pinkel, Daniel
; APPLICANT: Pinkel, Colin G.
; TITLE OF INVENTION: Repeat-Free Probes for Molecular
; TITLE OF INVENTION: Cytogenetics
; TILE REPREMENCE: 02307-111800US
; CURRENT APPLICATION NUMBER: US/09/766,450
; UNDRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FREESEQ for Windows Version 3.0
; ELENGTH: 19
                                                          Sequence 546, Application US/09853526
; Sequence 546, Application US/09853526
; Patent No. US20020163345A1
; GENERAL INFORMATION:
APPLICANT: CONDEN, Daniel
; APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
; TITLE OF INVERTION: PROSTATE CANCER GENE
; TITLE OF INVERTION: PROSTATE
CURRENT APPLICATION NUMBER: 09/9853,526
; CURRENT APPLICATION NUMBER: 09/338,907
PRIOR FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1998-00-09
; PRIOR FILING DATE: 1998-00-09
; PRIOR FILING DATE: 1998-12-22
NUMBER: OF SEQ ID NOS: 578
; SEQ ID NO 546
; LENGTH: 19
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; OTHER INFORMATION: primer 768.348.rl
US-09-766-450-48
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ORGANISM: Homo Sapiens
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GREERAL INFOWARTION:

GREERAL INFOWARTION:

APPLICANT: Ribosyme Pharmaceutical, Inc.

APPLICANT: Morrisesy, David

APPLICANT: Morrisesy, David

APPLICANT: Morrisesy, David

APPLICANT: Morrisesy, David

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION WHERE: US/10/244,647

CURRENT APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-03-26

PRIOR PILING DATE: 2002-03-26

PRIOR PILING DATE: 2002-03-26

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524

SOFTWARE: Patentin version 3.0

SEQ ID NO 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sinA sense r US-10-244-647-515
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
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44.4%; Pred. No. 7.1e+02;
tive 8; Mismatches 2; Indels
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Ubblication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morstissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
PRIOR APPLICATION NUMBER: US 09/916,466
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Publication No. US20030206887A1
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1 UUCCUCUUCAUCCUGCUG 18
                                  PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 429
LENGTH: 19
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ORGANISM: Artificial Sequence
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Best Local Similarity 44.45
Matches 8; Conservative
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Best Local Similarity 88.99
Matches 16; Conservative
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor in TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MRHB02-468-A)
CURRENT APPLICATION NUMBER: US/10/251,117
PRIOR PILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-00
                                     ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-180
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US-10-251-117-317
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                                                                                                                                                                                     Length 19;
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Pred. No. 7.1e+02;
3; Mismatches 2; Indels
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Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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: Sequence 429, Application US/10251117

: Publication No. US20030170891A1

: GENERAL INFORMATION:
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Best Local Similarity 72.2%;
Matches 13; Conservative
       ORGANISM: Artificial Sequence
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US-10-251-117-317/c
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LENGTH: 19
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TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
TITLE OF INVENTION: Short Interfering Nucleic Acid (sina)
FILE REFREENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-244-647-1161
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Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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TITLE OF INVENTION: Screening method
FILE REFERENCE: P02-0058PCT
CURRENT APPLICATION NUMBER: US/10/477,726
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 2001-145411
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 135
LENGTH: 19
                                                                                      CURKENT FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-07-05

PRIOR PILING DATE: 2002-03-26

PRIOR PILING DATE: 2002-06-08

NUMBER OF SEQ ID NOS: 1524

SOFTWARE: Patentin version 3.0

SEQ ID NO 1161
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Publication No. US20040138163A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 133, Application US/10477726
; Publication No. US20040110231A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 16; Conserv
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US-10-665-951-2244
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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-665-951-2244
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APPLICANT: Sirra Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leconid
APPLICANT: Bealsquan, Leconid
APPLICANT: Bayes, Pamela
TITLE OF INVENTION: Rowth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Growth Factor using Short Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/131 (MBHB02-742-P)
CURRENT APPLICATION NUMBER: US 10/664,668
PRIOR APPLICATION NUMBER: US 10/664,668
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-05-29
Gene Expression Using Short Interfering Nucleic Acid (siNA)
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PRIOR FILING DATE: 2003-09-18

PRIOR PILING DATE: 2003-09-18

PRIOR PILING DATE: 2003-02-18

PRIOR PILING DATE: 2003-02-20

PRIOR PILING DATE: 2003-02-02

PRIOR APPLICATION NUMBER: US 60/393,796

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-11-04

PRIOR PILING DATE: 2002-11-04

PRIOR PILING DATE: 2002-11-27

PRIOR PILING DATE: 2002-11-27

PRIOR PILING DATE: 2002-11-27

PRIOR PILING DATE: 2002-05-29

PRIOR PILING DATE: 2002-05-39

PRIOR PILING DATE: 2002-05-39

PRIOR PILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30
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                                              FILE REFERENCE: 400/131 (MBHB02-742-F)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
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Publication No. US20040138163A1
GENERAL INFORMATION:
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SEQ ID NO 2244
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Best Local Similarity
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Sequence 34, Application US/09454394

Sequence 34, Application US/09454394

Patent No. US20020034525A1

GENERAL INFORMATION:
APPLICANT: Tina McIntosh
APPLICANT: Steven Head
APPLICANT: Philip Goelet
TITLE OF INVENTION: Mcthods for the Detection of Multiple
TITLE OF INVENTION: Mchods for the Detection of Multiple
TITLE OF INVENTION: Mchods for the Detection of Multiple
TITLE REFERENCE: 04990.0029
CURRENT APPLICATION NUMBER: US/09/454,394
CURRENT FILING DATE: 1999-12-03
EARLIER FILING DATE: 1999-12-03
EARLIER FILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FateSEQ for Windows Version 3.0

SEQ ID NO 34
LENDITH: 20
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APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Michael T. Boyce-Jacino
APPLICANT: Michael T. Boyce-Jacino
APPLICANT: Michael T. Boyce-Jacino
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Michael Toleonide Polymorphisms in a Single Reaction
FILE REPERENCE: 04990.0029
CURRENT PILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 08/216,538
EARLIER FILING DATE: 1994-03-23
EARLIER FILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                   Indels
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Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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Pred. No. 7.5e+02;
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EARLIER APPLICATION NUMBER: 08/145,145
EARLIER FILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 20
TYPE: DNA
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; Equus caballus
; ORGANISM: Equus caballus
US-09-454-394-34
                                                                                                                                                                                       , ORGANISM: Equus caballus
US-09-454-394-33
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US-10-665-951-2265
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Patent No. US20020094525A1
GENERAL INFORMATION:

BAPLICANT: Steven Head
APPLICANT: Philip Goelet
APPLICANT: Michael T. Boyce-Jacino
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Mothods for the Detection of Multiple
FILE REFERENCE: 04990,0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/383,124
PRIOR PLING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR PLING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 2265
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 14.8; DB 1; Length 19; 72.2%; Pred. No. 7.1e+02;
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GENERAL INFORMATION:
APPLICANT: Itch, No. US20020082205Aluyuki
APPLICANT: Itch, No. US20020082205Aluyuki
APPLICANT: Kavanaugh, W. Michael
ITILE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-17150.001/201130.40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
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CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 08/216,538
BARLIER FILING DATE: 1994-03-23
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Patent No. US20020082205A1
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                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.2
Matches 13; Conservative
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US-09-801-968-5/c
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STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNATION:
NAME: COTUZZI, LAURA REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                         FILING DATE: 07-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seed and Berry LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 24. SEQUENCE CHARACTERISTICS.
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  CURRENT APPLICATION
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APPLICANT: Philip Goelet
APPLICANT: Philip Goelet
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Single Nucleotide Polymorphisms in a Single Reaction
FILE REFERENCE: 04990.0029
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Patent No. US20020142441A1
GENERAL INPORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                            0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02;
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88.9%; Pred. No. 7.5e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                        0; Mismatches
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CURRENT FILING DARE: 1999-12-03
EARLIER PILING DATE: 1994-03-23
EARLIER FILING DATE: 1994-03-23
EARLIER PILING DATE: 1994-03-23
EARLIER PILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NOS 36
LENGTH: 20
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ZIP: 10036-271
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/09454394
Patent No. US20020094525A1
GENERAL INFORMATION:
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 16; Conservative
                                                              ; TYPE: DNA
; ORGANISM: Equus caballus
US-09-454-394-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Equus caballus
                                                                                                                                            Query Match
Best Local Similarity
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SOFTWARE: Fa
SEQ ID NO 35
LENGTH: 20
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
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                                                                                                                           APPLICATION NUMBER: 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/386,844
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: Other SEQUENCE DESCRIPTION: SEQ ID NO: 24:
FILING DATE: 04-MAR-1998
APPLICATION UNMBER: 08/870,434
FILING DATE: 06-UTN-1997
APPLICATION NUMBER: 08/799,910
                                                                          FILING DATE: 13-FEB-1997
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
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ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-996-263-11
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 88.9%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Seguence
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APPLICANT: MCKAY, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nonia, Brett
APPLICANT: Brett
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS;
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS;
FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR PILING DATE: 1998-08-07
PRIOR PILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
LENGTH: 20
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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REPERENCE NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1214:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
FENGTH: 20 base pairs
TYPE: nucleic acid
US-09-263-959-1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Synthetic Sequence US-09-774-809-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/09774809
Publication No. US20030004120A1
GENERAL INFORMATION:
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Publication No. US20030004120A1
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                                                                                                                                                                                                                                                                                                                                                                                                                           3377 TTGCTGTGTCTCCAGGC 3394
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-774-809-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 906
US-09-774-809-42
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APPLICANT:
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APPLICANT: Phillip Dan Cook
Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325Alris
STREET: One Liberty Place - 46th Floor
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/996,263

FILING DATE: 28-NO. US20030004325A1-2001

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/471,973

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: 08/471,973

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
                   FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,609
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09
PRIOR FILING DATE: 1998-08
PRIOR FILING DATE: 1998-08
PRIOR FILING DATE: 1998-08
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 42
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Sequence US-09-774-809-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09996263
Publication No. US20030004325A1
GENERAL INFORMATION:
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1678 GACTICGGGCTGGCCCGG 1695
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STRANDEDNESS: single
TOPOLOGY: linear
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3 GGTGTGTGCATGTGT 20
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US-09-776-479-311/c
                                                                                                                                                                                                                                                                                                                              US-09-776-479-311/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Settlicant: WARDLAND, WARD

APPLICANT: WARDSTRADT, AND

TITLE OF INVENTION: IN INMUNE TOLERANCE

TITLE OF INVENTION: IN INMUNE TOLERANCE

TITLE OF INVENTION: UN UNMER: US/09/860,836B

CURRENT APPLICATION NUMBER: US/09/860,836B

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 36
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US-09-888-326-463/c

S-09-888-326-463/c

S-09-888-326-463/c

S-09-888-326-463/c

S-09-888-326-463/c

S-09-888-326-463/c

S-09-888-326

0.4%; Score 14.8; DB 1; Length 20; llarity 88.9%; Pred. No. 7.5e+02; Conservative 0; Mismatches 2; Indels
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|||||||| |||||||| 20 CTGCCAGGGGAGGAG 3
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Homo sapien
US-09-860-836B-36
Query Match
Best Local Similarity
Matches 16; Conserv
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Sequence 311, Application US/09776479
; Bublication No. US20030087848A1
; GENERAL INFORMATION:
    APPLICANT: Bratzler, Robert L.
    APPLICANT: Petersen, Deanna M.
    APPLICANT: Pouron, Yves
    TILLE OF INVENTION: Immunostimulatory Nucleic Acids for the
    TILLE OF INVENTION: 10037/7013 (HCL/MAT)
    CURRENT APPLICATION NUMBER: US/09/776,479
    CURRENT FILING DATE: 2000-02-03
    NUMBER OF SEQ ID NOS: 1093
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 311
    LENGTH: 20
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APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TYTLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: 1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Sequence US-09-776-479-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 311, Application US/09776479; Publication No. US20040067902A9; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GACTITGGCCTGGCCCGG
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Best Local Similarity 88.9
Matches 16; Conservative
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RESULT 912

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND THEIR USE IN GENETIC ANALYSIS
                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURSOT PAPLICATION DATA:

APPLICATION NUMBER: US/09/846,863

FILING DATE: 01-May-2001

CLASSIFICATION: -UNknown>

FRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/216,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                  Score 14.8; DB 1;
Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
SIREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 683-104-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-846-863-33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMUNICATION:
TELEPHONE: (202) 383-7451
TELEFAR: (202) 383-6610
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                   ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Sense PCR primer
US-09-802-154-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Equus caballus
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-846-863-33; Sequence 33, Application US/09846863; Publication No. US20030170624A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GOBLET, PHILIP
KNAPP, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                    825 CICTGCGTGGCTGGTGGT 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C. COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
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                                 SEQ ID NO 5
LENGTH: 20
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
ENGTH: 20
          SQUARENT APPLICATION OF HORMONE-SENSITIVE LIPASE EXPRESSION CURRENT APPLICATION NOUNDERS. 230 CURRENT EXPLICANT: Madeline M. Butler APPLICANT: Andrew T. Watt APPLICANT: Andrew T. Watt APPLICANT: Susan M. Freier APPLICANT: Susan M. Sensin M. Sensin
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llarity 88.9%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 0.4%; Score 14.8; DB 1; Length 20; Local Similarity 88.9%; Pred. No. 7.5e+02; hes 16; Conservative 0; Mismatches 2; Indels
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Publication No. US2003010530241
GENERAL INFORMATION:
APPLICANT: Itoh. No. US20030105302Aluyuki
APPLICANT: Kavanaugh, W. Michael
TITLE OF INVENTION: HUMAN FOF-23 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-17149.001/201130.409
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Antisense Oligonucleotide US-09-915-814-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97, Application US/09953318
Publication No. US20030105036A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 16; Conserv
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Sequence 36, APPLICATION US/09846863
PUBLICATION NO. US20030170624A1
GENERAL INFORMATION:
JAMAPP GOELET, PHILIP
TITLE OF INVENTION: SINGLE NUCLECTIDE POLYMORPHISMS AND THEIR USE IN GENETIC ANALYSIS
KONAPP, MICHAEL R.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND
THEIR USE IN GENETIC ANALYSIS
                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/09/846,863
FILING DATE: CURROWN-
PRIOR APPLICATION NUMBER: 08/216,538
FILING DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:
NAME: AUBERBACH, UFFREY I
REGISTRATION NUMBER: 32,680
TELEFRATION NUMBER: 32,680
TELEFRATION INFORMATION:
TELEFRANCE (202) 383-7451
TELEFRAX: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20,
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88.9%; Pred. No: 7.5e+02;
tive 0; Mismatches 2;
                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-846-863-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                      SEQUENCES: 95
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                                                                                                                                                           CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                                      NUMBER OF
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                                                                                                                                                                              Sequence 34, Application US/09846863
Publication No. US20030170624A1
GENERAL INFORMATION:
APPLICANT: GOBLET, PHILIP
TITLE OF INVENTION: SINGLE NUCLECTIDE POLYMORPHISMS AND
TITLE OF INVENTION: THEIR USE IN GENETIC ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TEACHER FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/846,863
FILING DATE: 01-May-2001
CLASSIFICATION NUMBER: 08/216,538
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/216,538
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: AUBRBACH, JEFFREY I
REGISTRATION NUMBER: 5890
REGISTRATION NUMBER: 683-104-CIP
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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US-09-846-863-35/c
; Sequence 35, Application US/09846863
; Publication No. US20030170624A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Equus caballus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2335 GTGTGTGTGTGTGTGC 2352
                        2826 ATATACATATATATAT 2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 383-6610 INFORMATION FOR SEQ ID NO: 34:
                                                3 ATATCAATATATATAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C. COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20004
                                                                                                                                                             US-09-846-863-34
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Gaps

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APPLICANT: Monia, Brett P.
IITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
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; Publication No. US2003060268A1
; Garbera Information:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES
; TITLE OF INTENTION: TESTATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT APPLICATION NUMBER: US 60/279,642
; RIOR SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 20
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2;
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; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301
                                                                                                                                                                                                                                                                                                                                                                      THIE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/057,550
CURRENT PILLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/506,073
PRIOR PILLING DATE: 2000-02-18
PRIOR PILLING DATE: 1998-08-28
PRIOR PILLING DATE: 1998-07-06
PRIOR PILLING DATE: 1998-07-06
PRIOR PILLING DATE: 1998-07-06
PRIOR PILLING DATE: 1998-07-06
PRIOR PILLING DATE: 1998-07-07
PRIOR PILLING DATE: 1996-07-07
PRIOR PILLING DATE: 1996-07-07
PRIOR PILLING DATE: 1996-07-07
PRIOR PILLING DATE: 1996-07-11-26
PRIOR PILLING DATE: 1996-07-11-26
PRIOR PILLING DATE: 1996-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: antisense sequence
                                                                                                                                                                    Sequence 27, Application US/10057550 Publication No. US20030032607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1678 GACTTCGGGCTGGCCCGG 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: artificial sequence
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Best Local Similarity 88.99
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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Sequence 101, Application US/10004551

Publication No. US20030004310A1

GENERAL INFORMATUON:

APPLICANT: SHIMKETS, RICHARD A

APPLICANT: FERNANDES, ELWA

TITLE OF INVENTION POLINUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

FILE REFERENCE: 15966-559

CURRENT APPLICATION NUMBER: US/10/004,551

CURRENT APPLICATION NUMBER: 09/635,949

PRIOR RILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 101

LENGTH:: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION TUMBER: US/99/846,863
FILING DATE: 01-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATE: ADMINISE: 08/216,538
FILING DATE: «Unknown»
ATPLICATION NUMBER: 08/216,538
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: AUBERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPRAT: (2021) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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Pred. No. 7.5e+02;
0; Mismatches 2;
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US-09-846-863-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Equus caballus
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2826 ATATACATATATATAT 2843
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LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 36:
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Best Local Similarity 88.9%;
Matches 16; Conservative
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION FILE REFERENCE: RISP-0363
                                        CURRENT APPLICATION NUMBER: US/10/181,846
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: PCT/US01/01416
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/490,692
PRIOR PILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/10173225B Publication No. US20030119769A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10238042
Publication No. US20030115618A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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US-10-238-042-20
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Publication No. US20030082602A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vamenco, No. US20030082602A1uko
APPLICANT: Suzuki, Tomohiro
APPLICANT: Suzuki, Tomohiro
TITLE OF INVERTION: Method for analyzing base sequence of nucleic acid
FILE REFERENCE: 03500.015203
CURRENT APPLICATION NUMBER: US/10/231,302
CURRENT FILING DATE: 2002-08-30
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                                                                                                                           Sequence 311, Application US/10017995
Publication No. US20030055014A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FESTESEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
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PRIOR FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Sequence US-10-017-995-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/10181846
Publication No. US20030083297A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1678 GACTTCGGGCTGGCCCGG 1695
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                          20 cacrirideccridecede
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
LENGTH: 20
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Best Local Similarity 88.9
Matches 16, Conservative
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Matches 16, Conservative
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US-10-231-302-72
                                                                                                                    US-10-017-995-311/c
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US-10-181-846-32/c
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APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
TITLE TO INVENTION INVERSE: US/10/173,225B
CURRENT PILING DATE: 2002-12-06
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 1998-08-28
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                                                                      0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; Live 0; Mismatches 2; Indel8
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Pred. No. 7.5e+02;
) OTHER INFORMATION: AntiBense Oligonucleotide US-10-181-846-32
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APPLICANT: Maga, Elizabeth A.
APPLICANT: Maga, Elizabeth A.
APPLICANT: Anderson, Gary B.
TOTLE OF INVENTION: METHOD OF GENERATING A THILE OF INVENTION: LIVESTOCK ANIMAL.
TITLE OF INVENTION: LIVESTOCK ANIMAL.
TITLE REFERENCE: UCAL.245
CURRENT FILING DATE: 2002-09-06
PRIOR PLING DATE: 2002-09-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 20
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; OTHER INFORMATION: PCR and DNA sequencing primer for exon 7 antisense US-10-321-555-10
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APPLICANT: Chuataleng Song
APPLICANT: Pamposh Ganju
APPLICANT: Pamposh Ganju
TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: VANILLOID RECEPTORS
FILE REPERENCE: 4-32048A
CURRENT APPLICATION NUMBER: US/10/171,319
CURRENT FILING DATE: 2002-0/297,835
PRIOR APPLICATION NUMBER: 60/397,835
PRIOR APPLICATION NUMBER: 60/351,238
PRIOR APPLICATION NUMBER: 60/352,914
PRIOR APPLICATION NUMBER: 60/352,914
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 20
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                  PRIOR FILING DATE: 1999-02-10
PRIOR PLING DATE: 1998-07-03
PRIOR PLING DATE: 1998-07-03
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 15
SOPTWARE: PATENTIN VETSION 3.1
APPLICATION NUMBER: GB 9903035.5
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Publication No. US20030157633A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Andrea Peier
APPLICANT: Peter McIntyre
APPLICANT: Stuart Bevan
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Publication No. US20030125276A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: C. Frank Bennet
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXF
TILE REPERENCE: RTS-031333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 21
LENGTH: 20
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Publication No. US20030134315A1
GENERAL INFORMATION:
APPLICANT: Waterenius, Hilmar Meek
APPLICANT: Waterenius, Hilmar Meek
APPLICANT: Beabra, Laurence Anthony
TITLE OF INVENTION: EXPRESSION OF DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED UF
TITLE OF INVENTION: EXPRESSION OF NEGATIVE AND POSITIVE SIGNAL TRANSDUCTION FACTORS
FILE REFERENCE: 1417-188
CURRENT APPLICATION NUMBER: US/09/622,277
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: PCT/GB99/00500
PRIOR FILING DATE: 1999-02-18
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-21
                PRIOR APPLICATION NUMBER: US 08/888,982
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-07-07
PRIOR PRILING DATE: 1996-11-26
PRIOR APPLICATION NUMBER: US 08/756,806
PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR PILING DATE: 1995-05-31
PRIOR PILING DATE: 1994-05-31
NUMBER OF SEQ ID NOS: 109
SEQ ID NO 26
LENGTH: 20
APPLICATION NUMBER: PCT/US98/13961
                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: antisense sequence
US-10-173-2258-26
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ORGANISM: artificial sequence
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Best Local Similarity 88.93
Matches 16; Conservative
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US-10-008-789-21/c
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                       Length 20;
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Pred. No. 7.5e+02;
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                 Indels
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| Publication No. US20030187240A1
| GENERAL INFORMATION:
| APPLICANT: Cook, Phillip Dan
| APPLICANT: Kawasaki, Andrew
| TITLE OF INVENTION: 2. Modified Oligonucleotides
| TITLE REFERENCE: 15155137
| CURRENT APPLICATION NUMBER: US/10/352,586
| CURRENT PILING DATE: 2003-01-28
| PRIOR APPLICATION NUMBER: 09/389,283
| PRIOR APPLICATION NUMBER: 09/389,283
| PRIOR APPLICATION NUMBER: 09/389,283
| STORFILING DATE: 1999-09-02
| NUMBER OF SEQ ID NOS: 37
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 11
| LENGTH: 20
                     Score 14.8; DB 1;
Pred. No. 7.5e+02;
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                     Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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; ORGANISM: Candida albicans
US-10-032-585-4779
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US-10-352-586-11/c
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GENERAL INFORMATION:
APPLICAMY: B.I. du Pont de Nemours and Company
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT PILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/297198
PRIOR APPLICATION NUMBER: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: MICROSOft Office 07
SEQ ID NO 32
LENGTH: 20
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APPLICANT: STUAT BECET MCINTYTE
APPLICANT: STUAT BEVAN
APPLICANT: CLUANZHERG SONG
APPLICANT: CLUANZHERG SONG
APPLICANT: CLUANZHERG SONG
APPLICANT: CNANILLOID RECEPTOR-RELATED NUCLBIC ACIDS
TITLE OF INVENTION: AND POLYFEFTIDES
FILE REFERENCE: 4-32048A
CURRENT PILING DATE: 2002-10-24
PRIOR PELING DATE: 2002-01-05-31
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR PELICATION NUMBER: 60/351, 314
PRIOR FILING DATE: 2002-01-29
PRIOR PELICATION NUMBER: 60/351, 161
PRIOR PLING DATE: 2002-02-12
PRIOR PLING DATE: 2002-02-12
PRIOR PLING DATE: 2002-02-12
PRIOR PLING DATE: 2002-05-15
PRIOR PLING DATE: 2002-05-15
PRIOR PLING DATE: 2002-05-15
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 114
SOPTWARE: FABELSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 73
LENGTH: 20
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                                                                                  US-10-171-319-73/c
; Sequence 73, Application US/10171319
; Publication No. US20030157633A1
; GENERAL INFORMATION:
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2 GGAGGACGAAGGTGAGGA 19
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US-10-167-547C-32
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ORGANISM: Artificial Sequence
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US-10-167-547C-32
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES
FILE REPERBENCE: RTS-0365
CURRENT APPLICATION WIMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
SEQ ID NOS: 134
SEQ ID NO 74
LENGTH: 20
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Publication No. US20030232443A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett

APPLICANT: C. Frank Bennett

TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION
FILE REPRENCE: HTS-0022

CURRENT APPLICATION NUMBER: US/10/176,277

CURRENT FILING DATE: 2002-06-18

NUMBER OF SEQ ID NOS: 77

LENGTH: 20
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Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 0.4%; Score 14.8; DB 1; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-176-277-17
                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide US-10-159-856-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 232, Application US/10094886 Publication No. US20040002120A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1262 AGGACCGGCCGCCAAGC 1279
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Taupier, Raymond J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Aggacregecagecaage 18
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Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 AráscraAsasarcac 2
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Boldog, Ferenc
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Susan M. Freier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li, Li
Gorman, Linda
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  Sequence 97, Application US/10446373

Faquence 97, Application US/10446373

Faquence 97, Application No. US20030204076A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: RTS-023

CURRENT APPLICATION NUMBER: US/10/446,373

CURRENT APPLICATION NUMBER: US/09/953,318

PRIOR FILING DATE: 2001-09-13

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 97

LENGTH: 20
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 311, Application US/10314578
Fublication No. US20030212026A1
GENERAL INPORMATION:
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US 60/156,113
FRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
SPRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
SPRIOR FILING DATE: 1999-09-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Sequence US-10-314-578-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-159-856-74/c, sequence 74, Application US/10159856; Publication No. US20030228689A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1352 TGCAGATGATGAGATGA 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1678 GACTTCGGGCTGGCCCGG 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conserv
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US-10-314-578-311/c
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                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: upstream amplification primer 99-8614 for SEQ 3898.
US-10-349-143-7832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                        PRIOR FILING DATE: BARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: BARLIER FILING DATE: 1998-11-23
PRIOR PILING DATE: BARLIER APPLICATION NUMBER: US 60/082,614
PRIOR PILING DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7832
  US 09/298,850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10407449

Publication No. US20040005601A1

GENERAL INFORMATION:
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Bearse, David
ITILE OF INVENTION: WETHODS FOR TARGETING QUADRUPLEX DNA
FILE REPERENCE: 53223-20004.00
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/404,966
PRIOR PLING DATE: 2002-08-04
PRIOR PLING DATE: 2002-08-04
PRIOR PLING DATE: 2002-04-05
PRIOR PLING DATE: 2003-04-05
PRIOR PLING DATE: 2003-04-05
PRIOR PLING DATE: 2003-04-05
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.8; DB 1;
Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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APPLICANT: Hurley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Grand, Cory
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%;
Best Local Similarity 88.9%;
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer_bind
LOCATION: 1..20
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhong, Mei, THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD CURRENT APPLICATION NUMBER: US/10/094,886

CURRENT FILING DATE: 2002-03-07
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105-10-349-143-7832, Application US/10349143

1 Publ.cation No. US20040005584A1

1 FUBLICATION TO US2004MATCH

1 APPLICANT: Cohen, Daniel

2 APPLICANT: Blumenfeld, Marta

3 APPLICANT: Chumakov, Ilya

3 TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

3 CURRENT APPLICATION NUMBER: US/10/349,143

3 CURRENT FILING DATE: 2003-01-21

3 FRIOR APPLICATION NUMBER: US/09/422,978

5 PRIOR PILING DATE: 1999-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PRINCATION NUMBER: 60/274,322
PRIOR PELING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR APPLICATION NUMBER: 60/28,052
PRIOR PELING DATE: 2001-05-02
PRIOR PELING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PELICATION NUMBER: 60/274,281
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
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                                                                                                                                                                                                                                     Fernandes, Elma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                                                                               Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
Pochart, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                       Pena, Carol
Gangolli, Esha
Gusev, Vladimir
Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 88.9
Matches 16; Conservative
                              Stacie
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LENGTH: 20
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Sequence 56, Application US/10210429
Publication No. US20040023379A1
Publication No. US20040023379A1
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION FILE REFERENCE: PTS-0048
CURRENT APPLICATION NUMBER: US/10/210,429
CURRENT PILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 56
LENGTH: 20
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US-10-210-429-127/c
US-10-210-429-127/c
US-10-210-429-127/c
US-10-210-429-127/c
Publication No. US20040023379Al
GENERAL INFORMATION:
APPLICANT: C Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION
TITLE OF INVENTION: UNDIRER: US/10/210,429
CURRENT APPLICATION UNDHER: US/10/210,429
CURRENT FILING DATE: 2002-07-31
SEQ ID NOS: 148
SEQ ID NO 127
LENGTH: 20
  ic sequence and polypeptides, fragments in particular for the diagnosis, prever
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                                                                                                                                                                                                                                                                                                            Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-429-56
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          743 TTCTCTCCTTGCACACG 760
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                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6513
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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ORGANISM: H. sapiens
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Matches 16; Conserv
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US-10-210-429-127
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Sequence 21, Application US/10422466

Sequence 21, Application US/10422466

Sequence 21, Application US/0606036A1

GENERAL INFORMATION:

APPLICANT: HU, Ji-Fan

APPLICANT: Bowersox, Scott

TITLE OF INVENTION: Silencing transcription by methylation

FILE REPERCES 112029.00005

CURRENT APPLICATION NUMBER: US/10/422,466

CURRENT FILING DATE: 2003-04-22

PRIOR FILING DATE: 2000-08-12

PRIOR APPLICATION NUMBER: 60/196,749

PRIOR APPLICATION NUMBER: 60/194,148

PRIOR APPLICATION NUMBER: 60/14,148

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 77

SEQ ID NO 21

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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            TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
                                                                                                   PRIOR APPLICATION NUMBER: US 60/404,966
PRIOR FILING DATE: 2002-08-04
PRIOR PILING DATE: 2002-08-04
PRIOR PILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: Unknown
PRIOR PILING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 20
                                    FILE REFERENCE: 53223-20004.00
CURRENT APPLICATION NUMBER: US/10/407,449
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2527 CAGGGAGCTGGGCCCGAC 2544
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-289-762-6513/c
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Best Local S
Matches 16
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APPLICANT: MCKAY, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULA
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULA
TITLE OF INVENTION: OF DAY PROTEINS
FILE REFERENCE: ISPH-0726
CURRENT FAPLICATION NUMBER: US/10/345,444B
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/774,809
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 09/287,796
PRIOR PILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
FILE REPERRNCE: P75-0028
CURRENT APPLICATION NUMBER: US/10/210,723
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 86
LENGTH: 20
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88.9%; Pred. No. 7.5e+02;
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Pred. No. 7.5e+02;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/210,723
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/10345444B Publication No. US20040029823A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-210-723-86/c
; Sequence 86, Application US/10210723
; Publication No. US20040023382A1
; GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 88.9°
Matches 16; Conservative
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Best Local Similarity 88.99
Matches 16; Conservative
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US-10-210-479-50/C

Squence 50, Application US/10210479

Fublication No. US20040023380A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION

TITLE OF INVENTION NUMBER: US/10/210,479

CURRENT APPLICATION NUMBER: US/10/210,479

WUMBER OF SEQ ID NOS: 123

SEQ ID NO 50

LENGTH: 20
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Publication No. US20040023380A1
Publication No. US20040023380A1
Publication No. US20040023380A1
APPLICANT: Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
FILE REPERENCE: RTS-0385
CURRENT APPLICATION NUMBER: US/10/210,479
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 123
SEQ ID NO 112
LENGTH: 20
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APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
FILE REFERENCE: PTS-0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; Live 0; Mismatches 2; Indels
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-479-50
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Publication No. US20040023382A1
GENERAL INFORMATION:
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                                                                     GCCTCTTCCTCTTCATCC 1
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9'
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ORGANISM: H. sapiens
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APPLICANT: Shimkets, Richard A
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 2402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
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PRIOR FILING DATE: 2000-03-30

PRIOR FILING DATE: 2000-03-30

PRIOR PELING DATE: 2000-03-30

PRIOR PELING DATE: 2000-08-10

PRIOR PELING DATE: 2000-08-10

PRIOR PELING DATE: 2000-08-10

PRIOR PELING DATE: 2000-08-10

PRIOR PELING DATE: 2000-08-12

PRIOR PELING DATE: 2000-09-12

PRIOR PELING DATE: 2000-09-14

PRIOR PELING DATE: 2000-09-17

PRIOR PELING DATE: 2000-09-17

PRIOR PELING DATE: 2000-09-07

PRIOR PELING DATE: 2000-09-09-07

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US09/540,763
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; Publication No. US20040067490A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1495 GGCCTGGACTACTCCTTC 1512
                                                                                                                                                                                                                                                                                                     Kekuda, Ramesh
LaRochelle, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adigaru, Muralidhara
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Reiger, Daniel K
Rothenberg, Mark E
Shenoy, Suresh
                                                                                                             Ellerman, Karen
Gerlach, Valerie
Gorman, Linda
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                      MacDougall, John R
Malyankar, Uriel M
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liet, Isabelle
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Pena, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peyman, John A
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US-10-236-392-402
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Publication No. US20040029823A1

GENERAL INFORMATION:

APPLICANT: MCKAY, Robert A.

APPLICANT: Dean, Nicholas M.

APPLICANT: Moria, Brett

APPLICANTON NUMBER: US/10/345,448

CURRENT APPLICANTON NUMBER: US 09/774,809

PRIOR APPLICANTON NUMBER: US 09/396,902

PRIOR FILING DATE: 1999-00-15

PRIOR APPLICANTON NUMBER: US 09/397,796

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR FILING DATE: 1999-00-07

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR FILING DATE: 1999-00-07

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR FILING DATE: 1999-00-07

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR FILING DATE: 1999-00-07

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR FILING DATE: 1999-00-07

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616

PRIOR APPLICANTON NUMBER: US 09/130,616
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: US 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 31
LENGTH: 20
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Publication No. US20040067490A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Gargess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic Sequence US-10-345-4448-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Sequence
US-10-345-444B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1678 GACTICGGGCTGGCCCGG 1695
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ORGANISM: Artificial Sequence
                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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Sequence 21, Application US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Renneth W. Dobie
APPLICANT: Sanjay Bhanot
TITLE OF INVENTION: ANTIESENSE MODULATION OF PATTY ACID SYNTHASE EXPRESSION
FILE REPERENCE: ISBH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 225
SEQ ID NO 21
LENGTH: 20
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Sensen W. Dobie
APPLICANT: Senseth W. Dobie
APPLICANT: Sensity Bhanot
TITLE OF INVANTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION FILE REPRENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 225
SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                               FEATURE:
, OTHER INFORMATION: Antisense Oligonucleotide
US-10-274-085-21
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Best Local Similarity 88.5
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICANT: Peyman, John A
ICANT: Reiger, Danniel K
ICANT: Reiger, Danniel K
ICANT: Rothenberg, Mark B
ICANT: Shenoy, Suresh
ICANT: Shinkets, Richard A
ICANT: Smirkets, Richard A
ICANT: Smithson, Glennda
B OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
REFERENCE: 21402-442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-12
PRIOR PILING DATE: 2000-09-12
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR PILING DATE: 2001-09-07
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Custom
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Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R FILING DATE: 2000-03-30
R PILING DATE: 2000-03-30
R APPLICATION NUMBER: US60/390,155
R FILING DATE: 2000-08-10
R APPLICATION NUMBER: US99/635,949
R FILING DATE: 2000-08-10
R APPLICATION NUMBER: US60/318,765
R FILING DATE: 2001-09-12
R APPLICATION NUMBER: US60/357,303
R RILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US60/367,753
FILING DATE: 2002-03-25
APPLICATION NUMBER: US60/369,479
FILING DATE: 2002-04-02
APPLICATION NUMBER: US09/659,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NT FILING DATE: 2002-09-06
APPLICATION NUMBER: US09/540,763
                                                                                                                                                                                                                                                       JaRochelle, William J
                                                                                                                                                                                                                                                                                                                                                                                           Padigaru, Muralidhara
Patturajan, Meera
Pena, Carol A
                                                                                                                                                                                                                                                                                              MacDougall, John R
Malyankar, Uriel M
Miller, Charles E
Millet, Isabelle
                              Catterton, Elina
Chapoval, Andrei
Crabtree, Julie
Edinger, Shlomit, R
Ellerman, Karen
Gerlach, Valerie
Gorman, Linda
Grosse, William M
Gusse, Vladamir
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Best Local Similarity 88.9%;
Matches 16; Conservative
         Casman, Stacie J
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Indels

Length 20;

RESUL: >> CUG-653-872-24

i Sequence 24, Application US/10653872

j Publication No. US20040081992A1

j GENERAL INFORMATION:

i APPLICANT: Falb, Dean

i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
STREET: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americae

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2; Indels

1495 GGCCTGGACTACTCCTTC 1512

GGCCTGGACTGCTTCTTC 20

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Length 20;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                               Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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Sequence 47, Application US/10303325
Publication No. US20040102395A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett;
APPLICANT: C. Frank Bennett;
APPLICANT: REPERENCE: TRS-0434
FILE REPERENCE: TRS-0434
CURRENT APPLICATION NUMBER: US/10/303,325
CURRENT FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 156
LENGTH: 20
                                                                                                                                                                                                                                                                                                      RESULT 958
US-10-302-027-105

Sequence 105, Application US/10302027

Publication No. US20040102391A1

GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean

TILLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION

FILE REFERENCE: PTS-0068

CURRENT FILING DATE: 2002-11-21

CURRENT FILING DATE: 2002-11-21

SEQ ID NO 105

LENGTH: 20
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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 960
US-10-688-706-153
; Sequence 153, Application US/10688706
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                                                                                                                                                                                   1447 GCGGCCAAGGGTAACCTG 1464
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Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-302-027-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Sequence 45, Application US/1030207;
Publication No. US20040102391A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: MODILATION OF GANKYRIN EXPRESSION
FILE REFERENCE: PTS-0068
CURRENT APPLICATION NUMBER: US/10/302,027
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 45
LENGTH: 20
                                                                COMPUTER: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MBDIUM TYPE: Diskette
COMPUTER: TBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FREASEQ Version 2.0
SPELICATION NUMBER: US/10/653,872
FRILING DATE: 03-58P-2003
FRILING DATE: 03-58P-2001
APPLICATION NUMBER: US/09/924,417
APPLICATION NUMBER: US/09/924,417
APPLICATION NUMBER: US/09/924,417
APPLICATION NUMBER: US/09/934,86
FILING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/870,434
FILING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/870,434
FILING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/89,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/89,573
FILING DATE: 09-FEB-1995
APPLICATION NUMBER: 08/89,573
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 08/89,573
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 08/386,844
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 03/36,573
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 30,742
REBERRENCE/DOCKET NUMBER: 30,742
MANE: COCUZZÍ, LAULRA
MANE: COCUZZÍ, LAULRA
MENESTANCE/DOCKET NUMBER: 30,742
MENESTANCE/DOCKET NUMBER: 30,742
MENESTANCE NUMBER: 30,742
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MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-653-872-24
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LENGTH: 20 base pairs
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 24:
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ORGANISM: Artificial Sequence
         CITY: New York
STATE: NY
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Squence 828, Application US/10688706

Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Broschat, Kay

TILE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

FILE REFERENCE: 01393/110/688,706

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT APPLICATION NUMBER: 60/419,268

PRIOR PILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: Patentin version 3.2

LENGTH: 20
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| Bublication No. US20040102412A1
| GENERAL INPORMATION:
| APPLICANT: Broschat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
| FILE REFERENCE: 01393/1
| CURRENT APPLICATION NUMBER: US/10/688,706
| CURRENT APPLICATION NUMBER: 60/419,268
| PRIOR PILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 3071
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     Ouery Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                OTHER INFORMATION: human GFAT antisense US-10-688-706-507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-508
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PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: PatentIn version 3.2
SEQ ID NO 507
LENGTH: 20
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Matches 16; Conservative
                                                                                                                            TYPE: DNA ORGANISM: artificial
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US-10-688-706-828
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| Sequence 285, Application US/10688706
| Publication No. US20040102412A1
| GENERAL INFORMATION:
| APPLICANT: Pharmacia Corp.
| APPLICANT: Broschat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
| FILE REFERENCE: 01393/1
| CURRENT APPLICATION NUMBER: US/10/688,706
| CURRENT PILING DATE: 2003-10-17
| PRIOR PILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 3071-17
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 285
| LENGTH: 20
                    GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Bracechat, Kay
TITLE OF INVENTION:
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR PILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 153
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay.
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION FILE REFERENCE: 01393/1
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CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: human GFAT antisense US-10-688-706-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: human GFAT antisense US-10-688-706-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3237 TAGTIGGAGGIGATICCA 3254
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     Publication No. US20040102412A1
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ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; tive 0; Mismatches 2; Indels
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                           Sequence 96, Application US/10316243
; Publication No. US20040110147A1
; Fublication No. US20040110147A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF BAF53 EXPRESSION
; FILE REFERENCE: RTS-0462
; CURRENT APPLICATION NUMBER: US/10/316,243
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 168
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-31-20-0
US-10-31-67/c
US-10-31-67/c
Sequence 167, Application US/10316243
Fublication No. US20040110147A1
GENERAL INFORMATION:
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF BAF53 EXPRESSION
FILE REFERENCE: RTS-046.2
CURRENT APPLICATION NUMBER: US/10/316,243
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 167
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-10-316-243-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/10660897; Publication No. US20040115706A1; GENERAL INFORMATION:
                                                                                                                   1473 TCTGCGGCGCGGCGCC 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3067 TCCCACACCCCAACACTT 3084
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                             Conservative
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ORGANISM: H. sapiens
                                      Query Match
Best Local Similarity
Matches 16; Conserv
US-10-688-706-828
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US-10-316-243-96
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US-10-303-588-42

US-10-303-588-42

Sequence 42, Application US/10303588

Publication No. US20040116364A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: MODULATION OF DEATH-ASSOCIATED PROTEIN KINASE 1 EXPRESSION
TITLE REFERENCE: HTS-0071

CURRENT APPLICATION NUMBER: US/10/303,588

CURRENT FILING DATE: 2002-11-22

NUMBER OF SEQ ID NOS: 78

SEQ ID NO 42

LENGTH: 20
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| Sequence 42, Application US/10303588 |
| Publication No. US20040116364A1 |
| Publication No. US20040116364A1 |
| GENERAL INFORMATION: |
| APPLICANT: Kenneth W. Dobie |
| TITLE OF INVENTION: MODULATION OF DEATH-ASSOCIATED PROTEIN KINASE 1 EXPRESSION |
| FILE REPERENCE: HTS-0071 |
| CURRENT APPLICATION NUMBER: US/10/303,588 |
| CURRENT PILING DATE: 2002-11-22 |
| SEQ ID NOS: 78 |
| LENGTH: 20 |
APPLICANT: Chung, Mary
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Whitten, John Siddiqui-Jain, Adam
APPLICANT: Farrell, Thomas
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
TITLE OF INVENTION: QUADRULEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
FILE REFERENCE: 532232000800
CURRENT FILING DATE: 2003-09-11
PRIOR PLILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: quadruplex forming sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Antisense Oligonucleotide US-10-303-588-42
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Sequence 1039, Application Us/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTIERNSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
                                                                                                                          US-010-316-540-18
Sequence 18, Application US/10316540
Sequence 18, Application US/10316540
Publication No. US20040126761A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
FILE REPERENCE: RYS-0471
CURRENT APPLICATION NUMBER: US/10/316,540
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 18
LENGTH: 20
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Publication No. US20040126761A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
FILE REFERENCE: RTS-0471
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Pred. No. 7.5e+02;
0; Mismatches 2;
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88.9%; Pred. No. 7.5e+02;
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  921 CTTCTTCCTGTTCATCCT 938
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Best Local Similarity 88.9%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                            Length 20;
                                                                                                         Query Match 0.4%; Score 14.8; DB 1; Length 2
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/763,992
FILING DATE: 22-Jan.2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5697.US.P1
TELECOMMUNICATION INFORMATION:
                         ; FEATURE:
- OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-588-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/418,887
FILING DATE: 15-0CT-1999
PILING DATE: 08-0CT-1997
FILING DATE: 08-0Ct-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-763-992-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 1L
                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/10763992
Publication No. US20040121397A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTS-RAPP, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COHEN, Maurice
FRIEDMAN, Paula N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GORDON, Julian
HODGES, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLASS, Michael R.
KRATOCHVIL, Jon D.
                                                                                                                                                                                                   2824 ATATATACATATATAT 2841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RUSSELL, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Best Local Similarity 88.9
Matches 16; Conservative
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US-10-763-992-21
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Gequence 1366, Application US/10671395
; Publication No. US20040132063A1
; Publication No. US20040132063A1
; Gentence 1366, Application Corp.
; Gentence 1366, Application Corp.
; APPLICANT: Diarracia Corp.
; APPLICANT: Gieree, James Modulation OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERRNCE: 1179/L/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR PILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SEQ ID NO 1366
; LENGTH: 20
                                                                                                                                                                                  Gaps
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                                                                                                                                 Query Match
0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1343
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ORGANISM: artificial
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## Sequence 1219, Application US/10671395

## Sequence 1219, Application US/10671395

## Sequence 1219, Application No. US20040132063A1

## SPELICANT: Pharmacia Corp.

## APPLICANT: Diamacia Corp.

## TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

## TITLE OF INVENTION: EXPRESSION

## TITLE OF INVENTION: EXPRESSION

## FILE REFERENCE: 1179/1/19 DATE: 2003-09-25

## CURRENT FILING DATE: 2003-09-25

## RIOR FILING DATE: 2002-09-25

## NUMBER OF SEQ ID NOS: 1809

## SOFTWARE: PatentIn version 3.2

## SOFTWARE: PatentIn version 3.2

## SOFTWARE: 2003-09-26

## SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-671-395-1106/c
; Sequence 1106, Application US/10671395
; Sequence 1106, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Giere, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1106
LENGTH: 20
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                           ; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1039
  CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION UNMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1039
LENGTH: 20
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Best Local Similarity 88.9 Matches 16; Conservative
                                                                                                                                                             TYPE: DNA
ORGANISM: artificial
FEATURE:
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ORGANISM: artificial
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US-10-671-395-1219/c
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APPLICANT: Hiromiten, TAKASE

APPLICANT: Hiromiten, TAKASE

APPLICANT: Hiromiten, TAKASE

APPLICANT: Hiromiten, TAKASE

APPLICANT: Hiromiten, METHOD OTO

TITLE OF INVENTION: METHOD ON MACS SPECTROMETRY

TITLE OF INVENTION: ION MACS SPECTROMETRY

FILE REFRENCE: CF017354US

CURRENT PAPLICATION NUMBER: US/10/744,730

CURRENT PILING DATE: 2003-12-23

PRIOR APPLICATION NUMBER: JP 2002-19010

PRIOR APPLICATION NUMBER: JP 2002-191391

PRIOR PILING DATE: 2002-66-28

PRIOR PRILING DATE: 2002-66-28

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PARCHIN VERSION 3.2

SEQ ID NO 5

LENGTH: 20
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Fatent No. US20020037508A1
GENERAL INPORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REPRENCE: 2255.2008-001
CURRENT FILING DATE: 2001-01-18
FRIOR APPLICATION NUMBER: US 60/176,861
FRIOR APPLICATION NUMBER: US 60/176,861
FRIOR PELLIKG DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 461
SOFTWARE: PRESECT for Windows Version 4.0
SEC ID NO 37
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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Local Similarity 88.9%; Pred. No. 7.5e+02;
les 16; Conservative 0; Migmatcher
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Pred. No. 7.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
FEATURE:
CTHER INFORMATION: Sequence for Target
US-10-744-730-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 266, Application US/09765081
                                                               Sequence 5, Application US/10744730
Publication No. US20040137491A1
GENERAL INFORMATION:
APPLICANT: Tadashi, OKAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2695 CCACTTCCCACCTGCCC 2712
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Matches 16, Conservative
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US-09-765-081-266/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Matches
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APPLICANT: Pharmacia Corp.
APPLICANT: Glerse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1728
LENGTH: 20
                                                                                                                                                                                                                                                                                               APPLICANT: Glerse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILLING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1597
LENGTH: 20
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; tive 0; Mismatches 2; Indels
                        2; Indels
  Pred. No. 7.5e+02;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Human PGE2 antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Human PGE2 antisense
                                                                                                                                                                                                                  sequence 1597, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION: APPLICANT: Pharmacia Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1728, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION:
                                                                 2315 GTCTGTGTGTGTGTGT 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2336 TGTGTGTGTGTGTGCA 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2316 TCTGTGTGTGTGTGTG 2333
                                                                                                        20 Grandrdrdrdrdrdr 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
  Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: artificial
                                                                                                                                                                            RESULT 978
US-10-671-395-1597/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-671-395-1728/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                        셤
                                                                    ઠે
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OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101-1688
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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US-09-864-426A-1134
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Publication No. US20030032788A1

GENERAL INFORMATION:

APPLICANT: GARVER, Eric

APPLICANT: ISRAEL, Yedy

TITLE OF INVENTION:

TITLE OF INVENTION NUMBER: US/09/932,300

CURRENT FILING DATE: 2001-08-20

CURRENT FILING DATE: 1997-07-03

PRIOR APPLICATION NUMBER: US 09/109,663

PRIOR FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 111

SOFTWARE PARENTING US: 111

SOFTWARE PARENTING US: 2011

SOFTWARE PARENTING US: 211

SOFTWARE PARENTING US: 211

SOFTWARE PARENTING US: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Candidate; OTHER INFORMATION: TNF(alpha) ASO
US-09-932-300-43
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Pred. No. 7.9e+02;
1; Mismatches 3; Indels
               GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2008-001
CURRENT APPLICATION NUMBER: US 60/1765,081
CURRENT PILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 461
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 21
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88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1134, Application US/09864636A Publication No. US20030104378A1 GREERAL INFORMATION:
APPLICANT: Third wave Technologies APPLICANT: Allwai, Watim APPLICANT: Bartholomay, Christian APPLICANT: Chehak, LuAnne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2082 GIACTCCCGGGTGGCCAGG 2101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 GICCIGCCCRGGAGGCCAGG 1
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Best Local Similarity 80.0%;
Matches 16; Conservative 1
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Best Local Similarity 88.99
Matches 16; Conservative
Patent No. US20020037508A1
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-765-081-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 984
US-09-864-636A-1134
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                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 6, Application US/10016505
Publication No. US20020086324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Peter W. Laird, Cindy A. Eads and Kathleen D. Danenberg
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT DNA METHYLATION
ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: May Wu Po
APPLICANT: May Wu Po
APPLICANT: May Wu Po
APPLICANT: Saiser, Michael
TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
FILE REFRENCE: FORS-04946
CURRENT APPLICATION NUMBER: US/09/864,426A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1134
ILENGTH: 21
                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 7.9e+02;
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Pred. No. 7.9e+02;
0; Mismatches 2;
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CORRESPONDENCE ADDRESS:
ADDRESSE: Davis Wright Tremaine LLP
STREET: 1501 Fourth Avenue
2600 Century Square
TITLE OF INVENTION: Detection of RNA Sequences FILE REFERENCE: FORS-04944
CURRENT APPLICATION NUMBER: US/09/864,636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1134
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1134, Application US/09864426A Publication No. US20040018489A1 GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2276 GACTCAGTGCAGATGGAG 2293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAATCAGTGAAGATGGAG 18
                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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APPLICANT: Kavanagh, T.
APPLICANT: Lao, N.
TITLE OF INVENTION: A NOVEL PLASTID-TARGETING NUCLBIC ACID SEQUENCE, A
TITLE OF INVENTION: A NOVEL BETA-AMYLASE SEQUENCE, A STIMULUS-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 14.8; DB 1; Length 21;
88.9%; Pred. No. 7.9e+02;
tive: 0; Mismatches 2; Indels
                                                                                                                                                                                    TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: D.S.1.7

COMPUTER READABLE FORM:
MEDIUM TYPE: FUCKHY
COMPUTER: DOEA

COMPUTER: DE COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: MICROSOFT WORD VERSION 2.0C
CURSOFTWARE: MICROSOFT WORD VERSION 2.0C
CURSOFT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      DU PONT DE NEMOURS
                                                                  Sequence 46, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT:
COMPANY
COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 46:
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LOCATION: 1..21
OTHER INFORMATION: /prc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835-20
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1353 GGAGATGATGAAGATGAT 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                 PLANTS
                                                                                                                                                                                                                                                                                                                                                            AND COMPANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GGAGAAGATGAAGAAGAT 1
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 107
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                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9<sup>§</sup>
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                              JS-10-023-066A-46/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-023-066A-46
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Publication No. US20030054371A1

FUBLICANT: Ying, Vincent

APPLICANT: Ying, Vincent

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

ITILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: UNMERR: US/10/085,906

CURRENT APPLICATION NUMBER: US 09/126,215

PRIOR FILING DATE: 1099-03-25

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 490

LENGTH: 21

LENGTH: 21

LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.8; DB 1; Length 21;
88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2; Indels
MEDIUM TYPE: Diskette-3.5 inch, 1.44 MB storage COMPUTER: PC compatible OPERATING SYCOMM Windows 95 SOFTWARE: Word 97
                                                                          SOFTWAKE: WOLD 9.7

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/016,505
FILING DATE: 10-Dec-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/311,912
FILING DATE: May 14, 1999
ATTORNEY/AGENT INFORMATION:
NAME: BATTY L. Davison
REGISTRATION NUMBER: 47,309
REFERENCE/DOCKET NUMBER: 47675-9
TELEPRONE (206) 628-7621
TELEPRONE: (206) 628-769
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FELCHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-505-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGGAGTTGGTGGAGGGTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
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US-10-085-906-490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-085-906-490/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Gaps

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APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
                                                                                                                                Gaps
         ; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide US-10-311-946-21
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                                                                                       Length 21;
                                                                                                                                Indels
                                                                                     Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vedvík, Kevín L.
TITLE OF INVENTION: RNA Detection Assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Allawi, Hatim
Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
                                                                                                                                                                                                                                                                                                                                        Sequence 1134, Application US/10084839 Publication No. US20030186238A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neri, Bruce P.
Olson, Sarah M.
Olson-Munoz, Marilyn C.
Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
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                                                                                                                                                                               2700 TCCCACCCTGCCCTCAG 2717
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Third Wave Technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymaicheva, Natalie E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
FEG ID NO 1134
                                                                                                                                                                                                                   3 TCCCACCCGCACCTCAG 20
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Lukowiak, Andrew A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-10-084-839-1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyamichev, Victor
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Best Local Similarity
Matches 16; Conserv
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US-10-452-510-204
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
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Publication No. US20030109481A1

GENERAL INFORMATION:

APPLICANT: Anne Isabelle Gallani, Georges Imbert, Wilhelm Krek

TITLE OF INVENTION: Tumour-Cell Specific Gene Expression and its Use in Cancer Therap

FILE REFERENCE: 1-3152021/FM1

CURRENT APPLICATION NUMBER: US/10/311,946

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.1
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| Sequence 49, Application US/10090011
| Publication No. US2030082810A1
| Publication No. US2030082810A1
| GENERAL INFORMATION:
| APPLICANT: Serup, Palle
| APPLICANT: Gradwohl Gerard
| TITLE OF INVENTION: Methods For Generating Insulin-Secreting
| TITLE OF INVENTION: Cells Suitable for Transplantation
| FILE REFERENCE: 6246-2200-US
| CURRENT APPLICATION NUMBER: US/10/090,011
| CURRENT FILING DATE: 2002-02-26
| PRIOR FILING DATE: 2001-02-26
| PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-261-189-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 1; Length 21; Pred. No. 7.9e+02; 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
  PROMOTER AND USES THEREOF
                FILE REFERENCE: 9341-017
CURRENT APPLICATION NUMBER: US/10/261,189
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US/09/375,140
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5.5
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapien
US-10-090-011-49
  TITLE OF INVENTION:
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LENGTH: 21
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US-10-648-593-311/c
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TITLE OF INVENTION: REGULATION OF HUMAN ADENYLATE CYCLASE, TYPE IV
FILL REFERENCE: RCK-6 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/398,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 135, Application US/10401520
| Publication No. US20040009506A1
| GENERAL INFORMATION:
| APPLICANT: Stephen, Jean-Philippe F. APPLICANT: Tsai, Siao Ping
| APPLICANT: Wong, Wai Lee Tan
| APPLICANT: Wong, Wai Lee Tan
| APPLICANT: Wong, Wai Lee Tan
| APPLICANT: Bileci, Todd
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| FILE REFERENCE: P1806R1US
| CURRENT APPLICATION NUMBER: US 60/368,669
| PRIOR APPLICATION NUMBER: US 60/368,669
| NUMBER OF SEQ ID NOS: 138
| LENGTH: 21
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larity 88.9%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 2; Indels
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FILE REFERENCE: 760050-93
CURRENT APPLICATION NUMBER: US/10/452,510
CURRENT FILING DATE: 2003-06-02
FRIOR APPLICATION NUMBER: US 09/526,193
PRIOR PILING DATE: 2000-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-06-08
PRIOR PILING DATE: 1999-06-08
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 287
SOFTWARE: FASTEREQ for Windows Version 4.0
SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Synthetic primer US-10-401-520-135
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Publication No. US20040029247A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens US-10-452-510-204
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Best Local Similarity
Matches 16; Conserv
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Sequence 311, Application US/10648593

Publication No. US20040106132A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

TITLE OF PROTEIN TYROSINE TYROSINE KINASE PATHWAYS IN BREAST CELLS

TITLE OF UNDENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

CURRENT APPLICATION NUMBER: US/10/648,593

CURRENT FILING DATE: 2003-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gequence 204, Application US/10617334

gequence 204, Application US/10617334

publication No. US20040058869A1

GENERAL INFORMATION:

APPLICANT: HAYGHAR MISCAN Michael R.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS

FILE REPRERENCE: 760050-91

CURRENT PILLING DATE: 2003-07-10

PRIOR PELLING DATE: 2003-07-10

PRIOR PELLING DATE: 1999-03-15

PRIOR PELLING DATE: 1999-03-15

PRIOR PILLING DATE: 1999-06-08

PRIOR FILLING DATE: 1999-06-17

PRIOR PELLING DATE: 1999-09-01

MUMBER OF SEQ ID NOS: 287

LENGTHARE: PALENTIN 3.0

SEQ ID NO 204
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88.9%; Pred. No. 7.9e+02;
vative 0; Mismatches 2; Indels
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Pred. No. 7.9e+02;
0; Mismatches 2;
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 60/24:
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
LENGTH: 21
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature

CTHER INFORMATĪON: Primer: AC4-L1

US-10-398-757-3
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
US-10-617-334-204
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Best Local Similarity
Matches 16; Conserv
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US-10-665-951-2275

Publication No. US20040138163A1

Publication No. US20040138163A1

GENERAL INFORMATION:

APPLICANT: Siran Therapeutics, Inc.

APPLICANT: Beigelman, beoind

APPLICANT: Pavoo. Pamela

ITILE OF INVENTION: Area Interference Mediated Inhibition of Vascular Endothelial

TITLE OF INVENTION: Growth Factor and Vascular Endothelial

FRIOR PAPELCATION WUMBER: US 60/399,348

PRIOR PILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-07-29

PRIOR PILING DATE: 2002-07-39

PRIOR APPLICATION WUMBER: US 60/383,124

PRIOR PILING DATE: 2002-03-11

PRIOR PILING DATE: 2002-03-1
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.8; DB 1; Length 21;
Pred. No. 7.9e+02;
0; Mismatches 2; Indel8
                               PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 09/526,193
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 256
SOFTWARE: Word for Windows Version 6.0 (ASCII Text)
LENGTH: 21
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      PRIOR APPLICATION NUMBER: US 60/151,977
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: homo sapien
US-10-745-377-118
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APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN

TITLE OF INVENTION: KINASE

FILE REFERENCE: AM101071

CURRENT APPLICATION NUMBER: US/10/702,496

CURRENT FILING DATE: 2003-11-07

PRIOR APPLICATION NUMBER: 60/429,381

PRIOR APPLICATION NUMBER: 60/429,381

NUMBER OF SEQ ID NOS: 306

SOFTWARE: Patentin version 3.2

LENGTH: 21

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APPLICANT: Hayden, Michael R.
APPLICANT: Hayden, Michael R.
APPLICANT: Hayden, Simon
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Dimetone, Simon
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Clee, Susanne M.
ITILE OF INVENTION: Compositions and Methods for Modulating
TITLE OF INVENTION: HDL Cholesterol and Triglyceride Levels
ITILE OF INVENTION: HDL Cholesterol and Triglyceride Levels
FILE REFERENCE: 76050-109
FILE REFERENCE: 2003-12-23
PRIOR APPLICATION NUMBER: 09/654,323
PRIOR APPLICATION NUMBER: US 60/124,702
PRIOR PILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-06-08
PRIOR PILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                       Score 14.8; DB 1; Length 21;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: Patentin version 3.2
SEQ ID NO 311
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2316 TCTGTGTGTGTGTGTG 2333
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Conservative
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Best Local Similarity 88.9°
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-311
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Best Local Similarity
Matches 16; Conserva
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McSwiggen, James
Beigelman, Leonid
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Sequence 2278, Application US/10665951
Sequence 2278, Application US/10665951
Sequence 2278, Application Wo. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Belgelman, Leonid
APPLICANT: Ravoingen, James
APPLICANT: McSwiggen, James
APPLICANT: Pavoo, Pamela
TITLE OF INVENTION: Townth Peator and Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REPRENKE: 400/131 (WHBMER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-20
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR PAPLICATION NUMBER: US 60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR PAPLICATION NUMBER: US 60/393,796
PRIOR PAPLICATION NUMBER: US 60/393,124
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-06-06
PRIOR PRIOR PRIOR PRIOR DATE: 2002-06-06
PRIOR PRIOR PLING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR PRIOR PLING DATE: 2002-06-06
PRIOR PRIOR PLING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR PRIOR PLANES PARCHIN Version 3.2
PRIOR FILING DATE: 2002-06-06
PRIOR PRI
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ch 0.4%; Score 14.8; DB 1; Length 21; I Similarity 72.2%; Pred. No. 7.9e+02; 13; Conservative 3; Mismatches 2; Indels
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// LOCATION: (20)...(21)

OTHER INFORMATION: n stands for thymidine

US-10-665-951-2278
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i. Sequence 2374, Application US/10665951
i. Publication No. US20040138163A1
j. GENERAL INFORMATION:
                                                                                                                                                  1953 CATGCGGGAGTGCTGGCA 1970
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ORGANISM: Artificial Sequence
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       Query Match
Best Local
                                            Best Loca
Matches
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88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                Sequence 245, Application US/10627253A Publication No. US20040161768A1 GENERAL INFORMATION: APPLICANT: BRINKWANN, ULRICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2791 TACATTTCTATAAATAGA 2808
                                                                           497 ACACGCTGGACGTGCTGG 514
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Best Local Similarity 88.9%;
Matches 16; Conservative
  Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                      RESULT 1005
US-10-627-253A-245/c
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APPLICANT: Hayden, Michael R.
APPLICANT: Hayden, Michael R.
APPLICANT: Pimestone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
TILE REFERENCE: 76050-92
CURRENT APPLICATION NUMBER: US/10/744,465
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US/617,334
PRIOR APPLICATION NUMBER: US/9/526,193
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UTHER INFORMATION: Description of Artificial Sequence: sink antisense region
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Pred. No. 7.9e+02;
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                       PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR PILING DATE: 2002-07-03
PRIOR PELLING DATE: 2002-11-04
PRIOR PELLING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: US 10/306,747
PRIOR PILING DATE: 2002-11-27
PRIOR PILING DATE: 2002-05-29
PRIOR PELLING DATE: 2002-02-0
PRIOR PELLING DATE: 2002-02-0
PRIOR PELLING DATE: 2002-02-0
PRIOR PELLING DATE: 2002-03-11
PRIOR PELLING DATE: 2002-03-11
PRIOR PELLING DATE: 2002-03-11
PRIOR PELLING DATE: 2002-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // NAME/KEY: misc_feature
// LOCATION: (20)_.(21)
// OTHER INFORMATION: n stands for thymidine
US-10-665-951-2386
                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2455 SOFTWARE: PatentIn version 3.2
     US 60/399,348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-10-744-465-204
Sequence 204, Application US/10744465
Sublication No. US20040157250A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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0.4%; Score 14.8; DB 1; Length 21;

Query Match

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APPLICANT: DALANCHANN, ULALCHANGE SVEN.

APPLICANT: HOFPMEYER, SVEN.

APPLICANT: HOFPMEYER, SVEN.

APPLICANT: MORNHINWEG, ESTHER

TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS.

FILE REFERENCE: VOS-42 CON

CURRENT APPLICATION NUMBER: US/10/627,253A

CURRENT APPLICATION NUMBER: PCT/EP02/00796

PRIOR FILING DATE: 2003-01-25

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 406

SOCITION NOWER: POSITION NOWER: POSITION NOWER: PRIOR FILING DATE: 2010-01-26

NUMBER OF SEQ ID NOS: 406

SEQ ID NO 246

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HOFFMETER, SUEN
APPLICANT: HOFFMETER, SUEN
APPLICANT: HOFFMETER, SUEN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (WRP-1) AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
FILE REFERENCE: VOS-42 CON
CURRENT APPLICATION NUMBER: PO10/627,253A
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: PO1101651.6
PRIOR APPLICATION NUMBER: EP 01101651.6
PRIOR PELING DATE: 2002-01-25
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOCTHARP: PATENTI VETSION 3.2
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA COGNISM: Artificial Sequence PRATURE: ORGANISM: AFTURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-245
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      Indels
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Pred. No. 7.9e+02;
0; Mismatches 2;
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US-10-786-720-3818/c
US-10-786-720-3818/c
Sequence 3818, Application US/10786720
Publication No. US20040191818A1
Sequence 3818, Application No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Usu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
TITLE REFERENCE: 031896-023000 (AMIO1331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SEQ ID NO 3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-786-720-3819
Sequence 3819, Application US/10786720
Sequence 3819, Application US/10786720
Sequence 3819, Application US/10786720
Sequence 3819, Application US/10786720
Sequence 3819, Application US/20040191818A1
Sequence 3819, Application O' US20040191818A1
APPLICANT: Wyeth
APPLICANT: Liu, Weith
APPLICANT: Liu, Weith
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION UNMER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 3819
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0.4%; Score 14.8; DB 1; Length 21;
ilarity 88.9%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 72.2%; Pred. No. 7.9e+02;
Matches 13; Conservative 3; Mismatches 2;
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2;
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                                                                                                               497 ACACGCTGGACGTGCTGG 514
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CRCANISM: RNAi-antisense strand
US-10-786-720-3819
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       Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-786-720-3820/c
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US-10-7817/c
Sequence 3817, Application US/10786720
Sequence 3817, Application US/10786720
Sequence 3817, Application US.00040191818A1
Sequence 3817, Application No. US20040191818A1
SEQUENCEMENT: West
TITLE OF INVENTION: O'TOOLE, Margot
TITLE OF INVENTION: DISEASES
STORMENT FILING DATE: 2004-02-26
NURBER OF SEQ ID NOS: 21135
SOFWHARE: PATENTIN VERSION 3.2
SEQ ID NO 3817
LENGTH: 21
                                                                                                                                                                                                                                                      Sequence 204, Application US/10833679

Sequence 204, Application US/10833679

Publication No. US20040185508A1

GENERAL INPORMATION:

APPLICANT: Hayden, Michael R.

APPLICANT: Hayden, Michael R.

APPLICANT: Pinactone, Simon N.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS

FILE REPERENCE: 760050-135

CURRENT APPLICATION NUMBER: US/10/833,679

CURRENT PELLING DATE: 2004-04-28

FRIOR APPLICATION NUMBER: 10/617,334

PRIOR PELLING DATE: 2003-06-02

PRIOR APPLICATION NUMBER: 09/526,193

PRIOR PELLING DATE: 2000-03-07-10

PRIOR PELLING DATE: 1999-06-08

PRIOR PELLING DATE: 1999-06-08

PRIOR PELLING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 287

SOFTWARE: PATENTH: 21
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11arity 88.9%; Pred. No. 7.98+02;
Conservative 0; Mismatches 2: InAPIR
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                                                                                                               2791 TACATTTCTATAAATAGA 2808
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; ORGANISM: Homo sapiens
US-10-833-679-204
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; ORGANISM: Homo sapiens
US-10-786-720-3817
       Query Match
Best Local Similarity
Matches 16; Conserv
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APPLICANT: 0'Toole, Margot
APPLICANT: 10'Toole, Margot
TITULGANT: Liu, Weil
TITULE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITULE OF INVENTION: DISEASES
TITULE OF INVENTION: DISEASES
TITULE OF INVENTION: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOCTHWARE: Patentin version 3.2
SEQ ID NO 4527
LENGTH: 21
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Beneral INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: 0'Toole, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: OCMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PAPLICATION NUMBER: US/10/786,720
CURRENT PAPLICATION NUMBER: US/10/786,720
CURRENT PAPLICATION NUMBER: SQL-02-26
NUMBER OF SEQ ID NOS: 21135 '
SOFTWARE: Parentin version 3.2
SEQ ID NO 4526
LENGTH: 21
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0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2. Thanh
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Pred. No. 7.9e+02;
3; Mismatches 2;
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US-10-786-720-4527
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Best Local Similarity 72.2%;
Matches 13; Conservative
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; ORGANISM: RNAi-sense strand
US-10-786-720-4526
                     , ORGANISM: Homo sapiens
US-10-786-720-4525
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US-10-786-720-4527
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US-10-796-720

Sequence 4525, Application US/10786720

Publication No. US20040191818A1

GENERAL INPORMATION:

APPLICANT: Wyeth

APPLICANT: O'Toole, Margot

APPLICANT: O'Toole, Margot
                         APPLICANT: Wyeth
APPLICANT: O'TOOLe, Margot
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Well
APPLICANT: Liu, Will
APPLICANT: US/10/786,720
CURRENT APPLICATION NUMBER: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 3820
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Sequence 3822, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wiweth
APPLICANT: Wiwe Weath
APPLICANT: Wiwe Wimper Compositions and MeTHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILLING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOCTHARRE: Patentin version 3.2
SEQ ID NO 3822
LENGTH: 21
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Pred. No. 7.9e+02;
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Pred. No. 7.9e+02;
3; Mismatches 2; Indels
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; ORGANISM: RNAi-antisense strand
US-10-786-720-3822
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il Similarity 72.2%;
13; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-10-786-720-3820
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Best Local Similarity
GENERAL INFORMATION:
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APPLICANT: 0'Toole, Margot
APPLICANT: 0'Toole, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT PAPLICATION WUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 5258
LENGTH: 21
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APPLICANT: Liu, Wei
TITLE O'INVENTION: DISBASES
FILE OF INVENTION: DISBASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
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                                                                                                                                                                                                                                                           Length 21;
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Pred. No. 7.9e+02;
0; Mismatches 2;
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Pred. No. 7.9e+02;
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; ORGANISM: RNAi-antisense strand
US-10-786-720-5259
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 5257
LENGTH: 21
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SEQ ID NO 5259
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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CRGANISM: RNAi-sense strand
US-10-786-720-5258
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                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-720-5257
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Best Local Similarity
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                                            Sequence 4528, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Win With WITHOUS TILL, Well
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
USBAGES
FILE REFERENCE: 011896-023000 (AM.013311.)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 4528
LENGTH: 21
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Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weeth
APPLICANT: Liu, Wei
APPLICANT: Liu,
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Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Weil
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 14.8; DB 1; Length 21;
88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2; Indels
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FILE REFERENCE: 031896-023000 (AM101331L)
VORRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-720-4528
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Best Local Similarity
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LENGTH: 21
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APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Liu, Weith APPLICANT: Liu, Weith APPLICANT: Liu, Weith APPLICANT: Liu, Weith COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: UNDABER: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SOFTWARE: Patentin version 3.2

SEQ ID NO 11108

LENGTH: 21
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Weit
APPLICANT: Liu, Weit
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE REPERENCE: 031896-023000 (AM101331L)
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11105
LENGTH: 21
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Pred. No. 7.9e+02;
0; Mismatches 2;
                    FILE REFERENCE: 031896-023000 (AMI01331L)
CURRENT PELLING NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17096
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                   TYPE: RNA
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US-10-786-720-5262
US-10-786-720-5262
Sequence 5262, Application US/10786720
Sublication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Weith
APPLICANT: O'TOole, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AMI01331L)
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
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Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Will, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
                                                                                                                                                                                                                                               APPLICANT: O'Toole, Margot
APPLICANT: D'Toole, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
MUNBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
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0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Pred. No. 7.9e+02;
3; Mismatches 2; Indels
                                                                                                                                                 Sequence 5260, Application US/10786720 Publication No. US20040191818A1 GENERAL INFORMATION: APPLICANT: Wyeth
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; ORGANISM; RNAi-antisense strand
US-10-786-720-5262
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                       2 ACACGCUGUACGUGCUCG 19
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Ouery Match
Best Local Similarity 72.2
Matches 13; Conservative
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ORGANISM: Homo sapiens
US-10-786-720-5260
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US-10-786-720-17096/c
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LENGTH: 21
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LENGTH: 21
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APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Liu, Weith COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES FILE REFERENCE: 031896-023000 (AM101331L) CURRENT FILLNG DATE: 2004-02-26 CURRENT FILLNG DATE: 2004-02-26 NUMBER OF SEQ ID NOS: 21135 SOFTWARE: PATENTIN VERSION 3.2 SOFTWARE: PATENTIN VERSION 3.2 LENGTH: 21
                                                         APPLICANT: Liu, Wei COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES FILE REFERENCE: 031896-023000 (AM101331L) CURRENT APPLICATION UNMBER: US/10/786,720 CURRENT FILING DATE: 2044-02-26 NUMBER OF SEQ ID NOS: 21135 SOFTWARE: Patentin version 3.2 SOFTWARE: Patentin version 3.2 LENGTH: 21
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APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISBASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
MUNBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
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88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.8; DB 1;
Pred. No. 7.9e+02;
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; Sequence 20857, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                           O'Toole, Margot
Liu, Wei
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Best Local Similarity 88.9
Matches 16, Conservative
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US-10-786-720-20857
   APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-786-720-20859
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SEQ ID NO 20859
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
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                                                                                                                                                                                                                                                                                                   Sequence 18281, Application US/10786720

Publication No. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Weeth
APPLICANT: O'Toole, Margot
APPLICANT: Liu, Wei
APPLICANT: US/00/080110NS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 18281
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-786-720-18290/c

Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

TITLE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
                                 2; Indels
   88.9%; Pred. No. 7.9e+02;
                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2342
                                                                                              2322 TGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2332 TGCGTGTGTGTGTGTG 2349
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88.9%;
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CRGANISM: RNAi-sense strand
US-10-786-720-18281
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; ORGANISM: RNAi-sense strand
US-10-786-720-18290
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Best Local Similarity 88.9
Matches 16; Conservative
                                 16; Conservative
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Matches 16; Conservative
Best Local Similarity
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US-10-786-720-18293/c
                                                                                                                                                                                                                                                          RESULT 1026
US-10-786-720-18281/c
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                                     Matches
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JOHNSTAL INCREMENT STUTCHING

JAPPLICANT: KANAGANA, TAKAHINO

JAPPLICANT: KANAGANA, TAKAHINO

JAPPLICANT: KANAGANA, YOLCHI

JAPPLICANT: KANAGANA, YOLCHI

JAPPLICANT: KANAGANA, VOLCHI

JAPPLICANT: YOKOMAKU, TOYOKAZU

JAPPLICANT: WOKOMAKU, TOYOKAZU

JAPPLICANTION: WUMBER: US/09/725,265

JAPPLICANTON WUMBER: US/09/725,265

JAPPLICANTON WUMBER: US/09/04-20

JAPPLICANTON WUMBER: WARDING WUMBE
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Sequence 7, Application US/09725265

Sequence 7, Application US/09725265

Publication No. US20010000175A1

GENERAL INFORMATION:

APPLICANT: KRANAGAWA, TAKAHIRO

APPLICANT: KANAGAWA, TAKAHIRO

APPLICANT: KANAGAWA, TAKAHIRO

APPLICANT: KANAGAWA, TAKAHIRO

APPLICANT: KANAGAWA, TOYOKAZU

APPLICANT: KANAGAWA, TOYOKAZU

APPLICANT: KOYAMA, OSAMU

APPLICANT: WUNGER: 1999-53USOXDIV

CURRENT APPLICATION NUMBER: US/09/725,265

FILE REFERENCE: 1999-53USOXDIV

CURRENT PLING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: UP 1999-111601

PRIOR PILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 70

SOPTWARE: PALCHING DATE: 1000-04-20

NUMBER OF SEQ ID NOS: 70

SOPTWARE: PALCHING DATE: DNA

TYPE: DNA
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0.4%; Score 14.8; DB 1;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
3309 ATTTTTTAGGAGATTTATTTTT 3334
                                                                                                                                                                                                                                                        Sequence 6, Application US/09725265 Publication No. US20010000175A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
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US-10-786-720-20990/C
i Sequence 20990, Application US/10786720
i Sequence 20990, Application US/10786720
i Publication No. US20040191818A1
i GENERAL INFORMATION:
i APPLICANT: Wyeth
i APPLICANT: Liu, Wei
i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
i TITLE OF INVENTION: DISEASES
i FILE REFERENCE: 031896-023000 (AM101331L)
i CURRENT PILLING DATE: 2004-02-26
i NUMBER OF SEQ ID NOS: 21135
i SOGTWARE PAEDELLATION OF SEQ ID NOS: 21135
i SOGTWARE PAEDELLATION OF SEQ ID NOS: 21135
i SEQ ID NO 20990
i LENGTH: 21
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Sequence 144, Application US/10085906

Publication No. US20030054371A1

GRENEAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: VUMBER: US/10/085, 906
CURRENT FILING DATE: 2002-27

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: US 69/534,061

PRIOR APPLICATION NUMBER: PCT/US00/07938

PRIOR PRILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 144

LENGTH: 26

LENGTH: 26
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                                                                                                  Score 14.8; DB 1; Length 21;
Pred. No. 7.9e+02;
3; Mismatches 2; Indels
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                1350 GATGGAGATGATGAAGAT 1367
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GAUGAAGAGGAUGAAGAU 18
; ORGANISM: RNAi-antisense strand
US-10-786-720-20859
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Best Local Similarity 88.9%;
Matches 16; Conservative (
                                                                                                          Query Match 0.4%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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Best Local Similarity 73.1%;
Matches 19; Conservative
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ORGANISM: RNAi-sense strand
US-10-786-720-20990
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ORGANISM: Homo sapiens
US-10-085-906-144
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APPLICANT: TORINDRA, MASAKI
APPLICANT: TORINDRA, MASAKI
APPLICANT: TORINDRA, MASAKI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOWAKU, TOYOKAZU
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
FILE REFERENCE: 2003-204-163-0-X
CURRENT APPLICATION NUMBER: US/09/891,517
CURRENT APPLICATION NUMBER: US/09/891,517
PRIOR APPLICATION NUMBER: US/000-236115
PRIOR PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 12
LENGTH: 30
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0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7;
PRIOR APPLICATION NUMBER: 0.2.0...
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: DP2000-236115
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 7
LENGTH: 30
LENGTH: 30
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Patent No. US20020106653A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAMA, YOLCHI
APPLICANT: TORIMURA, MASAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/10209608; Publication No. US20030082592A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Synthetic DNA US-09-891-517-12
                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Synthetic DNA US-09-891-517-7
                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                FEATURE:
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APPLICANT: KURAHINO
APPLICANT: KANAGAMA, TAKAHINO
APPLICANT: KANAGAMA, TAKAHINO
APPLICANT: KANADA, KAZUTAKA
APPLICANT: TANAGAMA, TAKAUDA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU

TITLE OF INVENTION: MUTHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAI
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 199953USOXDIV
CURRENT PLILING DATE: 2000-01-29
FRIOR FILLING DATE: 2000-04-20
FRIOR FILLING DATE: 1999-04-20
FRIOR FILLING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 12
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09891517
Sequence 7. US20020106653A1
GEMERAL INFORMATION:
GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: KANAGATA, YOICHI
APPLICANT: KANAGATA, YOICHI
APPLICANT: TORIMURA, MASAKI
APPLICANT: TORIMURA, MASAKI
APPLICANT: YOKOMAKU, TOYOKARA
APPLICANT: YOKOMAKU, TOYOKARA
APPLICANT: YOKOMAKU, TOYOKARA
APPLICANT: YOKOMAKU, TOYOKARA
APPLICANT: WINTON: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: WELHOD
TITLE OF INVENTION: WINDER: US/09/891,517
CURRENT APPLICATION NUMBER: US/09/891,517
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                                                                                                                                       Score 14.8; DB 1; Length 30;
Pred. No. 1.1e+03;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                    5 ATATTTTTTTTTGTTTTTTTTTTT 30
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/09725265; Publication No. US20010000175A1; GENERAL INFORMATION:
                                         ; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: SYNTHETIC DNA US-09-725-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
           ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                            Query Match
Best Local Similarity 73.1%;
Matches 19; Conservative
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## APPLICANT: KANAGAWA, TAKAHIRO
## APPLICANT: KANAGAWA, TAKAHIRO
## APPLICANT: KANAGARA, YOICHI
## APPLICANT: KANAGARA, YOICHI
## APPLICANT: KANAGARA, YOICH
## APPLICANT: KOKOMAKU, TOYOKAZU
## APPLICANT: YOKOMAKU, TOYOKAZU
## APPLICANT: YOKOWAKU, TOYOKAZU
## APPLICANT: KOYOWAKU, TOYOKAZU
## APPLICANT: KOYOWAKU, TOYOKAZU
## APPLICANT: KANAMA, OSAMU
## APPLICANT: KANAMA, OSAMU
## APPLICANT: KANAMA, OSAMU
## APPLICANT: TILLE OF INVENTION: THE METHOD FOR THE METHOD FOR ANALYZING DATY
## TILLE OF INVENTION: THE METHOD
## FILE REFERENCE: 199953USOKILV
## CURRENT APPLICATION NUMBER: US/09/725,265
## PRIOR APPLICATION NUMBER: US/09/725,265
## PRIOR PILLING DATE: 2000-04-20
## PRIOR PILLING DATE: 2000-04-20
## PRIOR PILLING DATE: 1999-111601
## PRIOR PILLING DATE: 1999-04-20
## PRIOR PILLING DATE: 1999-04-20
## PRIOR PILLING DATE: 1999-04-20
## NUMBER OF SEQ ID NOS: 70
## SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: WITHOH FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLEI
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATH
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: UNMBER: US/10/683,386
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US/09/556,127
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                                                                  Gaps
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                                                                  Indels
Pred. No. 1.1e+03;
                                                                  0; Mismatches
                                                                                                                                         3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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PRIOR APPLICATION NUMBER: JP 1999-111601
PRIOR FILING DATE: 1999-04-20
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/10209608
Publication No. US20030082592A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: SYNTHETIC DNA US-10-209-608-12
                               73.1%;
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                           Best Local Similarity 73.1
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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                                                   APPLICANT: KANAGAWA, TAKAHINO
APPLICANT: KANAGAWA, TAKAHINO
APPLICANT: KANAGAWA, YACTHI
APPLICANT: KANAGAWA, YACTHI
APPLICANT: YAMADA, YACTHAKA
APPLICANT: YAMADA, YACTHAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: FUNCHOW, KAUTHA
TITLE OF INVENTION: WICLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD
TITLE OF INVENTION WUMBER: US/10/209,608
TITLE OF INVENTION NUMBER: US/09/725,265
PRIOR APPLICATION NUMBER: US/09/725,265
PRIOR APPLICATION NUMBER: US/09/725,265
PRIOR APPLICATION NUMBER: US/09/725,265
PRIOR PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 6
TANDEL DATA
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APPLICANT: YANADA, KAZUTAKA

APPLICANT: YOKOMAKU, TOYOKAZU

APPLICANT: KOYAMA, OSAMU

TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI

TITLE OF INVENTION: METHOD

TITLE OF INVENTION: THE METHOD

FILE REFERENCE: 199953UGOXDIV

CURRENT APPLICATION NUMBER: US/09/725,265

PRIOR APPLICATION NUMBER: US/09/725,265

PRIOR APPLICATION NUMBER: US 09/556,127

PRIOR FILING DATE: 2000-11-29

PRIOR FILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LUMBER OF SEQ ID NOS: 70

LUMBER OF SEQ ID NOS: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Publication No. US20030082592A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
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KAMAGATA, YOICHI
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Best Local Similarity 73.1%;
Matches 19; Conservative
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ORGANISM: ARTIFICIAL SEQUENCE
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APPLICANT:
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APPLICANT: ULLMAN, EDWIN
APPLICANT: ULLMAN, EDWIN
APPLICANT: ULLMAN, EDWIN
APPLICANT: LIU, YEN PING
TITE COF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE FOF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REPERBNCE: 3817.05-1
CURRENT APPLICATION NUMBER: 02/10/219,195
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTHARE: PATENTION OF: 2.1
SEQ ID NO 30
LENGTH: 39
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Publication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, EDWIN
APPLICANT: ULLMAN: EDWIN
APPLICANT: LIU, YEN PING
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REPERBNCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
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US-10-219-195-30
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TITLE OF INVENTION: NUCLEIC ACID PROBES FOR TITLE OF INVENTION: THE METHOD FILE REFERENCE: 0163-0758-0X CURRENT PELLIS REPERIOR 1043-0758-0X CURRENT FILING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: US/09/556,127 PRIOR APLICATION NUMBER: US/09/556,127 PRIOR APLICATION NUMBER: JP 1999-111601 PRIOR FILING DATE: 1999-04-20 NUMBER OF SEQ ID NOS: 70 SOFTWARE: PATENTIN VETSION 3.1 SEQ ID NO 12 LENGTH: 30
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Sequence 30, Application US/10219195
Publication No. US20030165917A1
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PUDICATION NO. US20040063137A1

GENERAL INFORMATION:

APPLICANT: KURANG, YALAHIRO

APPLICANT: KANAGAMA, TAKAHIRO

APPLICANT: KANAGAMA, TAKAHIRO

APPLICANT: YAMADA, KAZUTAKA

APPLICANT: YOKOWAKU, TOYOKAZU

APPLICANT: FUNUSHY, OSAWU

APPLICANT: FUNUSHY, OSAWU

APPLICANT: FUNUSHY, OSAWU

APPLICANT: FUNUSHY, OSAWU

APPLICANT: TOYOKAZU

TITLE OF INVENTION: THE METHOD

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APPLICANT: KANAGAWA, TAKAHTRO
APPLICANT: KANAGAMA, YOICHI
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAWU
APPLICANT: KOYAMA, OSAWU
APPLICANT: FURUSHO, KENTA
ATILE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
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Pred. No. 1.1e+03;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                OTHER INFORMATION: SYNTHETIC DNA US-10-683-386-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: SYNTHETIC DNA US-10-683-386-7
                                                                                                                                                     TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
          NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%;
Best Local Similarity 73.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3259 AGATATTTATT
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nes 19; Conserva
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                                                                                SEQ ID NO 6
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RESULT 1049
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; Sequence 18, Application US/09827289
; Patent No. US20020009716A1
; GRERRAL INFORMATION:
    APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT PILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR RILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Abarzua, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US. 60/194843
PRIOR PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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Pred. No. 1.4e+03;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                           ch 0.4%; Score 14.8; DB 1; Length 39; l Similarity 73.1%; Pred. No. 1.3e+03; 19; Conservative 0; Mismatches 7; Indels
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION WUMBER: 60/312,505
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO LENGTH: 39
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; Sequence 14, Application US/09827289
; Patent No. US/0020009716A1
; GENERAL INFORMATION:
                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 73.1%;
Matches 19; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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LENGTH: 45
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Sequence 2, Application US/10362010

Sequence 2, Application No. US20040038247A1

GENERAL INFORMATION

APPLICAMT: Brenner, Sidney

APPLICAMT: Venkatesh, Byrappa

APPLICAMT: Venkatesh, Byrappa

APPLICAMT: Tan, Yin, Have

ITILE OF INVENTION: NUCLEIC ACID CONSTRUCTS INCLUDING A NOVEL T-CELL ACTIVE PROMOTER,

ITILE OF INVENTION: AND PHARMACEUTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR

ITILE REPERBNES: 01/22004

CURRENT APPLICATION NUMBER: US/10/362,010

CURRENT PILING DATE: 2003-08-19

CURRENT FILING DATE: 2003-08-19
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us-vs-car/-zev-14/C

patent No. US2002009716A1

gaugence 14, Application US/09827289

patent No. US20020009716A1

gaugence No. US20020009716A1

gaugence No. US20020009716A1

papelCANT: Abarzua, Patricio

TITLE OF INVENTION: Extension

TITLE OF INVENTION: Extension

FILE REFERENCE: 469290-55

CURRENT APPLICATION NUMBER: US/09/827,289

CURRENT APPLICATION NUMBER: U.S. 60/194843

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 45

TYPE: DNA

CRANISM: Artificial Sequence

FARTURE:

OTHER INFORMATION: use in allele discrimination

US-09-827-289-14
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
; TYPE: DNA; ORGANISM: Artificial Sequence; CRGANISM: Artificial Sequence; PEATURE: ... OTHER INFORMATION: Description of Artificial Sequence: P1 primer for; OTHER INFORMATION: use in allele discrimination US-09-827-289-14
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                     Query Match 0.4%; Score 14.8; DB 1; Length 45; Best Local Similarity 73.1%; Pred. No. 1.4e+03; Matches 19; Conservative 0; Mismatches 7; Indels
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0.4%; Score 14.8; DB 1; Length 45;
Best Local Similarity 59.5%; Pred. No. 1.40+03;
Matches 25; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1353 GGAGATGATGAAGATGATCGGGAAACACAAAAACATCATCAA 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Single strand DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                 3262 TATTITATTIGCTTIGCTTTTTCA 3287
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SEQ ID NO 2
LENGTH: 20
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ORGANISM: Artificial sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-827-289-14/c
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA US-09-828-034-1
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                                                                 APPLICANT: Lobse, Peter
APPLICANT: Lobse, Peter
APPLICANT: Lobse, Peter
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT PILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR APPLICATION NUMBER: 05/145,834
PRIOR APPLICATION NUMBER: 05/145,834
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: designed sequence to act as a linker US-10-208-357-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Forerari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: IN01165
CURRENT FAPLICATION UNMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR APPLICATION NUMBER: 2001-04-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3262 TATTTTATTTGCTTTGTCCTTTTTCAGGA 3290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09828034 Patent No. US20020064771A1
             Sequence 4, Application US/10208357
Publication No. US20020182687A1
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                                      GENERAL INFORMATION:
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSERS: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.6; DB 1; Length 20; Best Local Similarity 70.0%; Pred. No. 8e+02; Matches 14; Conservative 2; Mismatches 4; Indels
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                                                                   NAME/KEY: misc feature
LOCATION: (9)...(9)
OTHER INFORMATION: Any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)...(12)
OTHER INFORMATION: Any nucleotide
                                                                                                                                                                                                                                                                                                                                                  1750 AAGTGGATGGCGCCTGAGGC 1769
LOCATION: (6)..(6)
OTHER INFORMATION: Any nucleotide
FEATURE:
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Best Local Similarity 81.0
Matches 17; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Washing
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Gaps

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Gaps

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RESULT 1051 US-10-208-357-4/c

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GENERAL INFORMATION:
APPLICANT: Hood, Lercy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.4; DB 1; Length 16;
Pred. No. 6.8e+02;
0; Mismatches 1; Indels
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APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Blizabeth Blackburn
TITLE OF INVENTION: THERARY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: TELOMERASE ACTIVITY
TITLE OF INVENTION: TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAYE: ...__
COUNTRY: US
ZUP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
TIVING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 544:
                                                                                                                                                                    Sequence 544, Application US/09263959
Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/08463404 Publication No. US20020127634A1 GENERAL INFORMATION:
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3465 TATATATATATA 3480
3463 TATATATATCTATATA 3478
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Best Local Similarity 93.8%;
Matches 15; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: LOS Angeles
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                APPLICANT: FORSTHE, TOOM
APPLICANT: BISHOP, MICHAEL D.
TITLE OF INVENTION: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
TITLE OF INVENTION: CELLULAR REPROGRAMMING
FILE REPERBENCE: 028040-0209
FILE REPERBENCE: 028040-0209
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT FILING DATE: 2001-06-06
PRIOR PILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
WUMBER OF SEQ ID NOS: 1144
SOFTWARE: PATENTIN VERSION 3.0
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Pred. No. 1.4e+03;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3306 AGGALTITICITIAGGAGATTIAITITI 3334
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NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
PFISTER-GENSKOW, MARTHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 69.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Bovine
US-09-876-143-867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-263-959-541/c
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 867
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Sequence 540, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

APPLICANT: ROWEN, Lee

APPLICANT: ROWEN, Lee

APPLICANT: ADDRESS: 1279

CORRESPONDENCE ADDRESS:

ADDRESSES: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

STREET: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 6.8e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US.

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/09/263,959
FILING DATE: 05-MAR-1999
                                     920010.426C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASLETS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 540:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2824 ATATATACATATAT 2839
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2824 ATATATACATATAT 2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATATATATATATAT 16
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-263-959-540/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-263-959-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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; Patent No. US20020150891A1
; GENERAL INFORMATION:
    APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
APPLICANT: Seed and Berry LLP
STRAES Beed and Berry LLP
STRAES Washington
COUNTRY: Seattle
STRAES Washington
COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COUNTRY: LBM PC Compatible
COMPUTER: LBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 8torage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,404
FILING DATE: 05-UTN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 489-1600
TELER PAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTG 2333
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                RY: U.S.A.
90071-2066
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US-08-463-404-57
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APPLICANT: LI, YUAN
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HERMIDA, NANCY L.
APPLICANT: HOPPA, NANCY L.
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
TITLE OF INVENTION: LIBRABLES OF CDNAS
FILE REFERENCE: 0109015/026
CURRENT APPLICATION NUMBER: US/10/092,885
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEOLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONDITIONS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ for Windows 2.0
CURRENT APPLICATION DMARS:
APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MESULI -232-927A-80
1S-10-232-927A-80
Sequence 80, Application US/10232927A
Publication No. US20030190638A1
GENERAL INFORMATION:
APPLICANT: Michael_D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GICTGIGTGTGTGT 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           storage
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-885-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 231, Application US/10085906

Sequence 231, Application US/203064371A1

GENERAL INFORMATION:

APPLICANT: Ying, Vincent

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: POLYMORRPHIC ELEMENTS IN THE

TITLE OF INVENTION: POLYMORRPHIC ELEMENTS IN THE

TITLE OF INVENTION: COSTINULATORY RECEPTOR LOCUS AND USES THEREOF

FILE REPERENCE: GNN-5343CP2

CURRENT APPLICATION NUMBER: US/10/085, 906

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: PCT/US00/07938

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: PCT/US00/07938

PRIOR APPLICATION NUMBER: PCT/US00/07938

SOFTWARE: FRACEQ FOR WINGOWS VERSION 4.0

SEGOLD NOS: 545

LENGEN APPLICATION NUMBER: PCT/US00/07938
                                                                                             APPLICANT: Ying, Vincent
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Wu, Paul
APPLICANT: Gay, Gary, Gary
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 1202-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR APPLICATION NUMBER: US 999-03-25
PRIOR PILING DATE: 1209-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR SPELICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
PRIOR SEQ ID NOS: 545
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 6.8e+02; ve 0; Mismatches 1; Indels
                     Sequence 231, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2824 ATATATACATATAT 2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2824 ATATACATATAT 2839
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-231
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ઠે 원 RESULT 1061 US-10-092-885-28

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APPLICANT: Pavco, Pam
; APPLICANT: Bavco, Pam
; APPLICANT: Missinger, Jim
; APPLICANT: Missinger, Jim
; APPLICANT: Binchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Momber: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 2082-
SEQ ID NOS: 2082-
SEQ ID NO 6071
LENGTH: LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-287-949A-5819

US-10-287-949A-5819

Sequence 5819, Application US/10287949A

Sequence 5819, Application US/10287949A

Sequence 5819, Application Wo. US20040102389A1

Sequence 5819, Application Wo. US20040102389A1

SEQUENCE INFORMATION: Pavoo, Pam

APPLICANT: Richorom, Dan

APPLICANT: Escobed, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth.Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth.Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth.Factor Receptor

TITLE OF INVENTION: MUMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5819

LENGTH: 16
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                                                                                                                                                                                                                                                                                               Score 14.4; DB 1; Length 16; Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             1658 ACAACGTGATGAAGAT 1673
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NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 5848
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:|:|:|:|:
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Best Local Similarity 50.03
Matches 8; Conservative
                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-138-674-5848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674-6071
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US-10-287-949A-5819
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Publication No. US20040077565A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ravco, Pam
APPLICANT: Ravco, Pam
APPLICANT: Baccobed, Jam
APPLICANT: Becobed, Jam
APPLICANT: Becobed, Jaim
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refile REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin Version 3.0
SEQ ID NO 5819
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US-10-138-674-5848

Sequence 5848, Application US/10138674

Publication No. US20040077565A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Parco, Pam

APPLICANT: Stinchcomb, Dam

APPLICANT: Stinchcomb, Dam

APPLICANT: Stinchcomb, Dam

APPLICANT: Stinchcomb, Dam

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE STERENCE: MBHB00-876-N (400/049)

CURRENT APPLICANTION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03
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                                            NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 80: US-10-232-927A-80
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTG 2333
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                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                     PPLICANT: Michael D. Derry W. Shay
Woodring E. Wright
Blizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TELOMERASE ACTIVITY
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%; Score 14.4; DB 1; Length 16; Best Local Similarity 93.8%; Pred. No. 6.8e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTR: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FILING DATE: May 13,1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/691,633
FILING DATE: 22-Oct-2003
CLASSIFICATION: 514
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-691-633-57
                                                                                                                                                                                                                                                                                                   ADDRESSEB: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2002, Application US/09866108
Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
                       Sequence 57, Application US/10691633; Publication No. US20040198659A1
GENERAL INFORMATION: APPLICANT: Michael D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 57:
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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       US-10-691-633-57
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                                                                                                                                                                                                                             Sequence 5848, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Roskiggen, Jim
APPLICANT: Roskiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Mechod and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
NUMBER OF SEQ ID NOS: 2082-2
SOFTWARE: Patentin version 3.0
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Pred. No. 6.8e+02;
3; Mismatches 1; Indels
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50.0%; Pred. No. 6.8e+02;
ve 7; Mismatches 1; Indels
                          1; Indels
    75.0%; Pred. No. 6.8e+02;
                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-287-949A-6071; Sequence 6071, Application US/10287949A; Publication No. US20040102389A1; GENERAL INFORMATION: APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Pavco, Pam
                                                                     1295 TGAAGATGCTGAAAGA 1310
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1 UGAAAUGCUGAAAGA 16
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GUGUGUGUGUGUGGGU 16
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Best Local Similarity 75.0%;
Matches 12; Conservative
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                          12; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-287-949A-6071
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ORGANISM: Homo sapiens
Best Local Similarity
Matches 12; Conserva
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           PRIOR AFFLIANCE MANIER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
US 60/236,359
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Best Local Similarity 93.0x
Best Local Similarity
Best Local Similarity
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; ORGANISM: Homo sapiens
US-09-866-108-2003
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           APPLICANT: SHANNOW MARK:
TITLE OF INVERTION: MACSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PILING DITE: 2001-05-25
FRIOR PLILNG DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-05-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-00-37
PRIOR PILING DATE: 2000-00-37
PRIOR PILING DATE: 2000-00-37
PRIOR PILING DATE: 2001-00-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE
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Requence 2003, Application US/09866108

Retent No. US20020048800A1

GENERAL INFORMATION:

APPLICANT: GI, Yizhong

APPLICANT: PENN, Bharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David R.

APPLICANT: SHANK, David R.

APPLICANT: SHANK, David R.

APPLICANT: SHANKON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
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CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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CHEN, Wensheng
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APPLICANT
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GENERAL INPORMATION:

APPLICANT: GU'Y Yazhong
APPLICANT: J'Y Yazhong
APPLICANT: PENN, Sharron G.
APPLICANT: APPLICANT: APANEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-00-27
PRIOR FILING DATE: 2000-00-27
PRIOR FILING DATE: 2000-00-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30

                                         PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine SEQ ID NO 2006
LENGTH: 17
PRIOR APPLICATION NUMBER: PCT/US01/00670
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Patent No. US20020048800A1
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CORGANISM: Homo sapiens
US-09-866-108-2006
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: FENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, DAVIG C.
APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2000-09-21
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PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PRILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-21
PRIOR PRILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2005
LENGTH: 17
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CURRENT PEDELICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PELLINGTONION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
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CORGANISM: Homo sapiens
US-09-866-108-2005
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1 UUUAGUUUUAAAACUG 16
   1 ACCATCAAGCAGCTGG 16
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US-09-730-289B-156
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US-09-780-533A-1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUY, YiAhong
APPLICANT: GUY, YiAhong
APPLICANT: HAZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, WENST: US/09/866,108
CURRENT APPLICANTON NUMBER: US/09/866,108
FRIOR APPLICANTON NUMBER: US/01/0666
PRIOR APPLICANTON NUMBER: PCT/US01/0666
PRIOR APPLICANTON NUMBER: PCT/US01/0666
PRIOR APPLICANTON NUMBER: PCT/US01/0666
PRIOR PLIING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR P
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                                                                                                                             Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Patent No. US20020048800A1
                                                                                                                                                                                                                                                                  1992 CACCTTCAAGCAGCTG 2007
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7995
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ORGANISM: Homo sapiens
US-09-866-108-7997
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1993 ACCTICAAGCAGCTGG 2008

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US-09-730-289B-156

US-09-730-289B-156

Sequence 156, Application US/09730289B

Publication No. US20030050259A1

GENERAL INFORMATION:

APPLICANT: Blatt, Larry

CURRENT Blatt, Larry

CURRENT APPLICATION: WORDER: US/09/730, 289B

CURRENT APPLICATION NUMBER: US 60/169,100

PRIOR APPLICATION NUMBER: US 60/169,100

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PatentIn version 3.0

SEQ ID NO 156

LENGTH: ...
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Sequence 1807, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:
APPLICANT: Bilacyme Pharmaceuticals, Inc.
APPLICANT: Black Jim
APPLICANT: Black Jim
APPLICANT: Heaberli, Pete
APPLICANT: Heaberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT PILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: Patentin version 3.0

SEQ ID NO 1807

LENGTH: 17
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; Sequence 41, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
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APPLICANT: Ribozyme Fnarmaceuticats, 111...
APPLICANT: Brack, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jane
FILE REPREMENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT APPLICATION NUMBER: US 07/882,712
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR PLING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 2000-0-0-4
PRIOR PLING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-01-08
PRIOR PLING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 6586
SSQ ID NO 2089
FRANCH APPLICATION NUMBER: US 08/436,430
FRIOR PLING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SSQ ID NO 2089
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US-09-848-754A-2482
Sequence 2482, Application US/09848754A
PUBLICATION NO. US20030073207A1
GENERAL INFORMATION:
APPLICANT: Riboryme Pharmaceuticals, Inc.
APPLICANT: Riboryme Pharmaceuticals, Inc.
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE OF INVENTION: Levels of Machine 1 (400/018)
CURRENT APPLICATION NUMBER: US/09/9484,754A
CURRENT PILING DATE: 2001-05-03
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Pred. No. 7.2e+02;
5; Mismatches 1;
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Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                  853 GAGGAGGAGCTGGTGG 868
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Best Local Similarity 62.5%;
Matches 10; Conservative
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                                                                TYPE: RNA; Hepatitis B virus US-09-877-478-1412
; SEQ ID NO 1412
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                      APPLICANT: Blatt, Larry
APPLICANT: Mcwiggen, Jim
APPLICANT: Morrisesy, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT PRILING DATE: 2001-12-31
FRIOR PRICATION NUMBER: US 09/531,025
FRIOR PRILING DATE: 1992-05-14
FRIOR PRILING DATE: 2000-08-09
FRIOR PRILING DATE: 2000-08-09
FRIOR FILING DATE: 2000-10-24
FRIOR PRILING DATE: 1992-02-07
FRIOR FILING DATE: 1995-05-04
FRIOR PRILING DATE: 1995-05-04
FRIOR PRILING DATE: 1995-05-04
FRIOR PRILING DATE: 1995-05-04
FRIOR FILING DATE: 1995-05-04
FRIOR PRILING DATE: 1995-05-04
FRIOR FILING DATE: 1995
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Moriseey, Dave
TITLE CPE INVERTANTON: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT APPLICATION NUMBER: US 07/882,712
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-20
PRIOR PELING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 6866
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   Draper, Kenneth
Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1079
US-09-877-478-1412/c
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RESULT 1086
US-08-827-395A-424
| Sequence 424, Application US/09827395A
| Publication No. US20030113891A1
| GENERAL INFORMATION:
| APPLICANT: Bloozyme Pharmaceuticals, Inc.
| APPLICANT: James McSwiggen
| APPLICANT: Bharat Chowrira
| APPLICANT: CAURENCE: MSH000-878-C (400/017)
| CURRENT APPLICATION NUMBER: US/09/627,395A
                                                                          Sequence 391, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBHB00, 918-A 400/027
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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US-09-180-184-723
; Sequence 723, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Mcthod and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
CORGANISM: Homo Sapiens
US-09-930-423-391
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ORGANISM: Homo sapiens
US-09-780-164-723
                                                       US-09-930-423-391/c
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Sequence 2207, Application US/09848754A

Publication No. US20030073207A1

GENERAL INFORMATION:

APPLICANT: RIDEZYME Pharmaceuticals, Inc.

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

FILE REFERENCE: MBHB00-958-I (400/018)

CURRENT APPLICATION UNMERS: US/09/848,754A

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 9645

SOUTHWEATE: Patentin version 3.0

SEQ ID NO 2907
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US-09-930-423-390/c
; Sequence 390, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McGwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00, 918-A 400/027
; CURRENT FILING DATE: 2001-08-15
; UNMBER OF SEQ ID NOS: 4553
; SCFTWARE: PatentIn version 3.0
; SEQ ID NO 390
; LENGTH: 17
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NUMBER OF SEQ ID NOS: 9645
SOPTWARE: Patentin version 3.0
SEQ ID NO 2482
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                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2482
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ORGANISM: Homo sapiens
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CORGANISM: Homo Sapiens
US-09-930-423-390
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Best Local Similarity
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APPLICANT: Out.vis, indie
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
TITLE OF INVENTION: (GRID) Gene
TITLE OF INVENTION: MSHB00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-745-237A-390/c
US-09-745-237A-390/c
Sequence 390, Application US/09745237A
| Sequence 390, Application US/09745237A
| SENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: McSwiggen, Jim
| TITLE OF INVENTION: McHandel and Reagent for the Treatment of Alzheimer's Disease
| TITLE OF INVENTION: McHandel and Reagent for the Treatment of Alzheimer's Disease
| TILLE REFERENCE: 400/007 (MRHB00-918-A)
| CURRENT TRING DATE: 2002-04-15
| CURRENT FILMS DATE: 2002-04-15
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO. 390
| SEQ ID NO. 390
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 12; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                          0.4%; Score 14.4; DB 1; Length 17; 75.0%; Pred. No. 7.2e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 880, Application US/09792818
Publication No. US20030134806A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
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                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                            ; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-645
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CRGANISM: Homo sapiens
US-09-792-818-880
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ORGANISM: Homo sapiens
US-09-745-237A-390
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US-09-792-818-880
; SEQ ID NO 645
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Fublication No. US20030134806A1

GENERAL INFORMATION:

APPLICANT: Stbozyme Pharmaceuticals, Inc.

APPLICANT: Won Carlowitz, Ira

APPLICANT: McSwigen, Jim

APPLICANT: Hamblin, Paul

FILE OF INVENTION: (GRID) Gene

TITLE OF INVENTION: (GRID) Gene

TITLE OF INVENTION: (GRID) Gene

CURRENT APPLICATION NUMBER: US/09/792,818

CURRENT APPLICATION NUMBER: US/09/792,818

WUNDER OF SEQ ID NOS: 2304

SOFTWARE: PatentIn version 3.0

SEQ ID NO 382
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Sequence 455, Application US/09792818
Sequence 455, Application US.032030134806A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Narvis, Thale
APPLICANT: Wor Carlowitz, Ira
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
APPLICANT: Ellis, Jonathan
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: SIIS, Jonathan
TITLE OF INVENTION: (GRID) Gene
FILE REFERENCE: MBHB00-901-A (400/013)
CURRENT APPLICANTON NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.4; DB 1; Length 17; 81.2%; Pred. No. 7.2e+02; tive 2; Mismatches 1; Indels
                      PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2617
SOFTWARE: Patentin version 3.0
SEQ ID NO 424
  2001-04-05
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Best Local Similarity 81.2%
Matches 13, Conservative
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, ORGANISM: Homo sapiens
US-09-792-818-382
                                                                                                                                                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-09-827-395A-424
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US-10-238-700-3350/c

is Sequence 3350, Application US/10238700

is Sequence 3350, Application US/10238700

is Publication No. US20330153521A1

is CHARLAL INPORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

ITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/057 (MBHB01-1158-A)

CURRENT APPLICATION NUMBER: US/10/238,700

CURRENT APPLICATION NUMBER: DCT/US 02/16840

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-05-29

PRIOR FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 4666

SOFTWARE: Patentin version 3.0

SEQ ID NO 3350

LENGTH: 17
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Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REPRENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US 02/16840 PRIOR FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: US 60/318,471 PRIOR FILING DATE: 2001-09-10 NUMBER OF SEQ ID NOS: 4666 SOFTWARE: PATENTIN VETSION 3.0 SEQ ID NO 2806
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Best Local Similarity 93.8
Matches 15; Conservative
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US-10-238-700-2806
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US-10-238-700-3350
                                                                                                                                                                                                                          TYPE: RNA
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Sequence 2806, Application US/10238700

Publication No. US20030153521A1

Publication No. US20030153521A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: RoSwiggen, James

TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/PMBER: US/10/238,700

CURRENT APPLICATION NUMBER: US/10/238,700
                                                                                                                                               Sequence 391, Application US/09745237A

Sequence 391, Application US/09745237A

Publication No. US20030143708A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blact, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
TITLE OF INVENTYON: Method and Reagent for the Treatment of Alzheimer's Disease
TILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550

SOFTWARE: Patentin version 3.0

SEQ ID NO 391
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US-10-211-059-166/c
Sequence 166, Application US/10211059
Publication No. US20030100495A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
FILE REFERENCE: PB0149
CURRENT APPLICATION NUMBER: US/10/211,059
CURRENT APPLICATION NUMBER: US/0/211,059
CURRENT APPLICATION NUMBER: US/0/311,034
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 322
SOUTWARE: Acomica Sequence Listing Engine
SEQ ID NO 166
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     16 gccreckedeccred 1
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                    RESULT 1091
US-09-745-237A-391/c
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Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                   Publication No. US20030166229A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: HUMAN POSH-LIKE PROTEIN I
FILE REFERENCE: PB0178
FILE REFERENCE: PB0178
CURRENT PELIGATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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Publication No. US2003016622941

GENERAL INPORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

FILE REPERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666
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                                                                                                                             Sequence 444, Application US/10061201
Publication No. US20030166229A1
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ORGANISM: Homo sapiens
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Publication No US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SEQ ID NO 441
APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-061-201-441
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; ORGANISM: Homo sapiens
US-10-061-201-443
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Sequence 1412/c
Sequence 1412, Application US/10342902
Publication No. US20040054156A1
Sequence 1412, Application US/10342902
Publication No. US20040054156A1
SENDICANT: Sirna Therapeutics, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jum
SIRE REFRENCE: 400/075 (MBHB00-845-1)
CURRENT APPLICANT: WNBER: US 09/85-1)
FILE REFRENCE: 400/075 (MBHB00-845-1)
CURRENT APPLICATION NUMBER: US 09/837,478
PRIOR APPLICATION NUMBER: US 09/837,478
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR PELLING DATE: 2000-03-20
PRIOR PELLING DATE: 2000-06-09
PRIOR PELLING DATE: 2000-10-24
PRIOR PELLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/636,347
PRIOR PELLING DATE: 1994-02-07
PRIOR PELLING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
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                    FILE REFERENCE: 400/075 (MBHB00.0845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15,902
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 1994-02-07
PRIOR PILING DATE: 1994-05-14
PRIOR PILING DATE: 1999-11-08
NUMBER: US 09/436,430
PRIOR PILING DATE: 1999-11-08
NUMBER: OF SEQ ID NOS: 6592
SEQ ID NO 41
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SEQ ID NO 1412
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Best Local Similarity 93.8°
Matches 15; Conservative
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Best Local Similarity
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APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: James McSwiggen
APPLICANT: Blarat Chowira
APPLICANT: Bear Chowira
APPLICANT: Braret Chowira
APPLICANT: Brack Chowira
APPLICANTON: Mcthod and Reagent for the Inhibition of NOGO and NOGO Receptor G
FILE REFERENCE: MBB00-878-H (400/112)
CURRENT APPLICATION NUMBER: 05/04/30,882
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR APPLICATION NUMBER: PCT/US01/04273
PRIOR PELING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR APPLICATION NUMBER: 2001-02-01
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR APPLICATION NUMBER: 00-02-01
PRIOR APPLICATION NUMBER: 2001-02-01
PRIOR APPLICATION NUMBER: 2001-02-01
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR PILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 445
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Publication No. US20030203870A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 424
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Matches 15, Conservative
                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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US-10-430-882-424
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US-10-430-882-424
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Sequence 4753, Application US/10138674

Sequence 4753, Application US/10138674

Sequence 4753, Application US/10138674

Sequence 4753, Application US/10136541

Sequence 4753, Application US/10136674

Sequence 4753, Application US/10136674

Sequence 4753, Application US/10138674

Sequence 4753, Application US/10/138674

Sequence 4753, Application US/10/138674

Sequence 4753, Application US/10/138674

Sequence 4753, Application US/10/138674

Sequence 4753

Sequence 4753
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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/138, 674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6732
LENGTH: 17
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                                           Length 17;
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                                              Score 14.4; DB 1;
Pred. No. 7.2e+02;
                                              Query Match 0.4%; Score 14.4; Di
Best Local Similarity 81.2%; Pred. No. 7.2e
Matches 13; Conservative 2; Mismatches
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Publication No. US20040077565A1
GENERAL INFORMATION:
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1 Similarity 87.5%;
14; Conservative 1
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Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-4753
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US-10-138-674-6732
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Best Local Similarity
Matches 14; Conserv
US-10-138-674-2650
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                                                                                                                                                                                                                                                                                        RESULT 1104
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; Sequence 2650, Application US/10138674
; Bublication No. US20040077565A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Besobedo, Jaime
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEMBER: US/10/138,674
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; SOFTWARE: PETCH OF SEQ ID NOS: 20822
; SEQ ID NO 2650
                                                                                                                                                                                                                 Sequence 2089, Application US/10342902

Publication No. U820040054156A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Draper, Kenneth

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McRaigean, Jim

APPLICANT: McRaigean, Jim

APPLICANT: Workinger, Us/10,342,902

CURRENT PILIAG DATE: 2000-03-1-15

CURRENT PILIAG DATE: 2001-01-15

PRIOR APPLICATION NUMBER: US 09/877,478

PRIOR APPLICATION NUMBER: US 09/877,478

PRIOR PILING DATE: 2000-06-08

PRIOR FILING DATE: 2000-06-08

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 6592

SEQ ID NOS: 6592

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llarity 62.5%; Pred. No. 7.2e+02;
Conservative 5; Mismatches 1; Indels
  Indels
        1;
        Mismatches
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                                                         853 GAGGAGCTGGTGG 868
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                                                                                                          16 GAGGAGGAGCTGCTGG 1
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        15; Conservative
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Best Local Similarity
Matches 10; Conserve
                                                                                                                                                                                      RESULT 1102
US-10-342-902-2089
        Matches
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TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
SOFTWARE: Patentin Version 3.0
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APPLICANT: McSwiggen, Jim
APPLICANT: SECODED, Jaime
APPLICANT: Escobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 4753
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US-10-287-949A-6732

Sequence 6732, Application US/10287949A

Sequence 6732, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Riborayme Pharmaceuticals, Inc.

APPLICANT: Berobedo, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Becobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: UNMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822
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0.4%; Score 14.4; DB 1;
Best Local Similarity 81.2%; Pred. No. 7.2e+02;
Matches 13; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4753, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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Best Local Similarity 75.v.
Them 12; Conservative
Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
CORGANISM: Mus musculus
US-10-287-949A-2650
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; ORGANISM: Homo sapiens
US-10-287-949A-4753
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US-10-287-949A-4753
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Sequence 7696, Application US/2014077555A1

Publication No. US20040077555A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacobedo, Jaim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaim

APPLICANT: Bacobedo, Jaim

APPLICANT: Bacobedo, Jaim

APPLICANT: Bacobedo, Jaim

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: Malbado-876-N (400/049)

CURRENT APPLICATION WHERE: US/10/138,674

CURRENT PILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SEQ ID NO 7696

LENGTH: 17
                                       Sequence 7632, Application US/10138674

Forguence 7632, Application US/10138674

Forguence 7632, Application US/10138674

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Particon Family Forger, Jam
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 75.0%; Pred. No. 7.2e+02; Matches 12; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1397 TGCTGGGCGCCTGCAC 1412
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Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7632
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CORGANISM: Homo sapiens
US-10-138-674-7696
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Sequence 27, Application US/10712672

Sequence 27, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

FILE REPERBNCE: MSHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/10/712,672

CURRENT APPLICATION NUMBER: US/09/653,225

PRIOR APPLICATION NUMBER: US/09/653,225

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 1999-08-31

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14
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sequence 526, Application US/10712672

publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

FILE REFERENCE: MBHB00-88-C (400/019)

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SEQ ID NO 526

LENGTH: 17
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Pred. No. 7.2e+02;
3; Mismatches 1; Indels
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        Indels
    3; Mismatches
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                                                                                           1658 ACAACGTGATGAAGAT 1673
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Best Local Similarity 75.0%;
Matches 12; Conservative 3
                                                                                                                                       1 ACAACGUGGUGAAGAU 16
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12; Conservative
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ORGANISM: Homo sapiens
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        Matches
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Sequence 7632, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bacobed, Jaime
APPLICANT: Escobed, Jaime
APPLICANT: Bacobed, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stocked, Jaime
APPLICANT: Stocked, Jaime
APPLICANT: Scobed, Jaime
APPLICANT: Scoped, Jaime
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaim
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Cor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-87-6-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF ENQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7696
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                                                                                                                                                                                                                                                                                                Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 7.2e+02; Matches 14; Conservative 1; Mismatches 1; Indels
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1619 ACAGGGACCTGGCTGC 1634
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    SOFTWARE: PatentIn version 3.0
SEQ ID NO 6732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAGGGACCUGGCGGC 16
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-287-949A-7696
                                                                                                                                   TYPE: RNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 2682. Application US/10712672

Sequence 2682. Application No. US20040102413A1

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Chowitien, Bharat

APPLICANT: Chowitien, Bharat

APPLICANT: Marchcomb, Dan

TILE REPERBNCE: MBHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/10/712.672

CURRENT APPLICATION NUMBER: US/20/11-13

PRIOR PILING DATE: 2000-11-13

PRIOR PILING DATE: 2000-08-31

PRIOR PILING DATE: 2000-08-31

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2682

LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 81.2%; Pred. No. 7.2e+02; Matches 13; Conservative 2; Mismatches 1; Indels
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1479 GGCGCGGCGCCCCG 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-712-672-2682
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GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchoomb, Dan

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TITLE OF INVENTION: Momber: US/09/653,225

CURRENT APPLICATION NUMBER: US/09/653,225

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: Patentin version 3.0

SEQ ID NO 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 7.2e+02; Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                     Sequence 2019, Application US/10712672; Publication No. US20040102413A1; GENERAL INFORMATION:
                  1563 CTGTGCCTACCAGGTG 1578
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                                    CUGCGCCUACCAGGUG 17
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CORGANISM: Homo sapiens
US-10-712-672-2019
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CRGANISM: Homo sapiens
US-10-712-672-2330
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APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: UNINCEDENTIED INHIBITION OF HEPATITIS B VIRUS AND HEPAN
TITLE OF INVENTION: UNINCE REPLICATION
TITLE OF INVENTION: UNINCEDENTICATION
TITLE OF INVENTION: UNINCEDENTICATION
TITLE OF INVENTION: UNINCEDENTICATION
TITLE OF INVENTION: UNINCEDENTICATION
TOTHER REPERENCE: 400/04205 (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
PRIOR PELING DATE: 2002-09-23
PRIOR PELING DATE: 2002-09-24
PRIOR PELING DATE: 2001-06-08
PRIOR PELING DATE: 2001-10-24
PRIOR PELICATION NUMBER: US 60/337,055
PRIOR PELING DATE: 2001-10-24
PRIOR PELING DATE: 2001-10-24
PRIOR PELING DATE: 2001-10-34
PRIOR PELING DATE: 2001-10-34
PRIOR PELING DATE: 2001-10-3-11
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2000-03-12
PRIOR PELING DATE: 2000-03-12
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/410,332
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PELING DATE: 2000-01-15
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APPLICANT: Patrice, Lee
APPLICANT: Patrice, Lee
APPLICANT: Remath, Dapper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIE OF INVENTION: VIRUS REPLICATION
TITLE OF INVENTION: VIRUS REPLICATION
FILE REFERENCE: 400/402US (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILLING DATE: 2003-09-23
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PRIOR FILING DATE: 2002-03-26
PRIOR PELICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
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PRIOR PELICATION NUMBER: US 60/337,055
PRIOR FLING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      853 GAGGAGGAGCTGGTGG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.0 SEQ ID NO 1412 LENGTH: 17
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James, McSwiggen
David, Morrissey
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APPLICANT: James, McSarjagean
APPLICANT: David, Morrissey
APPLICANT: Patrice, Lee
APPLICANT: Riabeth, Exberts
APPLICANT: Riabeth, Draper
APPLICANTON: OLIGONOCLECOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
ITILE OF INVENTION: VIRUS REPLICANTON
FILE REFERENCE: 400/0420S (WHHB02-249-E)
CURRENT PILING DATE: 2003-03-26
FRIOR APPLICANTON NUMBER: US 60/236, 976
FRIOR APPLICANTON NUMBER: US 60/335, 059
FRIOR APPLICANTON NUMBER: US 60/335, 059
FRIOR PILING DATE: 2001-10-24
FRIOR PILING DATE: 2001-10-24
FRIOR PILING DATE: 2001-12-05
FRIOR PILING DATE: 2001-12-05
FRIOR FILING DATE: 2001-12-05
FRIOR PILING DATE: 2001-12-05
FRIOR APPLICANTON NUMBER: US 60/33, 124
FRIOR PELING DATE: 2001-12-18
FRIOR APPLICANTON NUMBER: US 60/340, 321
FRIOR APPLICANTON NUMBER: US 60/340, 321
FRIOR APPLICANTON NUMBER: US 69/440, 321
FRIOR APPLICANTON NUMBER: US 69/544, 321
FRIOR FILING DATE: 2000-07-07
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Pred. No. 7.2e+02;
0; Mismatches 1; Indels
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; Sequence 1412, Application US/10669841
; PUDIACATION No. US20040127446A1
; GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morriseey
                                                                                                                                                              RESULT 1113
US-10-669-841-41/C
; Sequence 41, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INPORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
. APPLICANT: James, McSwiggen
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1 AGGGAGGGGGGGCCC 16
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Best Local Similarity 93.8%;
Matches 15; Conservative
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ORGANISM: Hepatitis B Virus
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Patrice, Lee
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APPLICANT:
APPLICANT:
APPLICANT:
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                              Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Publication No. US20040137589A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3194 CCCCGGAGCTGGAGGA 3209
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Best Local Similarity 93.8
Matches 15; Conservative
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APPLICANT: PENN, Sharron
APPLICANT: HANZEL, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1124
US-10-723-361-2005/c
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US-10-723-361-2003/c
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Sequence 2002, Application US/10723361

Publication No. US20040137589A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: GU, Yizhong

APPLICANT: HANKEL, David R.

APPLICANT: BANG, David R.

APPLICANT: BROWN, Mark

TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

FILE REFERENCE: P80.03

APPLICANT: SHANON, Mark

TITLE OF INVENTION WIMBER: US 09/866,108

PRIOR PELING DATE: 2001-12-6

PRIOR PELING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: BE 2001-00-40

PRIOR APPLICATION NUMBER: BC 2003-00-40

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PELING DATE: 2001-01-40

PRIOR PELING DATE: 2001-01-30

PRIOR PELINGATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELING
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                   - See File Wrapper or PALM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-012-18
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 UUCCGGAAACUACUGU 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-723-361-2002
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
FILE REFERENCE: PB0105
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                                                            PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application data removed - See File Wrapper or PALM.
SEQ ID NOS: 15755
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Pred. No. 7.2e+02;
0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001
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CURRENT FILING DATE: 2003-11-26
APPLICATION NUMBER: PCT/US01/00664
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-723-361-2006
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US-10-723-361-7995
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Best Local Similarity
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             APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: POLOGE
CURRENT APPLICATION NUMBER: US/01/23,361
CURRENT PILING DATE: 2000-11.26
PRIOR PAPLICATION NUMBER: US/0866,108
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-01-04
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 
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APPLICANT: GU, Yizhong
APPLICANT: GU, Yongang
APPLICANT: DI, Yongang
APPLICANT: PENN, Sharron G,
APPLICANT: PENN, Sharron G,
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANKON, MARSH
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PRO105
CURRENT APPLICATION NUMBER: US/0/223,361
CURRENT PILING DATE: 2003-11-26
PRIOR PLILING DATE: 2000-105-25
PRIOR PLILING DATE: 2000-10-0-45
PRIOR FILING DATE: 2000-10-0-4
PRIOR PLILING DATE: 2000-0-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING PAPEL: 2001-09-30
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FILING DATE: 2001-01-30
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Publication No. US20040137589A1
GENERAL INFORMATION:
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Best Local Similarity 93.8
Matches 15; Conservative
RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-723-361-2006/c
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Patent No. US2020116735A1
GENERAL INFORMATION:
APPLICANT: Kunst et al.
TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
Involved In Very Long Chain Fatty Acid Synthesis
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
Leigh & Whinston, LLP
STREET: One World Trade Center, Suite
1600, 121 S.W. Salmon Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,325
FILING DATE: 26-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECHONE: (617) 7227-7400
TELEPHONE: (617) 7227-740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/058,947
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3658 GCCTGCAGGGCCATGG 3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 base pairs
Massachusetts: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         FILING DATE
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Sequence 7997, Application US/10723361

Publication No. US20040137583A1

SERVERAL INFORMATION:

APPLICAMT: GU, Yizhong

APPLICAMT: BENN, Sharron G.

APPLICAMT: PERN, Sharron G.

APPLICAMT: PERN, David R.

APPLICAMT: PHANEL, David R.

APPLICAMT: APPLICAMT: ANA EACH

TITLE OF INTENTION: HUMBER: US/10/723,361

CURRENT PAPLICATION NUMBER: US/20.01-26

FRIOR APPLICATION NUMBER: US/20.01-26

FRIOR APPLICATION NUMBER: US/20.01-26

FRIOR APPLICATION NUMBER: US/20.01-26

FRIOR APPLICATION NUMBER: US/20.01-06-25

FRIOR APPLICATION NUMBER: US/20.01-06-26

FRIOR APPLICATION NUMBER: US/20.01-06-27

FRIOR APPLICATION NUMBER: US/20.01-06-27

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00669
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      Gaps
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
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CORRESPONDENCE ADDRESS: ADDRESSE: LAHIUT & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
      1; Indels
   Mismatches
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Patent No. US20020099199A1
GENERAL INFORMATION:
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   15; Conservative
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; ORGANISM: Homo sapiens
US-10-723-361-7997
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      Matches
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: oligonucleotide probe US-09-320-229
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Pred. No. 7.7e+02;
0; Mismatches 1;
                                         APPLICATION NUMBER: PCT/US99/23089
                                PLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 229, Application US/09909088B
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Best Local Similarity 93.8%;
Matches 15; Conservative
                  1999-10-05
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CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
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REFERENCE/DOCKET NUMBER: 5493-50032/DJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/909,320 CURRENT FILING DATE: 2002-01-09 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR FILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: US 60/143,048
                                                                                                                                                 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-892-325-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-07-28
PEDLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-09-15
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229, Application US/09909320 Patent No. US20020132240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
               TELECOMMUNICATION INFORMATION TELEPHONE: (503) 226-7391
                                              TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 3106 GGCGGAGAGTTTTAAT 3121
                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                              2 GTCGGAGAGTTTTAAT 17
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Paoni, Nich
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IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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                                                                                           Query Match

0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-8
         ; OTHER INFORMATION: oligonucleotide probe
US-09-909-088B-229
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 229, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Stewart, Timothy A.
Fumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Pan, James
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Botstein, David
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Gao, Wei-Qiang
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APPLICANT: Ashkenazi, Avi
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Eaton, Dan L.
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PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: DCT/US00/0414

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-00-08

PRIOR PILING DATE: 1999-00-13

PRIOR PILING DATE: 1999-00-15

PRIOR PILING DATE: 1999-00-15

PRIOR APPLICATION NUMBER: PCT/US99/213089

PRIOR PILING DATE: 1999-00-15

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                              Gerber, Hanspeter
Gerritsen, Mary B
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Mather, Jennie P.
                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Baton, Dan L.
                                                                                                                                                                                                                                                                                                      Gao, Wei-Qiang
GENERAL INFORMATION:
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Patent No. US20020168708A1
GENERAL INFORMATION:
Andrew D.J. Goodearl and Sandra Glucksman
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02;
0.4%; Score 14.4; DB 1; Length 18; illarity 93.8%; Pred. No. 7.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,334
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/09/042,780
FILING DATE:
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNI-032CP
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                                                                                                            3658 GCCTGCAGGGCCATGG 3673
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          1 cccrccrcccchrcc 16
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, David
APPLICANT: Eaton, David
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Matches 15; Conservative
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STATE: Massachusetts
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                                Best Local Similarity
Matches 15; Conserv
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US-09-902-853-229
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             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09349755
Patent No. US20020166131A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TILLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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COUNTRY: USA

ZIP: 02109

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/349,755

FILING DATE: 08-Jul-1999

CLASSIFICATION NUMBER: US/09/042,780

FILING DATE: CURNOWN-

APPLICATION NUMBER: US/09/042,780

FILING DATE: O4-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A. Hanley

REGISTRATION NUMBER: 33,505

REGISTRATION NUMBER: 33,505

TELERCOMMUNICATION NUMBER: MAI-032CP

TELERCOMMUNICATION NUMBER: MAI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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STREET: 28 State Street
        PRIOR APPLICATION NUMBER: E.S., C.C. PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
THEORY ILING DATE: 2000-01-05
THEORY FILING DATE: 2000-01-05
THEORY FILING DATE: 2000-01-05
THEORY FILING DATE: 2000-01-05
THEORY FILING DATE: 2000-01-05
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-349-755-24
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INFORMATION FOR SEQ ID NO: 24:
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STRANDEDNESS: single
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Sequence 229, Application US/09907824 Publication No. US20020197671A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTUON: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTUON: Acids Encoding the Same
FILE REPRESSURS: 10466-130
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2000-09-18
FRIOR APPLICATION NUMBER: US/09/665,350
FRIOR APPLICATION NUMBER: US/09/665,360
FRIOR APPLICATION NUMBER: US/09/149,08
FRIOR PELING DATE: 1999-07-18
FRIOR APPLICATION NUMBER: US/09/20594
FRIOR PELING DATE: 1999-07-28
FRIOR PELING DATE: 1999-09-18
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-10-15
FRIOR PELING DATE: 1999-11-29
FRIOR PELING DATE: 1999-12-20
FRIOR PELING DATE: 1999-12-20
FRIOR PELING DATE: 1999-12-30
FRIOR PELIN
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                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E
                                                                                          Wei-Qiang
                                                                                                                                                                                            Goddard, A.
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APPLICANT: ROY, MATGATER AND
APPLICANT: ROY, MATGATER AND
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT PILLING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-11-30
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APPLICANT: Williams, Wickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: 02/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                        CTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Oligonucleotide probe US-09-907-841-229
                                                                                                                                                                                                                                                                                                                              Query Match

0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PLING APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 2000-02-22
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US-09-904-011-229
US-09-904-011-229
Sequence 229, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-907-824-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
          PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
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Grimaldi, Christopher J.
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Sequence 229, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                     LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same
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, OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-640-229
                                                                                                                                                                                                                                                                                                           Query Match

0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR PELLORICAN NUMBER: 09/665,350
PRIOR PELLORICAN NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21090
        PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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Eaton, Dan L.
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
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PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-06
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PRIOR PLING DATE: 2990-12-20
PRIOR PLING DATE: 2900-01-05
PRIOR PLING DATE: 2000-01-05
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary B.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-903-640-229
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Length 18;
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                               PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PRIOR PLING DATE: 1999-12-07
PRIOR PRIOR PLING DATE: 1999-12-07
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PRIOR PRIOR PLING DATE: 1999-12-07
PCT/US00/04414
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5. US20030027143A1
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Hillan, Kenneth, J
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Jao, Wei-Qiang
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GENERAL INFORMATION
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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, OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-908-093-229
                 PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PRIOR TILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3091
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3091
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Publication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
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ORGANISM: Artificial Sequence
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Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth,
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Mather, Jennie P.
Pan, James
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1990-12-20
PRIOR PILING DATE: 1990-12-30
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 10466-14
CURRENT PELLING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: CT/US00/04414
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PTING DATE: 1999-11-29
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Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                       Perrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paoni, Nicholas F
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                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
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Mather, Jennie P.
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Hillan, Kenneth,
                                                                                                                                                                                                                                                                                   Wei-Qiang
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                                                                                                                                                                                                           APPLICANT: THILLIAM, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERRICE: 1046-6.130
GURRENT APPLICATION NUMBER: US/09/906,838
GURRENT PILING DATE: 2001-00-16
PRIOR APPLICATION NUMBER: PC/1800/0441
PRIOR PILING DATE: 1099-70-70
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-77-26
PRIOR PILING DATE: 1999-77-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-20
PRIOR PILING DATE: 1999-10-20
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-00
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                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
                                                                                                    Nicholas F.
Kljavin, Ivar J.
Mather, Jennie P
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: Oligonucleotide probe US-09-907-613-229

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

RESULT 1144
US-09-907-613-229
Sequence 229, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:

GCTGTCCACAGGGGAG 18

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and Transmembrane Polypeptides and Nucleic
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1200-07-26
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
                      PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2090-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-904-859-229; Sequence 229, Application US/09904859; Publication No. US20030036060A1; GENERAL INPORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and
TITLE OF INVENTION: Acids Encod
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
FILE REPERDICATION NUMBER: US/09/907,942
CURRENT APPLICATION NUMBER: PCT/US00/04114
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-38
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
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                            Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Publication No. US20030027146A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botsoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goo, Wei-Qiang
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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APPLICANT:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: Oligonucleotide probe
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                                                       CURRENT PILING DATE: 2010-07-18

PRIOR APPLICATION NUMBER: DCT/USO0/04414

PRIOR PILING DATE: 2000-02-27

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1099-12-03

PRIOR PILING DATE: 1099-12-03

PRIOR PILING DATE: 1099-12-03

PRIOR PILING DATE: 1099-12-03
                                    CATION NUMBER: US/09/909,204
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5. US20030036094A1
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
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Best Local Similarity 93.88
Matches 15; Conservative
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Botstein, David
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Gao, Wei-Qiang
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic Oligonucleotide Probe
                                                       PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28655
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
                                        PCT/US99/21090
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Publication No. US20030036061A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT,
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Roy, Margaret Ann.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT FILING DATE: 2001-07-12
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Pred. No. 7.7e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-00
                      Application US/09904786
5. US20030039969A1
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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SEQ ID NO 229
LENGTH: 18
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URRENT APPLICATION NUMBER: US/09/904,820
URRENT FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-18
APPLICATION NUMBER: PCT/US00/04414
FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: 2000-01-05
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PLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/30999
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: 09/665,350
                             Christopher J.
                                                                                                                                                                                                                                                                                                                                             Williams, P. Mickey
Wood, William, I.
                                                                                                                     Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
                                                          Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Godowski, Paul J
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Godowski, Paul J. Grimaldi, Christopher J. errara, Napoleone Gerritsen, Mary E Goddard, A. Gerber, Hanspeter ilvaroff, Ellen Desnoyers, Luc Eaton, Dan L. ong, Sherman

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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PORGANISM: Artificial Sequence
PORGATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/21547
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PLICATION NUMBER: US 60/146,222
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FILING DATE: 1999-07-28
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-906-646-229
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                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembra TITLE OF INVENTION: Acids Encoding the Same FILE REFRENCE: 1046-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
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PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-8
PRIOR PLING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-06
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-04
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
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                                                                                                                                                                                                                                      Williams, P. Mickey
Wood, William, I.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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                                                                                                                   Nicholas F.
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SEQ ID NO 229
                                                                                    Pan, James
Paoni, Nich
                                                                                                                                                                              APPLICANT:
APPLICANT:
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US-09-906-700-229 ; Sequence 229, Application US/09906700 ; Publication No. US20030039972A1

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Gaps

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-786-229
                 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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RICH APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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PRIOR APPLICATION NUMBER: US 60/145,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 229, Application US/09902903
Publication No. US20030044839A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT:
APPLICANT:
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                                                                                                            Gaps
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                                                0.4%; Score 14.4; DB 1; Length 18; ilarity 93.8%; Pred. No. 7.7e+02; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/903,786

CURRENT PILING DATE: 2001-07-11

PRIOR FILING DATE: 2001-07-11

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-03-22

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR PILING DATE: 1999-00-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Pilvaroff, Ellen
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-906-700-229
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic;
COTHER INFORMATION: Oligonucleotide probe
US-09-903-749A-229
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Acids Encoding the Same
                                                                                                                           CURKENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PC7/US00/04414
PRIOR APPLICATION NUMBER: W5 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: W5 60/146,222
PRIOR PELICATION NUMBER: PC7/US99/20594
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
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o. US20030049621A1
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Filvaroff, Ellen
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Publication No. US20030049621A.
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bottetein, David
APPLICANT: Bestevers, Luc
APPLICANT: Eaton, Dan L.
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Matches 15; Conservative
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Gao, Wei-Qiang
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                                                   FRIOR APPLICATION NUMBER: PCI/0539/21030
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-12-02
FRIOR APPLICATION NUMBER: PCT/US99/3091
FRIOR FILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-06
FRIOR APPLICATION NUMBER: PCT/US99/3091
FRIOR FILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-07
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Sequence 229, Application US/09903749A
Publication No. US20030045693A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Paoni, Nicholas F
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
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Gao, Wei-Qiang
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/21547
RESULT 1156
US-09-904-556-229
; Sequence 229, Application US/09904956
; Publication No. US20030049622A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
noritCANT: Botstein, David
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF THE SOURCE: 2000-09-18
REIOR APPLICATION NUMBER: 05/06/143,048
REIOR APLICATION NUMBER: 06/04/14,048
REIOR PELLON FORTE: 1999-07-28
REIOR APPLICATION NUMBER: 06/0146,222
REIOR APPLICATION NUMBER: PCT/US99/20304
REIOR PELLOR DATE: 1999-00-15
REIOR PELLOR DATE: 1999-00-15
REIOR PELLOR DATE: 1999-10-20
REIOR PELLOR DATE: 1999-10-20
REIOR REILOR DATE: 1999-11-20
REIOR PELLOR DATE: 1999-11-20
REIOR REILOR DATE: 1999-11-30
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                                                         Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/004,956
CURRENT FILING DATE: 2001-07-12
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-09-09-09
PRIOR PILING DATE: 1999-09-09-09
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13 PRIOR APPLICATION WOMBER: PCT/05/2213
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ 1D NOS: 423
SEQ 1D NO 229
LENGTH: 18

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1101 GCTGTCCTCAGGGGAG 1116

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and Transmembrane Polypeptides and Nucleic
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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                                       PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Filvaroff, Ellen
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,736
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR PLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07-26
PRIOR PLING DATE: 1999-07-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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                                                                                                                                             0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02; tive 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PILING DATE: 1999-10-05
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Matches 15; Conservative
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Gao, Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File REPERRORS: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,943
CURRENT FILING DATE: 2001-07-11
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                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 99/665,350
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 1909-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-09-09
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-13
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/28214
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Publication No. US20030054351A1
GENERAL INFORMATION:
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Desnoyers, Luc
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APPLICANT:
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US-09-907-794-229
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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... LOATION NUMBER: PCT/US99/30911
... LLICATION NUMBER: PCT/US99/30999
... PRIOR PILING DATE: 1999-12-20
... PRIOR PLILING DATE: 2000-01-05
... NUMBER OF SEQ ID NOS: 423
... SEQ ID NO 229
... LENGTH: 19
                                             PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-01-15
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR FLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
PRIOR PRILING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
                           ION NUMBER: US 60/146,222
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Publication No. US20030054349A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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FILING DATE: 1999-07-26
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20949
PRIOR APPLICATION NUMBER: PCT/US99/2094
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CURRENT APPLICATION NUMBER: US/09/907,925
CURRENT FILING DATE: 2001-07-17
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                            Sequence 229, Application US/09907925
Publication No. US20030054352A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                             1101 GCTGTCCTCAGGGGAG 1116
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-02-2
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
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OR APPLICATION NUMBER: PCT/USO0/04414
OR APPLICATION NUMBER: PCT/USO0/04414
OR PILING DATE: 2000-02-22
OR PILING DATE: 1999-07-07
OR PILING DATE: 1999-07-07
OR PILING DATE: 1999-07-26
OR APPLICATION NUMBER: US 60/145,698
OR PILING DATE: 1999-07-28
OR PILING DATE: 1999-07-28
OR PILING DATE: 1999-09-08
OR PILING DATE: 1999-09-08
OR PILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/2054
OR PILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/2094
OR PILING DATE: 1999-09-18
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CURRENT APPLICATION NUMBER: US/09/904,462
CURRENT PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
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Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoni, Nicholas F.
                                                                                                                         Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                            Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                               PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1990-11-05
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APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 229, Application US/09903520 Publication No. US20030054401A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
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Eaton, Dan L.
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PPLICANT: Tumas, Daniel
PPLICANT: Tumas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
PPLICANT: Wood, William, I.
PPLICANT: Mood, Milliam, I.
PPLICANT: Mood, Milliam, I.
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                           , OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-907-925-229
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CURRENT FILING DATE: 2001-07-10
  PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Publication No. US20030054400A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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ilvaroff, Ellen
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                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Gerber, Hanspeter
Gerritsen, Mary B
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aoni, Nicholas F.
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Hillan, Kenneth,
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Wood, William, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PLICATION NUMBER: US/09/905.056

CURRENT FILING DATE: 2000-02-22

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-09

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-29

PRIOR PELING DATE: 1999-10-29

PRIOR PELING DATE: 1999-10-30

PRIOR PELING DAT
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Oligonucleotide probe
19.09-908-056-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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; Sequence 229, Application US/09909064
; Publication No. US20030059772A1
                                                                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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                                                                                                                                                       aoni, Nicholas F.
                                            lljavin, Ivar J.
Iather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
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                                                         PRIOR PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-05
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
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PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR PLING DATE: 1999-13-09
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-06
PRIOR PLING DAT
                                    CION NUMBER: PCT/US00/04414
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Grimaldi, Christopher J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Forgy, Sherman
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ORGANISM: Artificial Sequence
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Gerber, Hanspeter
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RESULT 1166
US-09-904-553-229
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CANT: Wood, William, I.
OP INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
JOTHER INFORMATION: Oligonucleotide probe
US-09-909-064-229
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RRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,522

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PILING DATE: 1999-12-0

PRIOR PILING DATE: 1999-12-0
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CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
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Ashkenazi, Avi
Botstein, David
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APPLICANT: Tumas, Dannel,
APPLICANT: Tumas, Dannel,
APPLICANT: Tumas, P. Mickey
APPLICANT: Wool, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US/09/904.553
CURRENT FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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Query Match

0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                                                      sequence 229, Application US/09904553; Publication No. US20030659828A1
GENERAL INFORMATION: APPLICANT: GENERAL INC.
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Grimaldi, Christopher J.
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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TANT: Roy, Margaret Ann
Stewart, Timothy A.
PANT: Stewart, Timothy A.
PANT: Tumas, Daniel
CANT: William, P. Mickey
CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Acids Encoding the Same
                                                            PRIOR FILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21547
PRIOR PELICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1990-12-20
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Grimaldi, Christopher J.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary B.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                    FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-553-229
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/905,381

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US/08/04414

PRIOR APPLICATION NUMBER: PCT/USO0/04414

PRIOR APPLICATION NUMBER: US 00/143,048

PRIOR FLING DATE: 2000-02-22

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PLING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222
                 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
PRIOR APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229, Application US/09905381 Publication No. US20030059829A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Ching
Gerber, Hanapeter
Gerritsen, Mary E.
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBYCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,348
CURRENT FILING DATE: 2001-07-13
RIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-36
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-20
                           Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                               Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams, P. Mickey
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                       Pan, James
Paoni, Nicholas F.
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APPLICANT:
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FILE REPERBUCE: 10466-14

CURRENT APPLICATION NUMBER: 09/665,350

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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US-09-905-348-229
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ATITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
                                                                                                                                                                             0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02; tive 0; Mismatches 1; Indels
                                                       FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-905-088-229
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20946
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 229, Application US/09907575
Publication No. US20030073079A1
GENERAL INFORMATION:
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Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                  1101 GCTGTCCTCAGGGGAG 1116
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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TYPE: DNA ORGANISM: Artificial Sequence
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Gerritsen, Mary E
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Mather, Jennie P.
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                                                                                                                                                                          Query Match 0.47
Best Local Similarity 93.87
Matches 15; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Gao, Wei-Qiang
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
                           Application US/09905088
5. US20030073077A1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gaps

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APPLICANT: KOY, MAIGHEL AND
APPLICANT: Stewart. Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Deniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPREMENT: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,759
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PRILING DATE: 1999-07-28
PRIOR RELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PRILING DATE: 1999-09-13
PRIOR PRILING DATE: 1999-09-13
                                                                    Score 14.4; DB 1; Length 18;
Pred. No. 7.7e+02;
0; Mismatches 1; Indels
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-12-02
; OTHER INFORMATION: oligonuclectide probe US-09-905-075-229
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US-00-302.759-229
Sequence 229, Application US/09902759
; Publication No. US20030077654A1
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Mather, Jennie P.
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,075
CURRENT FILING DATE: 2001-07-13
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                   PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
PRIOR RILING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Grimaldi, Christopher J.
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NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Stewart, Timothy A.
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ilvaroff, Ellen
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illan, Kenneth, J
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Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Artificial Sequence
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Tumas, Daniel
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                            PRIOR AFFLING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/2854
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                                                      FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
                                           FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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b. US20030082541A1
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Grimaldi, Christopher J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,634
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: oligonucleotide probe
US-09-902-759-229
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                   PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PAPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: "Milliams, Daniel, Baniel, Parkey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, D. Mickey
TITLE OF INVENTION: Acids Enceding the Same
TITLE OF INVENTION: Acids Enceding the Same
FILE REPRENCE: 10466-11 (1979) 1979
CURRENT APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/2034
PRIOR APPLICATION NUMBER: PCT/US99/2034
PRIOR FILING DATE: 1999-00-12
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR APPLICATION NUMBER: PCT/US99/2091
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PRIOR APPLICATION NUMBER: PCT
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
   Godowski, Paul J.
Grimaldi, Christopher J.
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ORGANISM: Artificial Sequence
                                                                                                                                             Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                           PPLICANT
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CTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-713-229
FILE REPREMENT: 1046-14
CURRENT PAPLICATION NUMBER: US/09/902,713
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1000-10-5
PRIOR PILING DATE: 1000-10-5
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PRIOR PILING DATE: 1000-10-5
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; Sequence 229, Application US/09907979
; Series Publication No. US2003082542A1
; GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-903-925-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-04
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
PLENGTH: 18
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FILING DATE: 1999-10-05
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US-09-906-760A-229
; Sequence 229, Application US/09906760A
                                                                                                                                     Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                                                Nicholas F
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,615
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              Application US/09902615
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Publication No. US20030096233A1
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Grimaldi, Christopher J.
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Grimaldi, Christopher J.
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
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Gao, Wei-Qiang
Gerber, Hanspeter
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ORGANISM: Artificial Sequence
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ilvaroff, Ellen
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Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
                                       US20030092002A
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Paoni, Nicholas F.
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Botstein, David
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Eaton, Dan L.
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                                                       GENERAL INFORMATION
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APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thuns, Daniel
APPLICANT: Williams, Daniel
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,823
CURRENT FILING DATE: 2001-07-11
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
; OTHER INFORMATION: oligonucleotide probe US-09-906-760A-229
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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RRICK APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229, Application US/09903823
Publication No. US20030104381A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: A Secreted and Transmembrane Polypeptides and Nucleic
ITILE REFERENCE: 10466-14
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR PRIOR DATE: 1999-12-03
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CURRENT APPLICATION NUMBER: US/09/906,760A
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
ong, Sherman
   tion No. US20030096340A1
INFORMATION:
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                     Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary E
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                      PRIOR FILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
            PCT/US99/21090
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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ORGANISM: Artificial Sequence
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
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Gao, Wei-Qiang
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, OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-823-229
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CURRENT APPLICATION NUMBER: US/09/907,652
CURRENT FILING DATE: 2002-01-16
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1099-07-07
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ. ID NOS: 423
; SEQ. ID NO 229
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FILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 229, Application US/09907652
Publication No. US20030104469A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-907-652-229
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,979
CURRENT PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-00-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR AFPLICATION NUMBER: PCT/US99/28113
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-10
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Ferrara, Napoleone
Filvaroff, Ellen
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ORGANISM: Artificial Sequence
FEATURE:
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Botstein, David
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-905-125-229
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                                                CURRENT FILING DATE: 2001-07-10

PRIOR PELING DATE: 2001-07-10

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PAPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR PILING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Publication No. US20030113718A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bestelin, David
APPLICANT: Beston, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT PEDLICATION NUMBER: US/09/906,815A

CURRENT PILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US(0414)

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20949

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28655
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
                                     Sequence 229, Application US/09906815A Publication No. US20030113838A1 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ACAGG ELICACALING COURRENT APPLICATION NUMBER: US/09/905,125
CURRENT APPLICATION NUMBER: US/09/905,125
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/3091
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-07
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                          Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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                             PRIOR APPLICATION NUMBEK: FL, CL, CL, PRIOR PLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Publication No. US20030130489A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Williams, P. Mickey
Wood, William, I.
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ORGANISM: Artificial Sequence
FEATURE:
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Roy, Margaret Ann
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
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APPLICANT:
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                          Gaps
) ORGANISM: Artificial Sequence; FEATURE: COTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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                                                                                                                                                                Query Match
0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/905,449
CURRENT FILING DATE: 2000-09-18
RRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28313
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 229, Application US/09905449 Publication No. US20030129592A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                   PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR RPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER PEG ID NOS: 423
LENGTH: 18
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CURRENT FILING DATE: 2001-09-18
PRICA APPLICATION NUMBER: PCT/USO0/04414
PRICA FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
              APPLICATION NUMBER: PCT/US99/30095
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 229, Application US/09904838 Publication No. US20030148370A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Hillan, Kenneth, J
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Mather, Jennie P.
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Best Local Similarity 93.8%
Matches 15; Conservative
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APPLICANT: Ashkenazi, Avi
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Gao, Wei-Qiang
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APPLICANT:
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APPLICANT: BOY, Margaret Ann.
APPLICANT: Stewart, Tinothy A.
APPLICANT: Stewart, Tinothy A.
APPLICANT: Stewart, Tinothy A.
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/904,992
CURRENT FILING DATE: 1000-02-20-01-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/2169
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2869
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2864
PRIOR APPLICATION NUMBER: PCT/US99/2864
PRIOR APPLICATION NUMBER: PCT/US99/2865
PRIOR APPLICATION NUMBER: PCT/US99/28655
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                                                                                          Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-806-229
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 229, Application US/09904992
Publication No. US20030135025A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                                                                                                                                                                                                             1101 GCTGTCCTCAGGGGAG 1116
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-906-777-229
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illarity 93.8%; Pred. No. 7.7e+02;
Conservative 0; Mismatches 1;
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PRIOR PILING DATE: 1939-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR FILING DATE: 1939-12-20
PRIOR FILING DATE: 1939-12-20
PRIOR PLILING DATE: 1939-12-20
PRIOR PLILING DATE: 1939-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
                                                                            CUCREMY AFFILMENT NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
                              FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,777
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
FEATURE:
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Ashkenazi, Avi
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Eaton, Dan L
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Best Local Similarity
Matches 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Discription of Artificial Sequence: Synthetic in OTHER INFORMATION: Oligonucleotide probe US-09-904-838-229
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
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Publication No. US20030148371A1
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Grimaldi, Christopher J.
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Stewart, Timothy A
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ilvaroff, Ellen
ong, Sherman
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ORGANISM: Artificial Sequence
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Gerber, Hanspeter
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Hillan, Kenneth,
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Mather, Jennie P
Pan, James
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Eaton, Dan L.
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Length 18;
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IIITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PLILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: PCT/USO0/04114
PRIOR PELICATION NUMBER: PCT/USO0/04114
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PLILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/904,532
PRIOR ADDITOR
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-11-30
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FILING DATE: 1999-11-29
                                                   Sequence 229, Application US/09904532
Publication No. US20030152922A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Desneyers, Luc
APPLICANT: Bateain, David
APPLICANT: Baton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Tumas, Daniel
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Filvaroff, Ellen
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Mather, Jennie P.
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APPLICAWY: Williams, Daniel
APPLICAWY: Williams, Deniel
APPLICAWY: Williams, Deniel
APPLICAWY: Wood, Williams, I
TITLE OF INVENTION: Acide Encoding the Same
FILE REPRENCETION: Acide Encoding the Same
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT PILLING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/00/414
PRIOR APPLICATION NUMBER: OF 00/145,698
PRIOR APPLICATION NUMBER: US/01/46,222
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-07-38
PRIOR PILLING DATE: 1999-07-18
PRIOR PILLING DATE: 1999-07-18
PRIOR PILLING DATE: 1999-07-18
PRIOR PILLING DATE: 1999-01-13
PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-11-29
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                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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Paoni, Nicholas F.
Gerritsen, Mary E.
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Best Local Similarity
Matches 15; Conserva
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229

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PRIOR APPLICATION NUMBER: PCT/US99/28564
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and-Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,766
                                                                                                                                               Gaps
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                                                                                                             Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                              ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-904-532-229
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RIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                     Sequence 229, Application US/09904766 Publication No. US20030152999A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Tjavin, Ivar .
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                           TYPE: DNA
ORGANISM: Artificial Sequence
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Beston, Luc
APPLICANT: Eaton, Dan L.
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Tumas, Daniel
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           LENGIH: 18
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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Pred. No. 7.7e+02;
0; Mismatches 1;
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CURRENT PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Grimaldi, Christopher J.
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acide Encoding the Same
FILE REPERBRÜCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,877A
CURRENT APPLICATION NUMBER: US/09/904,877A
CURRENT APPLICATION NUMBER: US/09/904,877A
CURRENT APPLICATION NUMBER: US/01/43,048
PRIOR APPLICATION NUMBER: US/01/45,698
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US/01/45,698
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
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Publication No. US20030187238A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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ORGANISM: Artificial Sequence
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                          PRIOR APPLICATION NUMBER: PCI/US99/20394
PRIOR PLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
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PRIOR PELING DATE: 1999-11-29
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PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
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PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-04
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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; Sequence 229, Application US/09904877A
; Publication No. US20030186358A1
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A
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Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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SEQ ID NO 229
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-8
PRIOR PELING DATE: 1999-07-8
PRIOR PELING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, P.
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                            Gerritsen, Mary E.
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Mather, Jennie P.
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Filvaroff, Ellen
                                         Song, Sherman
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                          APPLICANT: Roy, Margaret Ann
APPLICANT: Sewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACIDS ENCOLLING LIE SCRINGERINGS: 10466-14
CURRENT PELLING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILLING DATE: 1999-07-28
PRIOR FILLING DATE: 1999-07-28
PRIOR FILLING DATE: 1999-09-08
PRIOR FILLING DATE: 1999-09-13
PRIOR FILLING DATE: 1999-09-13
PRIOR FILLING DATE: 1999-09-13
PRIOR FILLING DATE: 1999-09-13
PRIOR FILLING DATE: 1999-09-15
PRIOR FILLING DATE: 1999-09-15
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PRIOR PRILING DATE: 1999-11-29
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-07
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                      Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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1101 GCTGTCCTCAGGGGAG 1116

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Ferrara, Napoleone

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APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14

FILE REFERENCE: 10466-14

FILE REPERENCE: 10466-18

FRICH APPLICATION NUMBER: 09/665,350

FRICH APPLICATION NUMBER: 05/6143,048

FRICH APPLICATION NUMBER: DC/US09/04414

FRICH APPLICATION NUMBER: US 60/145,698

FRICH APPLICATION NUMBER: US 60/146,222

FRICH APPLICATION NUMBER: PCT/US99/20944

FRICH APPLICATION NUMBER: PCT/US99/20944

FRICH APPLICATION NUMBER: PCT/US99/21090

FRICH APPLICATION NUMBER: PCT/US99/21090

FRICH APPLICATION NUMBER: PCT/US99/21090

FRICH APPLICATION NUMBER: PCT/US99/21090

FRICH FILING DATE: 1999-09-15

FRICH FILING DATE: 1999-09-15

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FRICH FILING DATE: 1999-09-15
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APPLICANT:
APPLICANT:
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APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,728

CURRENT APPLICATION NUMBER: US/09/907,728

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US/05/5350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28544

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR PILING DATE: 1999-12-06
                                                                                                                                                                                                     Sequence 229, Application US/09907728
Publication No. US20030190611A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Ashkenazi, Avi
APPLICANT: Destean, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Gao, Wei-Qiang
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Hillan, Kenneth, J.

Pan, James

Gurney, Austin L. Kljavin, Ivar J. Mather, Jennie P.

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Gaps
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                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-728-229
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER 0F SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Publication No. US20030211568A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Best Local Similarity 93.8
Matches 15; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICATION NUMBER: US 60/143,048
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Kljavin, Ivar J.
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APPLICANT: Sewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-805-229
                                           PRIOR FILING DATE: 1999-10-5

PRIOR PELICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR PELICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR PLING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-20

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PRIOR PILING DATE: 1999-12-30
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PRIOR FILING DATE: 2000-02-22
  APPLICATION NUMBER: PCT/US99/23089
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ilvaroff, Ellen
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Hillan, Kenneth, J
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Mather, Jennie P.
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                               FILING DATE: 1999-10-05
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-03
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PRIOR PLING DATE: 1999-11-20
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PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Botstein, David
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Matches 15; Conservative
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APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT PAPLICATION NUMBER: US/09/908,576
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-03-18
PRIOR FILING DATE: 2000-03-18
PRIOR PELICATION NUMBER: CG/U43,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
FOTHER INFORMATION: Oligonucleotide probe
78-09-908-576-229
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Grimaldi, Christopher J.
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                         Ferrara, Napoleone
Filvaroff, Ellen
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Mather, Jennie P.
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Jao, Wei-Qiang
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                                                                                                                                                               APPLICANT: Stewart, Timothy A. APPLICANT: Thuas, Daniel APPLICANT: Thuas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,722A
CURRENT FILING DATE: 2001-07-16
PRIOR PELING DATE: 2001-07-16
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 19
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Mather, Jennie P.
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; . Gaps ö Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels ; Sequence 24, Application US/10282958 ; Publication No. US20030110519A1 1101 GCTGTCCTCAGGGGAG 1116 GCTGTCCACAGGGGAG 18 GENERAL INFORMATION RESULT 1203 US-10-282-958-24 ð

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Sequence 229, Application US/09908576
Publication No. US20040005553A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi

RESULT 1202 US-09-908-576-229

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APPLICANT: KOY, MAGRATE AND
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFRENCE: P16182265
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-013
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR F
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Publication No. US20030185846A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                      Paoni, Nicholas F.
                                                                                                                                        Roy, Margaret Ann
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                                        lather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      COUNTER: USA

COUNTER READABLE FORM:

MEDIUM TYPER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/282,958

FILING DATE: 28-Oct-2002

CLASSIFICATION NUMBER: US/09/349,755

FILING DATE: 08-Jul-1999

APPLICATION NUMBER: US/09/042,780

FILING DATE: 08-Jul-1999

APPLICATION NUMBER: US/09/042,780

FILING DATE: 04-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A: Hanley

REGISTRATION NUMBER: 33,505

REFERENCE/DOCKET NUMBER: MNI-032CP

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ. DNO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: nucleic acid
; STRANDEDNESS: single
; POPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-282-958-24
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Publication No. US20030180312A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Blen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Matches 15; Conservative
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US-10-299-976-229
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Pred. No. 7.7e+02;
0; Mismatches 1; Indels
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PRIOR PELLING DATE: 2000-02-22
PRIOR PELLING DATE: 2000-02-22
PRIOR PELLING DATE: 1090-07-07
PRIOR PILLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-07-08
PRIOR PILLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR FILING DATE: 1996-01-12
PRIOR APPLICATION NUMBER: US 60/000,951
PRIOR FILING DATE: 1995-07-07
PRIOR FILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 2285
SOFTWARE: Patentin version 3.0
SEQ ID NO 1134
LENGTH: 18
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o. US20030211576A1
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Stewart, ...
Stewart, ...
                                                                                                                                                                                                                                 TYPE: RNA
COCCANISM: Mus musculus
US-10-440-850-1134
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Publication No. US20030207837A1

GENERAL INFORMATION:

APPLICANT: Riboryme Pharmaceuticals, Inc.

APPLICANT: Stinchcomb, Dan

APPLICANT: Jarvis, Thale

APPLICANT: Missinger, Jim

TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rever
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/299, 937
CURRENT APPLICATION NUMBER: US/10/299, 937
CURRENT APPLICATION NUMBER: US/10/299, 937
CURRENT APPLICATION NUMBER: PCT/USOO/04414
PRIOR FILING DATE: 2000-02-2
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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THER REPERSENCE: 250/130 (MRHBOD-900-A)
CURRENT APPLICATION NUMBER: US/10/440,850
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US/9/650,012
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: US 08/585,684
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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                               Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                            Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                 Fumas, Daniel
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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US-10-440-850-1134/c
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                    PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Oligonucleotide probe
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CURRENT APPLICATION NUMBER: US/10/448,923
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PCT/USO0/04114
PRIOR APPLICATION NUMBER: PCT/USO0/0414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/23089
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Publication No. US20030225253A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Mather, Jennie P
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Matches 15; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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    PRIOR FILING DATE: 1999-015
PRIOR FILING DATE: 1999-015
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: oligonucleotide probe US-10-448-923-229
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Pred. No. 7.7e+02;
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PCT/US99/21547
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Grimaldi, Christopher J.
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%;
Best Local Similarity 93.8%;
Matches 15; Conservative
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Kljavin, Ivar J.
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Filvaroff, Ellen
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Pan, James
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Botstein, David
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Eaton, Dan L.
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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Matches 15; Conserv
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US-10-425-447-229
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                           PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
ROBERTOR SEQ ID NOS: 423
ENGRH: 18
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 229, Application US/10448713; Publication No. US20040006211A1; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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                   FILING DATE: 1999-09-15
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 93.8<sup>1</sup>
Matches 15; Conservative
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Eaton, Dan L.
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APPLICANT:
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CURRENT FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 18
                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423 SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLING DATE: 1999-09-13
PRIOR PPLING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-05
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Publication No. US20040018497A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 39780-1618P2C78C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-10-215-371-229
                                             TITLE OF INVENTION: ACIDE ELECTRING CONTROLL OF THE REFERENCE: P1618P2C83
CURRENT APPLICATION NUMBER: US/10/215,371
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 99/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1998-09-10
PRIOR FILING DATE: 1997-10-17
SEQ ID NO 229
LENGTH: 18
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CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: 09/909,064
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 07/0500/0414
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT PAPLICATION NUMBER: US/10/425,447
CURRENT PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
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NUMBER OF SEQ ID NOS: 423
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. Sequence 229, Application US/10215371
. Publication No. US20040137561A1
. GENERAL INFORMATION:
                                                             Godowski, Paul J.
Grimaldi, Christopher J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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      Gerritsen, Mary E.
                                                                                                                                 Gurney, Austin L.
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APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin I
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Wood, William I
Yuan, Jean
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US-10-251-117-712
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APPLICANT: Egeland, Janice A.
APPLICANT: Beland, Janice A.
APPLICANT: Beland, Janice A.
APPLICANT: Paul, Steven
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITLE OF INVENTION: Susceptibility and Resistance Genes for TITLE OF INVENTION: Bipolar Affective Disorder
FILE REPRENCE: 015280-24811005
CURRENT PAPLICATION NUMBER: US/09/881,012
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US/09/175,158
PRIOR APPLICATION NUMBER: US 60/062,924
PRIOR FILING DATE: 1997-10-20
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                                             PRIOR FILING DATE: 1998-09-17
PRIOR PELING DATE: 1998-09-17
PRIOR PELING DATE: 1998-09-16
PRIOR PELING DATE: 1998-09-16
PRIOR PILING DATE: 1998-06-04
PRIOR PELING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/066,770
PRIOR APPLICATION NUMBER: 60/066,710
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-12
SEQ ID NOS: 423
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 230
LENCTH: 19
FILING DATE: 2000-02-22
APPLICATION NUMBER: PCT/US98/19437
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Publication No. US20020192655A1
GENERAL INFORMATION:
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; Publication No. US20030013669A1
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ORGANISM: Artificial Sequence
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hes 15; Conserva
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US-09-754-066-6/c
                                                                                                                                                                                                                                                                                                                                            LENGTH: 18
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Matches
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Sequence 712, Application US/10251117
Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MBHB02-466-A)
CURRENT APPLICATION NUMBER: US/10/251,117
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GENERAL INFORMATION:
APPLICANT: BURCOGLU, ARSINUR
TITLE OF INVENTION: METHOD OF TREATING HIV INFECTION
AND RELATED SECONDARY INFECTIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02939.04541
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/754,066
FILING DATE: 05-03n-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/848,013
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-88-1992
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-88-1992
APPLICATION NUMBER: 07/48,277
FILING DATE: 21-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 10/163,552
PRIOR PILING DATE: 2002-06-06
PRIOR APPLICATION UNMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 09/916,466
                                                                                                                                                                         ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 93.8
Matches 15; Conservative
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sinA sense r:
US-10-244-647-370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.4%; Score 14.4; DB 1; Length 19; Best Local Similarity 62.5%; Pred. No. 8.1e+02; Matches 10; Conservative 5; Mismatches 1; Indels
Short Interfering Nucleic Acid (siNA)
                     FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
FRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SEQ ID NO 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 380, Application US/10244647; Publication No. US20030206887A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA ORGANISM: Artificial Sequence
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RAM Interference Mediated Inhibition of Epidermal Growth Factor R
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION UNMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-468-4)
FRIOR PELING DATE: 2002-06-06
FRIOR PELING DATE: 2002-06-06
FRIOR PELING DATE: 2002-06-06
FRIOR PELING DATE: 2001-07-25
FRIOR PELING DATE: 2001-07-25
FRIOR PELING DATE: 2001-07-25
FRIOR PELING DATE: 2001-07-25
FRIOR PELING DATE: 2001-06-06
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FRIOR PILING DATE: 2001-07-25
FRIOR PILING DATE: 2001-07-26
FRIOR PILING DATE: 2001-07-25
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Publication No. US20030206887A1
Publication No. US20030206887A1
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
                                                                                                                                                                                                                                                                                                             Target sequence/siNA sense
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                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-251-117-712
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: US 60/296,249
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
SOFTWARE: Patentin version 3.0
SEQ ID NO 712
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1019, Application US/10251117; Publication No. US20030170891A1
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                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.8°
Matches 15; Conservative
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LENGTH: 19
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Best Local Similarity 62.5%; Pred. No. 8.1e+02;
Matches 10; Conservative 5; Mismatches 1
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.8°
Matches 15; Conservative
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US-10-244-647-1016/c
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                                                                                                                                              APPLICANT: Nationary Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: SEARCH Interfering Nucleic Acid (sinA)
FILE REPERBENCE: 400/060 (MBHB02-1000)
CURRENT ELING DATE: 2003-04-14
FRIOR PILING DATE: 2003-04-14
FRIOR FILING DATE: 2002-0-20
FRIOR FILING DATE: 2002-0-3-26
FRIOR FILING DATE: 2002-0-6-08
FRIOR FILING DATE: 2001-0-6-08
FRIOR FILING DATE: 2001-0-0-6
FRIOR FILING DATE: 2001-0-6-08
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morisaey, David
APPLICANT: Morisaey, David
APPLICANT: Morisaey, Javid
APPLICANT: Morisaey, Javid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
TITLE OF INVENTION: Short Interferring Nucleic Acid (siNA)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
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PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR PILING DATE: 2002-03-26
PRIOR PILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Parentin Version 3.0
LENGTH: 19
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Sequence 415, Application US/10244647
Publication No. US20030206887A1
                                 Application US/10244647
O. US20030206887A1
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

ITTLE OF INVENTION: Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)

FILE REPERENCE: 400/060 (MBHBO2-1000)

CURRENT FILING DATE: 2003-04-14

FRIOR FILING DATE: 2002-02-20

FRIOR PELICATION NUMBER: US 60/393,924

FRIOR FILING DATE: 2002-03-26

FRIOR FILING DATE: 2001-06-08

FRIOR FILING DATE: 2001-06-08
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrismey, David
APPLICANT: Mosrismey, David
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/060 (MEHBO2-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2001-06-08
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; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-244-647-1016
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1016, Application US/10244647; Publication No. US20030206887A1; GENERAL INFORMATION:
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Publication No. US20030206987A1
                                                                                              2776 TTCCGGAAACTAGTGT 2791
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Gaps

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Length 19; 1; Indels

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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r US-10-665-951-1042
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BESULT 12.2

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BEDICANT: Birna Therapeutics, Inc.

APPLICANT: Birna Therapeutics, Inc.

APPLICANT: Beavo, Pamela

TITLE OF INVENTIOR: ALT Interference Mediated Inhibition of Vascular Endothelial

TITLE OF INVENTIOR: Book and a thereference Mediated Inhibition of Vascular Endothelial

TITLE OF INVENTIOR: Book and a thereference Mediated Inhibition of Vascular Endothelial

TITLE OF INVENTIOR: Book and a thereference Mediated Inhibition of Vascular Endothelial

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TITLE OF INVENTIOR: BOOK and a thereference Mediated Inhibition of Vascular Endothelial

TITLE OF INVENTIOR: BOOK and a thereference Mediated Inhibition of Vascular Endothelial

FILIC REPRENCE: 400/13 (MEHBO: 742-79.742-7)

FRIOR APPLICATION NUMBER: US 10/665,951

CURRENT FILING DATE: 2002-01-09.18

FRIOR PELICOR TILL OF DATE: 2002-10-20

FRIOR APPLICATION NUMBER: US 60/393,796

FRIOR PELICOR TILL OF DATE: 2002-11-37

FRIOR APPLICATION NUMBER: US 60/393,796

FRIOR PELICOR TILL OF DATE: 2002-11-37

FRIOR PELICOR TILL OF DATE: 2002-02-20

FRIOR PELICOR TILL OF DATE: 2002-03-31

FRIOR PELICOR TILL OF DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-244-647-1061
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1;
                          PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-03-26
PRIOR PILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Patentin version 3.0
ENGTH: 19
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; Sequence 1057, Application US/10244647
; Publication No. US2003026887A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOEXIGEN, David
APPLICANT: MCSWiggen, James
APPLICANT: WA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TILLE REFERENCE: 400/060 (MBH02-1000)
CURRENT FILING DATE: 2003-04-4, 647
CURRENT FILING DATE: 2003-04-4, 647
CURRENT FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524-08
NUMBER OF SEQ ID NOS: 1524-08
LENGTH: 19
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: Morrissey, David
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/0500 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-244-647-1026
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0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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; Sequence 1061, Application US/10244647
; Publication No. US20030206887A1
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                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
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US-10-244-647-1057/c
SEQ 1D NO 1026
                                     LENGTH: 19
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1998 CAAGCAGCTGGTGGAG 2013
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SEQ ID NO 1734
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leconid
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION NUMBER: US 10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-07-29
PRIOR FILING DATE: 2003-07-29
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-01-10-4
PRIOR FILING DATE: 2002-01-10-4
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR PRILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/358,780
PRIOR PRILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/358,780
PRIOR PRILING DATE: 2002-02-20
PRIPARE PRILING DATE: 2002-02-20
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Publication No. US20040138163A1
GENERAL INFORMATION
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
IITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
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                                          1; Indels
   Similarity 81.2%; Pred. No. 8.1e+02; 13; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1366, Application US/10665951; Publication No. US20040138163A1; GENERAL INFORMATION:
                                                                                                                    1609 AAGTGCATCCACAGGG 1624
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                    RESULT 1228
US-10-665-951-1366/c
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TITLE OF INVENTION: Gene Procession and Vaccular Endethalial Growth Factor Receptor FITLE OF INVENTION: Gene Procession and Vaccular Endethalial Growth Factor Receptor FITLE OF INVENTION: Gene Procession and Vaccular Endethalial Growth Factor (1988)

FITLE SEREBBECH: 4001,100 (665.272)

CURRENT APPLICATION NUMBER: 107/10/665.581

FRICE APPLICATION NUMBER: 107/10/665.581

FRICE APPLICATION NUMBER: FOTUS 03/050.20

FRICE APPLICATION NUMBER: FOTUS 03/050.20

FRICE APPLICATION NUMBER: 107/06/33/148

FRICE APPLICATION NUMBER: 107/06/33/148

FRICE APPLICATION NUMBER: 107/06/34/148

FRICE APPLICATION NUMBER: 10
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N: Methods for Detecting, Grading or Monitoring an H. pylori Infec
EXT-048
                                                                                                                                                                   Gaps
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                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 8.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salmons, Brian
APPLICANT: Salmons, Brian
APPLICANT: Goller, Sabine
APPLICANT: Klein, Dieter
TITLE OF INVENTION: Targeted Integration Into Chromosomes
TITLE OF INVENTION: Using Retroviral Vectors
FILE RPEREMENT 216.2005-000
CURRENT APPLICATION NUMBER: US/09/752,110A
CURRENT FILING DATE: 2000-12-29
FRIOR APPLICATION NUMBER: PA 1998 01016
FRIOR FILING DATE: 1999-06-30
FRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGIN: AND APPLICANTON NUMBER: PA 1998 01016
FRIOR FILING DATE: 1998-07-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 8.5e+02;
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Pred. No. 8.5e+02;
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Patent No. US20020110810A1
GENERAL INFORMATION:
FAPLICANT: Shuber, Anthony
TITLE OF INVENTION: Methods for Detecting,
FILE REPRENCE: EXT-048
CURRENT APPLICATION NUMBER: US/09/755,004
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
LENGTH: 20
LENGTH: 20
TYPE: DNA
ORGANIEM: Artificial sequence
                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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OTHER INFORMATION: APC forward primer
US-09-755-004-10
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; Patent No. US20010043921A1
                                                                                                                                                                                                               2814 TGTATATGGTATATA 2829
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STRANDEDNESS: single
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity
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US-09-755-004-10/c
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US-10-768-089-6
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            PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: ParentIn version 3.2
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10768089
Publication No. US20040138167A1
GENERAL INFORMATION:
APPLICANT: BURCOGLU, ARSINUR
TITLE OF INVENTION:
AND RELATED SECONDARY INFECTIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 8.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORRUTER: IBM Compatible
CORRUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
FILING DATE: O2-Feb-2004
CLASSIFICATION NUMBER: US/09/754,066
FILING DATE: 03-Feb-2001
APPLICATION NUMBER: US/09/754,066
FILING DATE: 05-Jan-2001
APPLICATION NUMBER: 08/848,013
FILING DATE: 04-FEB-1992
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-FEB-1992
APPLICATION NUMBER: 07/830,886
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 02939.04541
TELECOMMUICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPRAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998 CAAGCAGCTGGTGGAG 2013
                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
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FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 CAAGAAGCTGGTGGAG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-10-768-089-6/c
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; Sequence 14, Application US/09920671; Publication No. US20030083283A1; GENERAL INFORMATION:
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                    1060 GCGTCCATGAGCTCCA 1075
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                                                            5 GCATCCATCAGCTCCA 20
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Pinus taeda L.
US-09-232-785-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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Publication No. US20030004120A1

GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Mero, Pam
APPLICANT: Mero, Pam
APPLICANT: Mero, Pam
APPLICANT: Caarde, William A.
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION NUMBER: US/09/774,809
CURRENT APPLICATION NUMBER: 09/396,902
FRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-08-07

PRIOR FILING DATE: 1999-08-07

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 17
  Gaps
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Sequence 3262, Application US/09969373

Fatent No. US2002013382A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Roger J.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping FILE REFERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

WINBER OF SEQ ID NOS: 4593

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 8.5e+02; tive 0; Mismatches 1; Indels
  1; Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2338 TGTGTGTGTGTGCA 2353
                                          856 GAGGAGCTGGTGGAGG 871
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Matches 15; Conservative
  15; Conservative
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CORGANISM: Glycine max
US-09-969-373-3262
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  Matches
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION
FILE REFERENCE: RTS-0297
CURRENT APPLICATION NUMBER: US/09/920,671
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 91
LENGTH: 20
                                                                                                                                                                                                                                                                                               Length 20;
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1; Indels
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Pred. No. 8.5e+02;
0; Mismatches 1;
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Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide US-09-920-671-14
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Sequence 12, Application US/10374932

Sequence 12, Application US/10374932

Publication No. US20030235566A1

GENERAL INFORMATION:

APPLICANT: van de Winkel, Jan G.J.

APPLICANT: Schuuran, Janine

APPLICANT: Schuuran, Janine

APPLICANT: Badagaard, Ole

APPLICANT: Badagaard, Ole

APPLICANT: Badagaard, Ole

APPLICANT: Breteren, Arnout F.

APPLICANT: WINGER: US/10/374,932

CURRENT APPLICATION UNMBER: US/10/374,932

CURRENT PILING DATE: 2003-02-26

PRIOR APPLICATION NUMBER: US 60/314,731

PRIOR APPLICATION NUMBER: US 10/226615

PRIOR APPLICATION NUMBER: US 10/226615

PRIOR APPLICATION NUMBER: US 10/226615

PRIOR APPLICATION NUMBER: US 00.208-23

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 20
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Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
              CURRENT PELLING DATE: 2002-10-25
PRIOR PILLING DATE: 2002-10-25
PRIOR PILLING DATE: 2002-10-25
PRIOR FILLING DATE: 2001-10-25
PRIOR FILLING DATE: 2001-10-08
PRIOR FILLING DATE: 2001-11-08
PRIOR PILLING DATE: 2001-11-08
PRIOR PILLING DATE: 2001-11-08
PRIOR PILLING DATE: 2001-11-09
PRIOR PILLING DATE: 2001-11-09
PRIOR PILLING DATE: 2001-11-09
PRIOR PILLING DATE: 2001-12-04
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Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-374-932-12
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TITLE OF INVENTION: ATTENDED MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION FILE REFERENCE: RTS-0259
CURRENT APPLICATION NUMBER: US/09/967,669
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 88
LENGTH: 20
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| Sequence 38, Application US/10090011
| Publication No. US20030082810A1
| Publication No. US20030082810A1
| Publication No. US20030082810A1
| Publication No. US20030082810A1
| APPLICANT: Serup, Palle
| APPLICANT: Gradwohl Gerard
| TITLE OF INVENTION: Methods For Generating Insulin-Secreting
| TITLE OF INVENTION: Cells Suitable for Transplantation
| FILE REFERENCE: 6246-200-US
| CURRENT APPLICATION NUMBER: US/10/090,011
| CURRENT FILING DATE: 2002-226
| PRIOR APPLICATION NUMBER: US 60/271,474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 14.4; DB 1; Length 20; Best Local Similarity 93.8%; Pred. No. 8.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 363, Application US/10282174
Publication No. US20030224380A1
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                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-011-38
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LENGTH: 20
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Sequence 1, Application US/10425037

Sequence 1, Application US/10425037

Publication No. US20040054162A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Molecular Detection Systems Utilizing Reiterative Oligonucleotide
TITLE OF INVENTION: Synthesis
FILE REPERENCE: 2072.0010005
FILE REPERENCE: 2072.0010005
FILE REPERENCE: 2072.0010005
FRICK RAT PELICATION NUMBER: PT/US02/34419
FRICK APPLICATION NUMBER: US 09/984,664
FRICK APPLICATION NUMBER: US 09/984,664
FRICK APPLICATION NUMBER: US 09/984,664
FRICK FILING DATE: 2001-10-30
FRICK APPLICATION NUMBER: US 09/984,664
FRICK FILING DATE: 2001-10-30
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; Sequence 65, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-124-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
APPLICANT: van de Winkel, Jan G.J.
APPLICANT: van Dijk, Marcus Antonius
APPLICANT: Schuurman, Janine
APPLICANT: Gerritsen, Arnout F.
APPLICANT: Baadsgaard, Ole
APPLICANT: Petersen, Jorgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: P16DF2 Primer US-10-425-037-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1209 TGGGGAGGCTGCTTC 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 93.89
Matches 15; Conservative
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-379-741-12
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                                                                                                                                                                                                                                                                          OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10264958B
Publication No. US20040038224A1
GENERAL INFORMATION:
BAPLICANT: Hoffman, Hal
APPLICANT: Kolodner, Richard
TITLE OF INVENTION: TSOLated Cryopyrins, Nucleic Acid Molecules Encoding These, and UTITLE OF INVENTION: TSOLated Cryopyrins, Nucleic Acid Molecules Encoding These, and UTITLE OF INVENTION: TSOLated Cryopyrins, Nucleic Acid Molecules Encoding These, and UTITLE OF INVENTION: Thereof
FILE REFERENCE: LUD 5738.1 CIP (10209575)
CURRENT APPLICATION NUMBER: US60/327,728
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 18
LENGTH: 20
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93.8%; Pred. No. 8.5e+02;
trive 0; Mismatches 1; Indels
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                                                                                                                                                       APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTIERNSE OLIGONUCLEOTIDE
TITLE OF INVENTION: OF JNK PROTEINS
FILE REPERENCE: ISPH-0726
CURRENT PELLING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/774,809
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-04-07
PRIOR PRILING DATE: 1999-04-07
PRIOR PRILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: US 09/130,616
PRIOR FILING DATE: 1999-08-07
PRIOR PRILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 168
SENGTH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Synthetic Sequence US-10-345-4448-17
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ORGANISM: Artificial Sequence
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                         Publication No. US20040029823A1
GENERAL INFORMATION:
                                                                                                APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.8<sup>†</sup>
Matches 15; Conservative
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Matches 15; Conservative
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US-10-380-124-65/c
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US-10-264-958B-18
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2107 CCCAGCTCCAGCTCCT 2122
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                                                                                                     Conservative
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ORGANISM: H. sapiens
                                                   Query Match
Best Local Similarity
Matches 15; Conserv
              US-10-303-266-130
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TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15) FILE REFERENCE: GMI-024CP2
CURRENY APPLICATION NUMBER: US/10/379,741
CURRENY FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: US 60/314,731
PRIOR FILING DATE: 2001-08-23
PRIOR PAPLICATION NUMBER: US 10/226615
PRIOR FILING DATE: 2002-08-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 54, Application US/10303266;
Publication No. US20040101848A1
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Alexander H. Borchers
APPLICANT: Renneth W. Dobie
TITLE OF INVENTION: MODILATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
FILE REFERENCE: RTS-0426
CURRENT APPLICATION NUMBER: US/10/303,266
CURRENT APPLICATION NUMBER: US/10/303,266
NUMBER OF SEQ ID NOS: 157
ILENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
FILE REFERENCE: RTS-0426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-266-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/303,266
CURRENT FILING DATE: 2002-11-23
NUMBER OF SEQ ID NOS: 157
SEQ ID NO 130
LENGTH: 20
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US-10-303-266-130
; Sequence 130, Application US/10303266
; Publication No. US20040101848A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 GAGGAGCTGGTGGAGGC 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2107 CCCAGCTCCAGCTCCT 2122
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                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-10-379-741-12
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ORGANISM: H. sapiens
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                                                                                                                                                                                                                                                                                        TYPE: DNA
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  Length 20;
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; Sequence 155, Application US/10316243
; Publication No. US20040110147A1
; GENERAL INPORMATION:
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MOULATION OF BAF53 EXPRESSION
; FILE REFERENCE: RTS-0462
; CURRENT APPLICATION NUMBER: US/10/316,243
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 168
; SRQ ID NO 155
; LENGTH: 20
                                                                                                                                                                                                                     US-10-316-243-82
; Sequence 82, Application US/10316243
; Publication No. US20040110147A1
; Publication No. US20040110147A1
; GENERAL INFORMATION:
; APPLICANT: Renneth W. Dobie
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF BAF53 EXPRESSION
; FILE REFERENCE: RTS-0462
; CURRENT APPLICATION NUMBER: US/10/316,243
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 8: LENGTH: 20
0.4%; Score 14.4; DB 1;
93.8%; Pred. No. 8.5e+02;
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Best Local Similarity 93.8%; Pred. No. 8.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.4%; Score 14:4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-243-82
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                                            Mismatches
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US-10-317-279-22/c
'Sequence 22, Application US/10317279
'Publication No. US20040110703A1
'GENERAL INFORMATION:
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Gaps

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Sequence 1086, Application US/10671395
; Sequence 1086, Application US/10671395
; Bedication No. US20040132063A1
; Bublication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: 05/10,503
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1086

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APPLICANT: Baadsgaard, Ole
APPLICANT: Baadsgaard, Ole
APPLICANT: Huang Haichun
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
FILE REFERENCE: GMI-055
CURRENT APPLICATION NUMBER: US/10/687,799
CURRENT PILING DATE: 2003-10-17
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-04-02
NUMBER OF SEQ ID NOSE: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 14.4; DB 1; Length 20;
                             Indels
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    93.8%; Pred. No. 8.5e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.4; DB 1; Best Local Similarity 93.8%; Pred. No. 8.5e+02; Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/10687799
Publication No. US20040167319A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Teeling, Jessica
APPLICANT: Rulls, Sigrid
APPLICANT: Glennie, Martin
APPLICANT: van de Winkel, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                         18 GGCTGCAGGTGCTGGA 3
                                                                            53 GGCTGCAGGTGCTGAA
                             15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parren, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: artificial
  Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                             RESULT 1254
US-10-671-395-1086/c
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LENGTH: 20
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APPLICANT: Memeth W. Dobie
TITLE OF INVENTION: MODULATION OF DRI-ASSOCIATED PROTEIN 1 EXPRESSION
FILE REPRESENCE: HTS-0027
CURRENT APPLICATION NUMBER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
SEQ ID NOS: 59
LENGTH: 20
APPLICANT: Ming-Yi Chiang
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: WODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
FILE REFERENCE: HTS-0027
CURRENT APPLICATION NUMBER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 59
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LENOTH: 20
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Fublication No. US20040115640A1
GENERAL INFORMATION:
APPLICANT: Kathleen Wyers
APPLICANT: Kanneth W. Dobie
FITE REFERENCE: RTS-0454
CURRENT APPLICATION NOWLER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 116
LENGTH: 20
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O.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-279-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-317-279-51
, Sequence 51, Application US/10317279
; Publication No. US20040110703A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1545 CTTCAAGGACCTGGTG 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1545 CTTCAAGGACCTGGTG 1560
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                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 CTTGAAGGACCTGGTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-317-803-116/c
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US-10-317-279-51
                                                                                                                                                                                                                        TYPE: DNA
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US-10-085-906-147
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Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wu, Paul

APPLICANT: Gray, Gary, Gary S.

ITILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

FILE REFERENCE: GNN-543CP2

CURRENT RELING DATE: 1999-02-27

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: US 09/534,061

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 78

LENGTH: 27
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| Sequence 51, Application US/10781142
| Publication No. US20040192630A1
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION: SECTORS HAVING BOTH ISOFORMS OF
| TITLE OF INVENTION: BETA-HEXOSAMINIDASE AND USES OF THE SAME
| TITLE OF INVENTION: BETA-HEXOSAMINIDASE AND USES OF THE SAME
| FILE REFERENCE: 21108.004001
| CURRENT APPLICATION NUMBER: PS10/10/781,142
| CURRENT FILING DATE: 2004-02-18
| PRIOR FILING DATE: 2003-05-03
| PRIOR PILING DATE: 2003-05-03
| PRIOR PILING DATE: 2002-05-03
| NUMBER OF SEQ ID NOS: 71
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 51
| LENGTH: 20
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0.4%; Score 14.4; DB 1; Length 27;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence; note OTHER INFORMATION: synthetic construct US-10-781-142-51
                          3; Indels
Best Local Similarity 75.0%; Pred. No. 8.5e+02; Matches 15; Conservative 2; Mismatches 3
                                                                             853 GAGGAGCTGGTGGAGGC 872
                                                                                                          288 CGTCCGCTTCCGCTGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CGTCCGCTTCCGCTAC 20
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; ORGANISM: Homo sapiens
US-10-085-906-78
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US-US-725-265-11

Sequence 11, Application US/09725265

Publication No. US20010000175A1

Sequence 11, Application US/09725265

Publication No. US20010000175A1

SEQUENCE RANAGAMA, TAKAHIRO

APPLICANT: KURANG, YOLCHIRO

APPLICANT: YAMAGAMA, TOYOKAZU

APPLICANT: YAMAGAMA, TOYOKAZU

APPLICANT: YOKOMAKU, TOYOKAZU

APPLICANT: YOKOMAKU, TOYOKAZU

APPLICANT: WOYAMA, OSAMU

APPLICANT: WOYENTION: MUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT:

TITLE OF INVENTION: THE METHOD

TITLE OF INVENTION: WUMBER: US/09/725,265

CURRENT FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: UF 1999-111601

PRIOR PILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 30

MANCHER DATE

LENGTH: 30

LENGTH: 30

LENGTH: 30
                                                                                                                                                                                                     Sequence 147, Application US/10085906

Sequence 147, Application US/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Ving, Vincent

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: COLIMORDIC ELEMENTS IN THE

TITLE OF INVENTION: COSTUMILATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTUMILATORY RECEPTOR LOCUS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: US 69/534,061

PRIOR APPLICATION NUMBER: PCT/US00/07938

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: PCT/US00/07938

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 147

LEMETER OF SEQ ID Windows Version 4.0

LEMETER OF SET OF WINDOWS SET OF WINDOWS SET OF TANGENT 200
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3310 TITITCTITAGGAGATITATTIT 3333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-085-906-147
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vivlemore401-10.rnpb

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APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAKADA, OSAWU
TYKOWAKU, TOYOKAZU
APPLICANT: KOYOMAKU, OSAWU
APPLICANT: KOYOMAK, OSAWU
TITLE OF INVENTION: WUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: WUMBER: US/10/683,386
TITLE OF INVENTION: WUMBER: US/10/683,386
CURRENT APPLICATION NUMBER: US/09/556,127
PRIOR APPLICATION NUMBER: US/09/556,127
PRIOR RILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: JP 1999-111601
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
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Publication No. US20030143604A1
GENERAL INFORMATION:
APPLICANT: Storhoff, James
APPLICANT: Firiz, Brett
APPLICANT: Herrmann, Mark
TITLE OF INVENTION: Real-Time Monitoring of PCR Amplification Using Nanoparticle Prob
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PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: UP 1999-111601
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 11
LENGTH: 30
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; Publication No. US20040063137A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    FEATURE:
COTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: SYNTHETIC DNA US-10-683-386-11
                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: ARTIFICIAL SEQUENCE
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APPLICANT: KURANE, YUICHIRO
APPLICANT: KANGAMA, TAKAHIRO
APPLICANT: KANGAMA, TAKAHIRO
APPLICANT: KANGAMA, TAKAHIRO
APPLICANT: TORIMURA, MASAXI
APPLICANT: TORIMURA, MASAXI
APPLICANT: TORIMURA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
TITLE OF INVENTION: NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: NUCLEIC ACID 94-163-0-X
TITLE OF INVENTION: NUMBER: US/09/891,517
CURRENT PELICATION NUMBER: US/09/891,517
FRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOCTHARE: PALCHLIN VERSION 3.1
LENGTH: 30
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APPLICANT: KGNAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, YOICHI
APPLICANT: YOXOMAKU, TOYOKAZU
APPLICANT: YOXOMAKU, TOYOKAZU
APPLICANT: YOXOMA, OSAMU
APPLICANT: PURUSHO, KENTA
TITLE OF INVENTION: WETHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOU
TITLE OF INVENTION: THE METHOD
FILE REPERENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US/10/209,608
CURRENT APPLICATION NUMBER: US/09/725,265
PRIOR FILING DATE: 2000-011-29
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                                  Query Match 0.4%; Score 14.4; DB 1; Length 30; Best Local Similarity 75.0%; Pred. No. 1.2e+03; Matches 18; Conservative 0; Mismatches 6; Indels
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; Sequence 11, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09891517
Patent No. US20020106653A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic DNA US-09-891-517-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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US-09-263-959-923

US-09-263-959-923

Sequence 923, Application US/09263959

Patent No. US20020150891A1

Patent No. US20020150891A1

Patent No. US20020150891A1

APPLICANT: Rowen, Lee

APPLICANT: Rowen, Lee

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES. 1279

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 8.7e+02;
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; Sequence 4190, Application US/09969373
; Patent No. US20020133822A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of General Referent Application NUMBER: US/09/969,373
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; RECORDER OF SEQ ID NOS: 4593
; SEQ ID NO 4190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 8.7e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                 PRIOR APPLICATION NUMBER: 08/955,841
PRIOR FILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-11-19
PRIOR FILING DATE: 1966-11-19
PRIOR PILING DATE: 1966-11-20
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 51
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Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-548-51
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CORGANISM: Glycine max
US-09-969-373-4190
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; OTHER INFORMATION: Description of artificial sequence: APC gene probe mutant
US-10-306-630-2
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Publication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, BONIN
APPLICANT: ULV, WIN DIM
APPLICANT: ULLWAN, YEN PIN
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
CURRENT FILING DATE: 2002-08-14
PRIOR PILING DATE: 2001-08-14
PRIOR PLINIG DATE: 2001-08-14
PRIOR PLINIG DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOUTHARE PATENTIN VET. 2.1
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0.4%; Score 14.4; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels
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65.6%; Pred. No. 1.4e+03;
tive 0; Mismatches 11; Indels
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Patent No. US20020107216A1

GENERAL INFORMATION:

APPLICANT: Dedhar, Shoukat

APPLICANT: Hannigan, Greg

APPLICANT: Hannigan, Greg

TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES

FILE REFERENCE: KINSO010CIP4

CURRENT APPLICATION NUMBER: US/09/925,548

CURRENT APPLICATION NUMBER: 09/390,425

PRIOR FILING DATE: 1999-09-03

PRIOR APPLICATION NUMBER: 09/305,706
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                 CURRENT APPLICATION NUMBER: US/10/306,630
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/334,644
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3262 TATTTTATTTGCTTTGTCCTTTTT 3285
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FILE REFERENCE: 01-1747-A
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial
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Matches 21; Conserv
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LENGTH: 39
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Sequence 19, Application US/09835371

Publication No. US2002018747341

GENERAL INFORMATION:
APPLICANT: ULLMANN, Eugen
APPLICANT: ULLMANN, Eugen
APPLICANT: ULLMANN, Eugen
APPLICANT: WILL, David W
ITILE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
ITILE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REFERENCE: 02401.1743 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/835,371
CURRENT FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 19
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Sequence 19, Application US/09835370

Publication No. US20030022172A1

GENERAL INFORMATION:

APPLICANT: UHLMANN, EUGEN

APPLICANT: WILL, DAVID W

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

CURRENT APPLICATION NUMBER: US/09/835,370

CURRENT APPLICATION NUMBER: US/09/835,370

CURRENT PILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 19
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. OTHER INFORMATION: Description of Artificial Sequence: base sequence
; OTHER INFORMATION: of PNA targeting CMV
US-09-835-371-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: nucleotide
CTHER INFORMATION: base sequence of PNA derivatives that bind to
CTHER INFORMATION: viral and cellular targets
US-09-835-370-19
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                                                                                                                                                                                                                      Length 19;
                                                                                                                                                                                                              0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3;
TYPE: nucleic acid
STRANDEDRESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                              184 GGGGAGGACGAGGCTGAGG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GGGGAGGACGAGGCTGAGG 202
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                                                                                                                                                                                                                                                   Best Local Similarity 84.2
Matches 16; Conservative
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US-09-860-784-18
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US-09-835-370-19
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US-09-835-371-19
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UHLMANN, Eugen
TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
              MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PAPELIANE
COMPUTER:
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APPLICATION NUMBER: US/09/860,784
FILING DATE: 21-May-2001
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,452
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COlin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/264/HOCE
TELECOMMUNICATION:
TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 8.7e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2924 GGGGCGTGGGGGCGTGG 2942
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.2°
Matches 16; Conservative
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US-09-263-959-923
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA US-09-793-146-17
                            GENERAL INFORMATION:
APPLICANT: ULHAANN, EUGEN
APPLICANT: HERIPOHL, GERHARD
TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFREENCE: 02481.1437-02
CURRENT APPLICATION NUMBER: US/09/793,146
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: P 44 08 528.1
PRIOR APPLICATION NUMBER: 08/402,838
PRIOR APPLICATION NUMBER: 08/402,838
PRIOR FILING DATE: 1994-03-14
PRIOR FILING DATE: 1995-03-13
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
    US20030203359A1
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Score 14.2; DB 1; Length 19;
Pred. No. 8.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCOMMENTION: GENERAL INCOMPATION: GENERAL INCOMMENTION: Adaptors and Methods of Use TITLE OF INVENTION: Adaptors and Methods of Use FILE REFERENCE: 9397/1000 CURRENT APPLICATION NUMBER: US/09/880,313A CURRENT FILING DATE: 2001-06-13 NUMBER OF SEQ ID NOS: 276 SEQ ID NOS: 277 SEQ ID NOS: 276 SEQ ID NOS: 277 SEQ ID NOS: 276 SE
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APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, Lubane
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT APPLICATION NUMBER: US/09/864,636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1955
LENGTH: 19
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APPLICANT: Third Wave Technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/09880313A Publication No. US20030044791A1
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US-09-793-146-17
; Sequence 17, Application US/09793146
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        0.4%;
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ORGANISM: Artificial Sequence
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        Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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US-09-864-636A-1955
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Gaps

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Length 19; Indels

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Sequence 1955, Application US/09864426A

Sequence 1955, Application US/09864426A

Publication No. US20040018489A1

GENERAL INPORMATION:

APPLICANT: Third Wave Technologies

APPLICANT: Lyamichev, Victor

APPLICANT: Lyamichev, Victor

APPLICANT: Saiser, Michael

TITLE OF INVENTION: Barymes for the Detection of RNA Sequences

FILE REFERENCE: FORS-04946

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 2640

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1955

LENGTH: 19
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Pred. No. 8.7e+02;
0; Mismatches 3; Indels
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; Sequence 177, Apr.
; Publication No. US2003004-1.
; GENERAL INFORMATION:
; APPLICANT: BENEFIE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
. APPLICANT: ARNOULD-REGUIGNE, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2485 GTGCAGAATGTAAGTGGGC 2503
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1 gegaageaageareage 19
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic US-09-864-426A-1955
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; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-226-992-24
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Sequence 107, Application US/10226992

Publication No. US20030148507A1

GENERAL INFORMATION:

APPLICANT: Riboryme Pharmaceuticals, Inc.

APPLICANT: Rosnaugh, Kathy

TITLE OF INVENTION: and Prostaglandin D2 Synthetase (PTGDS) Gene Expression Using Sh;

TITLE OF INVENTION: RNA

TITLE OF INVENTION: RNA

FILE REFERENCE: 400/055 (MBHB01-1110-B)

CURRENT APPLICATION NUMBER: US/10/226,992

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/315,315

PRIOR FILING DATE: 2001-08-21

NUMBER OF SEQ ID NOS: 184

SOFTWARE: Patentin version 3.0

SEQ ID NO 107
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Publication No. US20030170691A1
GENERAL INFORMATION:
APPLICANT: Gimeno, Ruth
APPLICANT: Wu, Zhidan
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Hubbard, Brian K.
TITLE OF INVENTION: (DGAT2) FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: MP101-265P2RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
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Pred. No. 8.7e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
   FILE REFERENCE: 400/055 (MBHB01-1110-B)
CURRENT APPLICATION NUMBER: US/10/226, 992
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
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CURRENT FILING DATE: 2002-12-19
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Best Local Similarity 73.7%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                      TYPE: RNA
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                                                                                                                                                                                                                                              LENGTH
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APPLICANT: DUVERGER, Nicolas
APPLICANT: ALLIKWETS, Rando
APPLICANT: ALLIKWETS, Rando
APPLICANT: DEAN, Michael
TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCAS, ABCA6, ABCA9, AND ABCA10 GENES
TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
FILE REFERENCE: ABCA5, 6, 9, 10
CURRENT APPLICATION NUMBER: US/10/005,338B
CURRENT FILING DATE: 2001-01-20
PRIOR APPLICATION NUMBER: FR 004263,231
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR FILING DATE: 2000-12-07
SOFTWARE: PATENTING DATE: 2010-12-07
SOFTWARE: PATENTING DATE: 2010-12-07
SOFTWARE: PATENTING DATE: 2010-12-07
SOFTWARE PATENTING DATE: 2010-12-07
SOFTWARE: PATENTING DATE: 2010-12-07
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Publication No. US20030148507A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Fosnaugh, Kathy
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Prostaglandin D2 Receptor TITLE OF INVENTION: RNA Interference Synthetase (PTGDS) Gene Expression Using Sh TITLE OF INVENTION: RNA
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| Publication No. US20030113726A1
| GENERAL INFORMATION:
| APPLICANT: Bristol-Myers Squibb Company
| TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
| FILE REFERENCE: D0053NP
| CURRENT APPLICATION WOBER: US/10/005,956
| CURRENT APPLICATION NUMBER: US/11/005,956
| CURRENT FILING DATE: 2000-12-03
| PRIOR APPLICATION NUMBER: 60/251,015
| PRIOR APPLICATION NUMBER: 60/263,678
| PRIOR PILING DATE: 2001-01-23
| PRIOR PILING DATE: 2001-01-23
| PRIOR FILING DATE: 2001-03-02
| NUMBER OF SEQ ID NOS: 1579
| SOFTWARE: Patentin Version 3.0
| SEQ ID NO 596
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity .84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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CORGANISM: Homo sapiens
US-10-005-956-596
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CORGANISM: Homo sapiens
US-10-005-338B-177
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US-10-005-956-596/c
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US-10-226-992-24/c
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AFPLICANT: MCSWiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
TITLE OF INVENTION: Gane Bxpression Using Short Interfering RNA
TITLE OF INVENTION: Gane Bxpression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US 10/0/251,117
CURRENT APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
NUMBER: US 60/296,249
PRIOR FILING DATE: 2001-06-06
NUMBER: OF SEQ ID NOS: 1213
SEQ ID NO 650
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; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-251-117-400
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84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
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                     CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
FRIOR APPLICATION NUMBER: US 60/393,924
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-02-0
FRIOR APPLICATION NUMBER: US 60/358,580
FRIOR APPLICATION NUMBER: US 60/296,249
FRIOR APPLICATION NUMBER: US 60/296,249
FRIOR APPLICATION NUMBER: US 60/296,249
FRIOR FILING DATE: 2001-07-25
FRIOR FILING DATE: 2001-07-36
NUMBER OF SEQ ID NOS: 1213
SOFTWARE: PATENTIN VERSION 3.0
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Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
: 900/042 (MBHB02-468-A)
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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APPLICANT: Ribozyme Pharmaceuticals, Inc.

ITILE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (WEHB02-468-A)

CURRENT FILING DATE: 2003-02-24

PRIOR FILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-06-06

PRIOR PILING DATE: 2002-06-06

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOCTWARE: PatentIn version 3.0
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Sequence 400, Application US/10251117

Sequence 400, Application US/10251117

Sequence 400, Application No. US20030170891A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: MSGAYIGAN, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
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US-10-251-117-151
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                        PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/411,859
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151, Application US/10251117
Publication No. US20030170891A1
   PRIOR APPLICATION NUMBER: 60/341,947
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LENGTH: 19
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Gaps

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Gaps

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JULY SEQUENCE 957, Application US/10251117

j Publication No. US20030170891A1

j GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaccuticals, Inc.
    APPLICANT: Rowiggen, James
    TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
    FILE REPERENCE: 900/042 (MBHB02-468-A)
    CURRENT APPLICATION NUMBER: US 60/339,924
    PRIOR APPLICATION NUMBER: US 60/339,924
    PRIOR FILING DATE: 2002-05-03
    PRIOR PILING DATE: 2002-06-06
    PRIOR PILING DATE: 2002-06-06
    PRIOR PILING DATE: 2001-06-06
    PRIOR PILING DATE: 2001-07-25
    PRIOR FILING DATE: 2001-07-25
    PRIOR FILING DATE: 2001-07-25
    PRIOR FILING DATE: 2001-06-06
    PRIOR FILING DATE: 2001-06-06
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Sequence 972, Application US/10251117

SERVERAL INFORMATION:

APPLICANT: McSaviggen, James

TITLE OF INVENTION: Ran Interference Mediated Inhibition of Epidermal Growth Factor R

TITLE OF INVENTION: Ran Interference Mediated Inhibition of Epidermal Growth Factor R

TITLE OF INVENTION: WAS US (10/251,117

CURRENT APPLICATION NUMBER: US (0/393,924

PRIOR FILING DATE: 2002-02-03

PRIOR APPLICATION NUMBER: US (0/393,924

PRIOR APPLICATION NUMBER: US (0/358,580

PRIOR APPLICATION NUMBER: US (0/358,580

PRIOR PILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-02-20

PRIOR PILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR PILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: US (0/296,249)
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US-10-251-117-957
                                                                                              Gaps
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    Length 19;
                                                                                                   Indels
0.4%; Score 14.2; DB 1;
57.9%; Pred. No. 8.7e+02;
tive 5; Mismatches 3;
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                                                                                                                                                                                         1938 CGACCTGTACATGATCATG 1956
                                                                                                                                                                                                                                             | | | | : : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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SOFTWARE: PatentIn version
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    Query Match
Best Local Similarity
Matches 11; Conserva'
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| Sequence 720, Application US/10251117 |
| Sequence 720, Application US/10251117 |
| Publication No. US20030170891A1 |
| Publication No. US20030170891A1 |
| CENERAL INFORMATION: Pharmaccuticals, Inc. |
| APPLICANT: Ribozyme Pharmaccuticals, Inc. |
| APPLICANT: McSwiggen, James |
| APPLICANT: McSwiggen, James |
| TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R |
| TITLE OF INVENTION: Gene Expression Using Short Interfering RNA |
| FILE REPERENCE: 900/042 (MBH802-468-A) |
| CURRENT APPLICATION NUMBER: US/10/251,117 |
| CURRENT FILING DATE: 2003-02-24 |
| PRIOR APPLICATION NUMBER: US 60/393,924 |
| PRIOR PILING DATE: 2002-05-06 |
| PRIOR PILING DATE: 2002-05-06 |
| PRIOR PILING DATE: 2002-02-20 |
| PRIOR PILING DATE: 2001-06-06 |
| PRIOR PILING DATE: 2001-06-06 |
| NUMBER OF SEQ ID NOS: 1213 |
| SOFTWARE: PatentIn version 3.0 |
| SEQ ID NO 720 |
| LANGTH: 19 |
| LANGTH: 19 |
| LANGTH: 19
                                                                                                                                                            GENERAL INCRMATION:

GENERAL INCRMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor F TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (WHB02-468-A)

CURRENT FILING DATE: 2003-02-24

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE: PatentIn version 3.0

LENGTH: 19
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; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-720
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                                                                                                   Sequence 665, Application US/10251117
Publication No. US20030170891A1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
TITLE OF INVENTION: Interfering RNA
TITLE OF INVENTION: Interfering RNA
TITLE OF INVENTION: Interfering RNA
TITLE OF INVENTION: 101033
CURRENT APPLICATION NUMBER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 19
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US-10-205-309-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: Petentin version 3.1
SEQ ID NO 1955
LENGTH: 19
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; Publication No. US20030190635A1
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thompson, Lisa C. PapLICANT: Vedvik, Kevin L. TILLE OF INVENTION: RNA Detection Assays PILE REFERENCE: FORS-06666
                                                 Kwiatkowski, Jr., Robert W.
Lukowiak, Andrew A.
                                                                                                                                                                                 Neri, Bruce P.
Olson, Sarah M.
Olson-Munoz, Marilyn C.
Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
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; Publication No. US20030190635A1
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                                                                                                                                  ymaicheva, Natalie E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                         yamichev, Victor
                        Caiser, Michael
                                                                                                                                                             , WuPo
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US-10-205-309-343
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CURRENT APPLICATION NUMBER: US /10/251,117

PRIOR FILING DATE: 2003-02-24

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-02-20

PRIOR PLILNG DATE: 2002-02-25

PRIOR PLILNG DATE: 2001-02-25

PRIOR PLILNG DATE: 2001-02-25

PRIOR PLILNG DATE: 2001-02-25

PRIOR PLILNG DATE: 2001-02-26

PRIOR PLILNG DATE: 2001-06-06
                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-251-117-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-251-117-1027
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                                                                                                                                                                                                                                        Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1027, Application US/10251117
Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allawi, Hatim
Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
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APPLICANT: Third Wave Technologies
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SOFTWARE: Patentin version 3.0
SEQ ID NO 972
LENGTH: 19
                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1027
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ORGANISM: Artificial Sequence
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Hall, Jeff G.
Ip, Hon S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-251-117-1027/c
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Gaps

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Length 19;

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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/060 (MBHB02-100/244,647
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: DCT US02/09187
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Patentin Version 3.0
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US-10-454-323-3/c
; Sequence 3, Application US/10454323
; Publication No. US20040001833A1
; GENERAL INFORMATION:
; APPLICANT AGUS David B.
; TITLE OF INVENTION: Method of Treating Cancer Using Kinase Inhibitors
; FILE REFERENCE: 81476-250159
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,622
; RAPOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3.3
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84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
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Publication No. US20040005584A1
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ORGANISM: Artificial Sequence
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 16; Conserv
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US-10-349-143-4702/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-244-647-1157
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                                                                       APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using FILE OF INVENTION: Interfering RNA PILE REFERENCE: 900/033
CURRENT APPLICATION NUMBER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 511, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
Morisaey, David
APPLICANT:
Morisaey, David
APPLICANT:
Morisaey, David
APPLICANT:
Morisaey, David
TITLE OF INVENTION:
FILE OF INVENT
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; OTHER INFORMATION: Description of Artificial Sequence:
US-10-205-309-343
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Pred. No. 8.7e+02;
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                                                  Ribozyme Pharmaceuticals, Inc
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PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
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US-10-244-647-1157/c
Sequence 1157, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 511
LENCTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 42.1%;
Matches 8; Conservative
                 GENERAL INFORMATION:
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; Deblication No. US20040009946A1
; GENERAL INFORMATION:
   APPLICANT: Lewis, Stephen Patrick
   APPLICANT: Klinghoffer, Richard
   APPLICANT: Wilson, Linda K.
   TITLE OF INVENTION: MODULATION OF PPP1B SIGNAL TRANSDUCTION
   TITLE OF INVENTION: BY RNA INTERFERENCE
   TITLE OF INVENTION: BY RNA INTERFERENCE
   CURRENT APPLICATION NUMBER: US/10/444,925
   CURRENT FILING DATE: 2003-05-23
   NUMBER OF SEQ ID NOS: 599
   SOFTWARE: PastSEQ for Windows Version 4.0
   LENGTH: 19
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                                                                                                       APPLICANT: Lewis, Stephen Patrick
APPLICANT: Lewis, Stephen Patrick
APPLICANT: Klinghoffer, Richard
APPLICANT: Wilson, Linda K.
TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
TITLE OF INVENTION: BY RNA INTERFERENCE
FILE REFERENCE: 20015-441
CURRENT APPLICATION NUMBER: US/10/444,925
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 372
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Publication No. US20040009946A1
GENERAL INFORMATION:
APPLICANT: Lewis, Stephen Patrick
APPLICANT: Klinghoffer, Richard
APPLICANT: Wilson, Linda K.
APPLICANT: Wilson, Linda K.
APPLICANT: WILSON INVENTION: MODULATION OF PTPLE SIGNAL TRANSDUCTION
TITLE OF INVENTION: BY RNA INTERPERENCE
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US-10-444-925-392
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                     Sequence 372, Application US/1044925
Publication No. US20040009946A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-444-925-372/c
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Sequence 6183, Application No. US20040005584A1

Sequence 6183, Application No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

TITLE REPRENCE: GENSET. 0200701

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER PILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER PILING DATE: 1998-11-23

NUMBER OF SEQ ID NOS: 11796

LENGTH: 19
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
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; OTHER INFORMATION: upstream amplification primer 99-11075 for SEQ 2449, US-10-349-143-6383
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                                                                              CURRENT FILING DATE: 2003-01-21
PRIOR PLICATION NUMBER: US/09/422,978
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PELING DATE: EARLIER PELLING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER PELLON NUMBER: US 60/109,732
PRIOR PELING DATE: EARLIER PILING DATE: 1998-11-23
PRIOR PELING DATE: EARLIER FILING DATE: 1998-11-23
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PRIOR PELING DATE: EARLIER PELLING DATE: 1998-04-21
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Pred. No. 8.7e+02;
0; Mismatches 3; Indels
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84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
                        FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4702
LENGTH: 19
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Matches 16, Conservative
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ORGANISM: Homo Sapiens
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LOCATION: 1..19
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US-10-349-143-6383/c
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; OTHER INFORMATION: Description of Artificial Sequence: PCR primer US-10-182-644A-6
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                                                                                                                                                 Length 19;
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                                                                                                                                                                                 Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                            Score 14.2; DB 1;
Pred. No. 8.7e+02;
0; Mismatches 3;
                                                                                                                                                                                                                    2687 AGGCTTTCCCACTTCCCAC 2705
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Publication No. US20040137470A1
                                                                                                                                                                                                                                                       19 ATGCTTTCACACTTCCAAC 1
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                                                                                                                                              Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative (
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   TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 19
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US-10-376-770-89/C

Sequence 89, Application US/10376770

Publication No. US20040106102A1

GENERAL INFORMATION:

APPLICANT: Dhallan, Ravinder S.

TITLE OF INVENTION: RAPID ANALYSIS OF VARIATIONS IN A GENOME

FILE REFERENCE: 543312000320

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US/10/376,770

PRIOR PILING DATE: 2002-03-11

PRIOR PILING DATE: 2002-03-11

PRIOR PILING DATE: 2002-03-01

PRIOR PILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-06-08

NUMBER OF SEQ ID NOS: 262

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTH: 19
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TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
FILE REPERENCE: 200125449
CURRENT APPLICATION NUMBER: US/10/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 372
LENGTH: 19
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0.4%; Score 14.2; DB 1;
Best Local Similarity 52.6%; Pred. No. 8.7e+02;
Matches 10; Conservative 6; Mismatches 3;
FILE REFERENCE: 200125.441
CURRENT APPLICATION NUMBER: US/10/444,925
CURRENT FILING DATE: 2003.05-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                             ) OTHER INFORMATION: Small interfering RNA US-10-444-925-486
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, OTHER INFORMATION: Small interfering RNA US-10-444-7958-372
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 372, Application US/10444795B
Publication No. US20040077574A1
GENERAL INFORMATION:
APPLICANT: Klinghoffer, Richard
                                                                                                                                                                                                                                                                                                         3188 AGCCTGCCCCGGAGCTGGA 3206
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ORGANISM: Artificial Sequence
                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
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                                                                                        SEQ ID NO 486
LENGTH: 19
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SOFTWARE: FastSEQ for Windows Version 4.0

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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANTON: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor 3003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-07
PRIOR PARTICAL DATE: 2002-07-07
PRIOR PARTICAL DATE: 2002-07-07
PRIOR PARTICAL DATE: 2002-07-0
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/131 (MBHB02-742-F)
CURRENT APPLICATION NUMBER: US/0/665,951
CURRENT FILING DATE: 2003-09-18
FRIOR APPLICATION NUMBER: US 10/664,668
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NUMBER OF SEQ ID NOS: 2455
SOFWARE: Patentin version 3.2
SEQ ID NO 815
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84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
                                                                                                        Sequence 815, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
                                                                         JS-10-665-951-815/c
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US-10-665-951-1041
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Fublication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Sitna Therapeutics, Inc.
APPLICANT: Backedman, Leonid
APPLICANT: Barco, Pamela
ITILE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
FRIOR APPLICATION NUMBER: US 60/399,348
FRIOR FILING DATE: 2002-01-30
FRIOR PILING DATE: 2002-01-30
FRIOR PILING DATE: 2002-11-04
FRIOR APPLICATION NUMBER: US 60/389,789
FRIOR PILING DATE: 2002-11-04
FRIOR PILING DATE: 2002-11-04
FRIOR PILING DATE: 2002-11-04
FRIOR PILING DATE: 2002-01-30
FRIOR FILING DA
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US-10-665-951-388
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (5)...(9)
COTHER INFORMATION: These nucleotides may be absent
US-10-661-165-89
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                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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SEQ ID NO 388
SEQ ID NO 89
LENGTH: 19
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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r US-10-665-951-1046
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US-10-665-951-1052
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/131 (MBHB02-742-F)
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CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
FRIOR PILING DATE: 2003-09-18
FRIOR PLING DATE: 2003-09-18
FRIOR PLING DATE: 2003-09-18
FRIOR PLING DATE: 2003-09-18
FRIOR APPLICATION NUMBER: US 60/399,348
FRIOR PLING DATE: 2002-07-03
FRIOR APPLICATION NUMBER: US 60/393,796
FRIOR PLING DATE: 2002-07-03
FRIOR APPLICATION NUMBER: US 60/393,796
FRIOR APPLICATION NUMBER: US 60/393,796
FRIOR PLING DATE: 2002-11-04
FRIOR PLING DATE: 2002-11-04
FRIOR PLING DATE: 2002-11-07
FRIOR PLING DATE: 2002-11-07
FRIOR PLING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: US 60/363,124
FRIOR PLING DATE: 2002-05-05
FRIOR PLING DATE: 2002-05-06
FRIOR FLING DATE: 2002-06-06
FRIOR FLING DATE: 2002-05-06-06
FRIOR FLING DATE: 2002-03-11
FRIOR FLING DATE: 2002-03-03-03
FRIOR FLING DATE: 2002-03-03-03
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PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 1046
LENGTH: 19
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Publication No. US20040138163A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 13; Conserv
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Sequence 1046, Application US/10665951

Publication No. US20040138163A1

GRNERAL INFORMATION:
APPLICANT: Sitma Therapeutics, Inc.
APPLICANT: HCORAGE James
APPLICANT: Beacle Leconid Application of Vascular Endothelial
TITLE OF INVENTION: Rome Leconid APPLICANT: Bavoco, Pameal
TITLE OF INVENTION: Rome Expression Using Short Interfering Nucleic Acid (sina)
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Fa
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                                                                            PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-02-29
PRIOR PELING DATE: 2002-07-29
PRIOR PELING DATE: 2002-07-29
PRIOR PPLICATION NUMBER: US 60/393,796
PRIOR PPLICATION NUMBER: US 10/287,949
PRIOR PILING DATE: 2002-11-04
PRIOR PILING DATE: 2002-11-27
PRIOR PLING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: PCT/US 02/17674
PRIOR APPLICATION NUMBER: PCT/US 02/17674
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-06-60
PRIOR PILING DATE: 2002-06-06
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Pred. No. 8.7e+02;
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Best Local Similarity 57.9%; Pred. No. 8.7e
Matches 11; Conservative 5; Mismatches
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APPLICATION NUMBER: US 10/664,668
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sequence 1190, Application Us/L0605951
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sirnar Therapeutics, Inc.
APPLICANT: Bitan Therapeutics, Inc.
APPLICANT: Baselgelman, Leenid
APPLICANT: Beagelman, Leenid
APPLICANT: Bamela
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Us/10/665,951
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT APPLICATION NUMBER: US/10/665,951
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-05-29
PRIOR PILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
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Sequence 1370, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sina)
FILE REPERENCE: 400/131 (MSHB02-742-F)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
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NUMBER OF SEQ ID NOS: 2455
SOFTWARE: PatentIn version 3.2
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Pred. No. 8.7e+02;
0; Mismatches 3; Indels
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Publication No. US20040138163A1
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    UACACAAUCCAGAGUGACG 19
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Best Local Similarity 84.2%;
Matches 16; Conservative
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; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-665-951-1370
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PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR FILING DATE: 2002-02-02
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR PLING DATE: 2002-11-27
PRIOR PLING DATE: 2002-11-27
PRIOR PLING DATE: 2002-01-27
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-03-11
PRIOR PLING DATE: 2002-06-06
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APPLICATION NUMBER: US 60/358,580
ELLING DATE: 2002-02-20
APPLICATION NUMBER: US 60/363,124
FILING DATE: 2002-03-11
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Publication No. US20040138163A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: BASWIGGEN, James
APPLICANT: Beigelnan, Leonid
APPLICANT: Berco. Pamela
TITLE OF INVENTION: Raw Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
FILE REFERENCE: 400/131 (MBHB02-742-F)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-20
PRIOR FILING DATE: 2002-02-20
PRIOR PLILING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-01-04
PRIOR PLILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR PLILING DATE: 2002-01-04
PRIOR PLILING DATE: 2002-01-04
PRIOR PLILING DATE: 2002-02-20
PRIOR PLILING DATE: 2002-03-11
PRIOR PRILING DATE: 2002-06-66
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                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-665-951-1376
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PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 1376
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1786 TACACTCACCAGAGTGACG 1804
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-665-951-1674
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GURREAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Meswiggen, James
APPLICANT: Meswiggen, James
APPLICANT: Beacol James
APPLICANT: Beacol James
APPLICANT: Beacol James
APPLICANT: Beacol James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION UNMER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR PELLOR TON NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR PELLOR DATE: 2003-07-29
PRIOR PELLOR APPLICATION NUMBER: US 60/399,348
PRIOR PELLOR DATE: 2002-07-29
PRIOR PELLOR DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/359,580
PRIOR PELLOR DATE: 2002-05-29
PRIOR PELLOR DATE: 2002-02-20
PRIOR PELLOR DATE: 2002-02-20
PRIOR PELLOR PELLOR NUMBER: US 60/359,782
PRIOR PELLOR DATE: 2002-02-20
PRIOR PELLOR DATE: 2002-02-20
PRIOR PELLOR DATE: 2002-02-20
PRIOR PELLOR PELLOR NUMBER: US 60/359,782
PRIOR PELLOR DATE: 2002-02-11
PRIOR PELLOR DATE: 2002-02-11
PRIOR PELLOR DATE: 2002-02-11
PRIOR PELLOR DATE: 2002-03-11
PRIOR PELLOR DATE: 2002-03-11
PRIOR PELLOR DATE: 2002-03-11
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US-10-665-951-1683
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (SINA)
CURRENT APPLICATION NUMBER: US/10/665,951
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Sequence 1683, Application US/10665951; Publication No. US20040138163A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SEQ ID NO 1683
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1573 CAGGTGGCCCGGGGCATGG 1591

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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-665-951-2263
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APPLICANT: Beigelman, Leonid
APPLICANT: Bavoo, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sinA)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-665-951-1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR PLILING JAHE: 2003-02-20
PRIOR PLILING DATE: 2003-02-20
PRIOR PLILING DATE: 2003-02-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR PLILING DATE: 2002-07-29
PRIOR PLILING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-11-04
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-02-20
PRIOR PLILING DATE: 2002-02-20
PRIOR PLILING DATE: 2002-03-11
PRIOR PLILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARR: PRECENTIN VERSION 3.2
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2265
SOFTWARE: PATENTIN version 3.2
SEQ ID NO 1930
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Sequence 2263, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 68.4
Matches 13; Conservative
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                                                                                 PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR FILING DATE: 2003-02-120
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2003-02-20
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-12-07
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-03-11
PRIOR PLING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
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           CURRENT FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: US 10/664,668
PRIOR FILING DATE: 2003-09-18
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PEDLICATION NUMBER: US 60/358,580
FILING DATE: 2002-02-20
APPLICATION NUMBER: US 60/363,124
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
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ORGANISM: Artificial Sequence
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LENGTH: 19
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APPLICANT: LI, JUNG
APPLICANT: LI, JUNG
APPLICANT: SIN, WIN CHEX
APPLICANT: SIN, WIN CHEX
APPLICANT: SIN, WIN CHEX
TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
FILE REFERENCE: 38002-0062
CURRENT APPLICATION NUMBER: US/10/715,117
CURRENT PILING DATE: 2003-11-18
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 13
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/10715117

Sequence 14, Application US/10715117

Publication No. US2040171037A1

GENERAL INFORMATION:

APPLICANT: LI JUNG

APPLICANT: SIN, WUN CHEY

APPLICANT: SIN, WUN CHEY

TITLE OF INVENTY AMELIFIED GENES INVOLVED IN CANCER

FILE REFERENCE: 38002-0062

CURRENT PELLOATION NUMBER: US/10/715,117

CURRENT FILING DATE: 2003-11-18

PRIOR FILING DATE: 2003-11-19

PRIOR FILING DATE: 2002-11-19

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 202-12-19

PRIOR FILING DATE: 202-12-19
                                                                                                                                                                                   Score 14.2; DB 1;
Pred. No. 8.7e+02;
0; Mismatches 3;
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Publication No. US20040171037A1
GENERAL INFORMATION:
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      2003-06-20
CURRENT FILING DATE: 2003-06-2
NUMBER OF SEQ ID NOS: 206
SOFTWARE: Patentin version 3.2
SEQ ID NO 37
LENGTH: 19
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                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                      FEATURE:
COTHER INFORMATION: Synthetic
US-10-600-070-37
                                                                                                                                                                                   Query Match
Best Local Similarity 84.21
Matches 16; Conservative
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Best Local Similarity 84.4.
Best Local Similarity 64.4.
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ORGANISM: Homo sapiens
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US-10-715-117-14
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                                                                                                           Sequence 37, Application US/10600070
Publication No. US20040139500A1
GENERAL INFORMATION:
APPLICANT: Otteryoung, Katherine W.
APPLICANT: Vitha, Stanislav
APPLICANT: Koksharova, Olga A.
APPLICANT: Gao, Hongo
TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-665-951-2264
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CURRENT APPLICATION NUMBER: US/10/600,070
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        1950 GATCATGCGGGAGTGCTGG 1968
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                           1 GACCAUGCUGGACUGCUGG 19
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                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: SIRNA sequence
US-10-715-117-14
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                                                                                                                                                                                                                0.4%; Score 14.2; DB 1; Length 19; 78.9%; Pred. No. 8.7e+02;
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APPLICANT: Halbert, Donald N.
APPLICANT: Halbert, Donald N.
APPLICANT: McDowell, Jeffrey A.
APPLICANT: Schurdak, Mark E.
APPLICANT: Schurdak, Mark E.
APPLICANT: Sarthy, Aparna V.
TITLE OF INVENTION: Method Of Killing Cancer Cells FILE REPERENCE: 7046.US.01
CURRENT APPLICATION NUMBER: US/10/385,163
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 19
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APPLICANT: Halbert, Donald N.
APPLICANT: Halbert, Donald N.
APPLICANT: Schurdak, Mark E.
APPLICANT: Schurdak, Mark E.
APPLICANT: Sarthy, Aparna V.
ITLE OF INVENTION: Method Of Killing Cancer Cells
FILE REFERENCE: 7046.02.21
CURRENT APPLICATION NUMBER: US/10/796,177
CURRENT PILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/60/453,420
PRIOR PILING DATE: 2006-03-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 19
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US-10-385-163-95
                                                                                                                                                                                                                                                           1; Mismatches
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Publication No. US20040180844A1
GENERAL INFORMATION:
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Publication No. US20040180848A1
GENERAL INFORMATION:
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                                                TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 78.99
Matches 15; Conservative
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SEQ ID NO 14
LENGTH: 19
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense rous-10-683-990-22
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PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
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                                                                                                                                                                                      Length 19;
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                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                      Ouery Match 0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                             FEATURE:
; OTHER INFORMATION: antisense oligonucleotide US-10-796-177-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-02-20
PRIOR PELING DATE: 2002-02-20
PRIOR PELING DATE: 2002-02-20
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR PELING DATE: 2002-08-29
PRIOR PELING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR PELING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 119, Application US/10683990
; Publication No. US20040198682A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10683990 Publication No. US20040198682A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  1950 GATCATGCGGGAGTGCTGG 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 AGCTGCTGGCCGTGCCGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGCUCCUGGCCGGGCUGGC 19
                                                                                                                                                                                                                                                                                                                                                                            19 GATGATGCGAGAGTGTTGG 1
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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SEQ ID NO 22
LENGTH: 19
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Sequence 139, Application US/09758881

Sequence 139, Application US/09758881

Sequence 139, Application US/09758881

GENERAL INFORMATION:
APPLICANT: Karras, James G

TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
CURRENT APPLICATION NUMBER: US/09/758,881
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR PILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
SOFTWARE: Patentin Ver. 2.1
SEC ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-758-881-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pendication No. US2002003915229
pichlication No. US20020039789A1
general Application No. US20020039789A1
general information No. US20020039789A1
general information No. US2002003978A1
papticant: THER REGENTS OF THE UNIVERSITY OF CALIFORNIA
papticant: Ray, Jasodhara
rithe OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
FILE REFERENCE: REGENII60-5
CURRENT APPLICATION NUMBER: US/09/915,229
CURRENT APPLICATION NUMBER: 08/884,427
PRIOR APPLICATION NUMBER: 08/445,075
PRIOR PILING DATE: 1997-06-27
PRIOR PELING DATE: 1993-11-03
PRIOR PLILOG DATE: 1993-11-03
PRIOR PLILOG DATE: 1993-11-03
PRIOR PLILOG DATE: 1993-11-03
PRIOR PLILOG DATE: 1993-10-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
                                                                                       3; Indels
                  Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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                                                                                                                                                            2850 TATGGAAGAGGAAAAGGCT 2868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 GIGCACAAGAICICCCGCT 1024
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ORGANISM: Artificial Sequence
                  Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conserva
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APPLICANT: Sirra Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: WcSwiggen, James
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RAM Interference Mediated Inhibition of Placental Growth Factor
TITLE OF INVENTION: Gene Expression Using SHort Interfering Nucleic Acid (sink)
FILE REFERENCE: 400/114 (02-742-H)
FILE REPERENCE: 400/114 (02-742-H)
CURRENT APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-09-05
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-09-09
PRIOR P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 243, Application US/09216393
Patent No. US2001001447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA

CRGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-216-393-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.2; DB 1; Length 19;
84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1999-12-18
EARLIER APPLICATION NUMBER: 08/994,825
SARAINER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin Ver. 2.0
SENGTH: 20
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Best Local Similarity
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0.4%;
  Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%
Matches 16; Conservative
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APPLICANT: SETHURAMAN, NATARAJAN
APPLICANT: SETHURAMAN, NATARAJAN
APPLICANT: SETHURAMAN, NATARAJAN
TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
TITLE OF INVENTION: ANTIVIRAL AND ANTICANCER THERAPY
TITLE OF INVENTION: ANTIVIRAL AND ANTICANCER THERAPY
FILE REFERENCE: 023032/0108
CURRENT FILING DATE: 1095-04-27
PRIOR FILING DATE: 1995-04-25
PRIOR FILING DATE: 1995-12-04
PRIOR FILING DATE: 1992-12-04
PRIOR FILING DATE: 1991-12-04
PRIOR FILING DATE: 1991-12-04
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Jiang, Shan
TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
TITLE OF INVENTION: METHYLATED CPG ISLANDS
FILE REFERENCE: 01107.00128
CURRENT APPLICATION NUMBER: US/09/861,893
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/206,161
PRIOR APPLICATION NUMBER: 60/206,161
PRIOR PELING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
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0.4%; Score 14.2; DB 1; Length 20; ilarity 84.2%; Pred. No. 9.1e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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US-09-842-628-11/c
1S-09-842-628
Sequence 11, Application US/09842628
Fatent No. US2002064862A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1346 CTGAGATGGAGATGAA 1364
                                                                                                 2385 TGCCTCCAGGTGCAGAGGT 2403
                                                                                                                                                                                                                                                                     Sequence 3, Application US/09861893
Patent No. US20020045257A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 20
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-893-3
  Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                   US-09-861-893-3/c
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LAION US/09416384A

LAMPORMATION:
AMPLICANT: BLUMENFELD, MATTA
APPLICANT: GUNGUELERET, Lydie
APPLICANT: GUNGUELERET, Lydie
APPLICANT: CHARANCO, IIya
APPLICANT: CHARANCO, IIya
APPLICANT: CHARANCO, LAUREN
APPLICANT: CHARANCO, LAUREN
APPLICANT: CHARANCO, LAUREN
APPLICANT: DASSET 0445.384A
TITLE REFERENCE: GENSET 0445.384A
FILE REFERENCE: GENSET 0450-01.2
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: 06/103,955
FRIOR FILING DATE: 1999-10-12
FRIOR FILING DATE: 1999-10-13
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Moro, Pam
APPLICANT: Garde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS;
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS;
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS;
FILE REFERENCE: ISPH-0412
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 09/396,902
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR PLLING DATE: 1999-08-07
PRIOR PLLING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 65
                                                                                                 Gaps
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         Length 20;
Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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US-09-416-384A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/09774809 Publication No. US20030004120A1 GENERAL INFORMATION:
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Gaps
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OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
OTHER INFORMATION: primer
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                                       RESULT 1333
US-09-982-262B-62
| Sequence 62, Application US/09982262B
| Sequence 62, Application US/09982262B
| Publication No. US20030077565A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett
| APPLICANT: C. Frank Bennett
| TITLE OF INVENTION: OLGGONUCLEOTIDE MODULATION OF CELL ADHESION FILE REPERENCE: 15PH-6612
| CURRENT APPLICATION NUMBER: US/09/982,262B
| PRIOR APPLICATION NUMBER: 09/659,288
| PRIOR PILING DATE: 2000-09-12
| PRIOR PILING DATE: 1998-06-12
| PRIOR PILING DATE: 1998-06-12
| PRIOR PILING DATE: 1995-05-12
| PRIOR PLILING DATE: 1995-05-12
| PRIOR PAPLICATION NUMBER: 09/663,167
| PRIOR PILING DATE: 1993-05-17
| PRIOR PAPLICATION NUMBER: 09/063,167
| PRIOR PILING DATE: 1993-02-10
| PRIOR PILING DATE: 1993-01-10
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| Sequence 4, Application US/09760285
| Publication No. US20030091997A1
| GENERAL INFORMATION:
| APPLICANT: Nicolaides, Nicholas C
| APPLICANT: Grasso, Luigi
| APPLICANT: Grasso, Luigi
| APPLICANT: Grasso, Luigi
| TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
| FILE REPRENCE: MOR -0017
| CURRENT APPLICATION NUMBER: US/09/760,285
| CURRENT FILING DATE: 2001-01-15
| NUMBER OF SEQ ID NOS: 44
| SEQ ID NO 4
| LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3380 CTGTGTGTCCCAGGCAGGG 3398
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     2 GAAGGTTTCCAGGGAAGAG 20
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US-09-760-285-4
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US-09-865-686-68
US-09-865-686-68
Sequence 68, Application US/09865866
Publication No. US20030045487A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFRENCE: RIS-021
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 68
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 160, Application US/09771933

Publication No US20030023387A1

GENERAL INFORMATION:
APPLICANT: Gill-Garrison, Rosalynn D

APPLICANT: Martin, Christopher J

APPLICANT: Martin, Christopher J

APPLICANT: Martin, Camputer-assisted Means for Assessing Lifestyle Risk

TITLE OF INVENTION: Factors

FILE REFERENCE: 620-130

CURRENT APPLICATION NUMBER: US/09/771,933

CURRENT APPLICATION NUMBER: US/09/771,933

CURRENT PILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 205

SEQ ID NO 160

LENGTH: 20
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                                                                                                                                                             Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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US-09-865-866-68
                                                     FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-774-809-61
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-771-933-160/c
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TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
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| Sequence 2531, Application No. US2004018489A1 |
| Seneral Information: US2004018489A1 |
| General Information: Application Mave Technologies |
| APPLICANT: Third Wave Technologies |
| APPLICANT: Lyamichev, Victor |
| APPLICANT: Lyamichev, Victor |
| APPLICANT: Saiser, Michael |
| TITLE OF INVENTION: Braymes for the Detection of RNA Sequences |
| TITLE OF INVENTION: Braymes for the Detection of RNA Sequences |
| TITLE OF INVENTION: Braymes for the Detection of NA Sequences |
| TITLE OF INVENTION: Braymes for the Detection of NA Sequences |
| TITLE OF INVENTION UNMBER: V8/09/864,426A |
| CURRENT FILING DATE: 2001-05-24 |
| SOFTWARE: PatentIn version 3.0 |
| SEQ ID NO 2331 |
| LENGTH: 20 |
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Publication No. US20030022311A1
GENERAL INFORMATION:
TRAILS, James D.
Shoelson, Steven B.
TITLE OF INVENTION: HUMAN CIS PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Sweedland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antisense Oligonucleotide US-09-908-147-26
                                        FILE REFERENCE: RTS-0185
CURRENT APPLICATION NUMBER: US/09/908,147
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 26
LENGTH: 20
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                  Sequence 2, Application US/09899440
Publication No. US20030092158A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENT: Stein, CY
TITLE OF INVENT: SPISSENCE: 0575/63180
CURRENT APPLICATION NUMBER: US/09/899,440
CURRENT FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 18
SSOFTWARE: Patentin version 3.0
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2531, Application US/09864636A; Sequence 2531, Application US/09864636A; Publication No. US20030104378A1; GENERAL INFORMATION: US20030104378A1; APPLICANT: Third Wave Technologies; APPLICANT: Bartholomay, Christian; APPLICANT: Chehak, Ludane; TITLE OF INVENTION: Detection of RNA Sequences; FILE REFERENCE: FORS-04944; CURRENT APPLICATION NUMBER: US/09/864,636A; CURRENT FILING DATE: 2002-10-15; SEQ ID NOS: 2640; SEQ ID NOS: 2640; SEQ ID NOS: 2640; SEQ ID NO 2531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature; LOCATION: ()..(); OTHER INFORMATION: antisense oligonucleotide LB62 US-09-899-440-2
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                  20 GACAGAGICTICACTAACC 2
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conservative
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APPLICANT: Andrew T. Watt
                                                                                                                        RESULT 1335
US-09-899-440-2/c
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US-09-908-147-26
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US-10-079-429-66
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0
Length 20;
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORPATION:
GENERAL INCORPATION:
APPLICATUR: Haseltine et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
FILE REPERENCE: PF106F911
CURRENT APPLICATION NUMBER: US/10/079,429
CURRENT FILING DATE: 2002-02-2
FRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR FILING DATE: 1995-01-05
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1994-03-18
PRIOR PLING DATE: 1994-03-16
PRIOR APPLICATION NUMBER: 08/240,13
PRIOR PLING DATE: 1994-03-16
PRIOR PLING DATE: 1994-01-27
NUMBER OF ELING DATE: 1994-01-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN VERSION 3.0
FEBRIOR OF SEC ID NOS: 78
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TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
CURRENT APPLICATION NUMBER: US/10/079,429
CURRENT PILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1994-08-23
PRIOR FILING DATE: 1994-08-23
PRIOR PLILING DATE: 1994-08-23
PRIOR PLILING DATE: 1994-08-23
PRIOR PLILING DATE: 1994-08-23
PRIOR PLILING DATE: 1994-08-23
PRIOR FILING DATE: 1994-08-36
PRIOR FILING DATE: 1994-08-16
PRIOR PRILING DATE: 1994-08-16
PRIOR FILING DATE: 1994-08-16
Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-429-69/c
; Sequence 69, Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                US-10-079-429-66/c

: Sequence 66, Application US/10079429

: Publication No. US20030027177A1

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1777 GACCGAGTCTACACTCACC 1795
                                                                                                                   1777 GACCGAGTCTACACTCACC 1795
                                                                                                                                                                            20 GACAGAGTCTTCACTAACC 2
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   Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-U0-4-25-55/C

| Sequence 55, Application US/10079429
| Publication No. US2003002717741
| GENERAL INFORMATION:
| APPLICANT: Hascline et al.
| TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
| FILE REFERENCE: PF1067511
| CURRENT FILING DATE: 2002-02-22
| PRIOR PELICATION NUMBER: US/10/079,429
| CURRENT FILING DATE: 1995-01-25
| PRIOR FILING DATE: 1995-01-65
| PRIOR FILING DATE: 1995-06-06
| PRIOR FILING DATE: 1994-01-23
| PRIOR FILING DATE: 1994-06-23
| PRIOR FILING DATE: 1994-01-27
| WHERR OF SEQ ID NOS: 78
| SOFTWARE: PatentIn version 3.0
| SOFTWARE: PATENTIN VERSION 100-27
| LENGTH: 20
| LENGTH: 20
| LENGTH: 20
                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/262,130
FILING DATE: 01-0ct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/655,327
FILING DATE: 21-MAY-1996
ATTORNEY, AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 33,833
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2965 CCATGCAAGCAGAGCCA 2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: hMLH3 primer US-10-079-429-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERIZTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 cccrcaacccagacca 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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OF SEQ ID NOS: 78

NUMBER

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Score 14.2; DB 1; Length 20; Pred. No. 9.1e+02; 0; Mismatches 3; Indels

0.4%;

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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-10-067-125-195
                                                                                                                                                                                                                                                                                                             1998 CAAGCAGCTGGTGGAGGAC 2016
                                                                                                                                                                                                        Query Match 0.45
Best Local Similarity 84.25
Matches 16; Conservative
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SEQ ID NO 195
                          LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Letternan, Michael I.
APPLICANT: Latif, Farida
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Latif, Farida
APPLICANT: Mei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Gao, Boning
APPLICANT: Gao, Boning
APPLICANT: OR NUMBER: William Channel Compositions and Methods of Use Thereof
FILE REFERENCE: NIH-05043
CURRENT APPLICANTON NUMBER: US/10/116,949
CURRENT APPLICANTON NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
PRIOR FILING DATE: EARLIER FILING DATE: 1990-12-22
PRIOR FILING DATE: EARLIER FILING DATE: 1990-12-30
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                     ; OTHER INFORMATION: primer useful for amplifying codons 415 to 863 of hMLH3
US-10-079-429-69
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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 195, Application US/10067125
; Publication NO. US20030055015A1
; Publication NO. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Coweart, Lex M.
; APPLICANT: Wonia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                             0.4%; Score 14.2; DB 1; Length 20;
ilarity 84.2%; Pred. No. 9.1e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/10116949
Publication No. US20030044911A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      1777 GACCGAGTCTACACTCACC 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3706 TGGTGGCCAGAGGTGTCAC 3724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
SOFTWARE: PatentIn version 3.0
                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                           Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-067-125-195
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                        SEQ ID NO 69
LENGTH: 20
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LENGTH: 20
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                                                     LENGTH:
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APPLICANT: Van Tol, Hubert H.M.
Civelli, Olivier
TITLE OF INVENTION: A No. US20030059845Alel Human Dopamine Receptor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER: F10PDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/224,260
FILING DATE: 20-Aug-2002
CLASSIPICATION: UDKNOWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Intron1
/note= "This is the 5' sequence of an intron
estimated to be 2.0 kilobases in length"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 22
CORRESPONDENCES ADDRESS:
ADDRESSES: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /partiāl
/cons splice= (5'site: YES, 3'site: NO)
/evidēnce= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030059845Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..20
IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/928,611
                                                                                                                   Sequence 3, Application US/10224260 Publication No. US20030059845A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
2 chadececiceradadahe 20
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TELEX: 810-221-831.7
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                   US-10-224-260-3/c
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APPLICANT: Chader, Gerald J
APPLICANT: Becerrar, Sofia P
APPLICANT: Becerrar, Sofia P
APPLICANT: Rodriguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
TITLE OF INVENTION: RETINAL BIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
TITLE OF ILLUGATION NUMBER: US/08/520,373
CURRENT FILING DATE: 1995-08-29
PRIOR FILING DATE: 1995-08-29
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR PLING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                     APPLICANT: Dona T. Ward
APPLICANT: Dona T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECQLS EXPRESSION
FILE REPERENCE: RTS-0203
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US/09/798,185
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ 1D NOS: 92
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-238-443-75
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                Sequence 75, Application US/10238443 Publication No. US20030083302A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/10216373
Publication No. US20030096750A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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SEQ ID NO 30
     Conservative
                                                        3260 GATATTTTATTTGCT
                                                                                                                                                                                                             JS-10-238-443-75
Matches 16;
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| Sequence 92, Application No. US20030083296A1
| GENERAL INFORMATION:
| APPLICANT: Hong Zhang
| APPLICANT: Hong Zhang
| APPLICANT: Lex M. Coweert
| TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
| FILE REFERENCE: RTSP-0334
| CURRENT APPLICATION NUMBER: US/10/181,177
| CURRENT APPLICATION NUMBER: US/10/181,177
| PRIOR APPLICATION NUMBER: 09/487,445
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2000-01-19
| NUMBER OF SEQ ID NOS: 176
| SEQ ID NO 92
| LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: 3' human rhodopsin primer over BstEII site US-10-000-773A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 9.1e+02;
                                                        3; Indels
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Farrar, Gwenyth Jane
APPLICANT: Humphries, Peter
APPLICANT: Humphries, Peter
APPLICANT: Humphries, Peter
APPLICANT: Humphries, Peter
APPLICANT: Millington-Ward, Sophia
TITLE OF INVENTION: Suppression of Polymorphic Alleles
FILE REFERENCE: MIN-001CP
CURRENT FILING DATE: 2001-11-30
PRIOR PILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR PLICATION NUMBER: PCT/GB97/00574
PRIOR PLICATION NUMBER: PCT/GB97/00574
PRIOR PLICATION NUMBER: B9604449.0
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-03-03
SPRIOR FILING DATE: 1997-03-01
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 20
                             9.1e+02;
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Query Match 0.4%; Score 14.2; I
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                          US-10-000-773A-3/c; Sequence 3, Application US/10000773A; Publication No. US20030069195A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1897 AAGGAGGCCACCGCATGG 1915
                                                                                                                                                          19 GCGGCCGGACGCGCCTCAC 1
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ORGANISM: Artificial Sequence
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Best Local Similarity
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                   Query Match
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                                     Best Loca
Matches
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US-10-016-149-35/c

US-10-016-149-35/c

Sequence 35, Application US/10016149

Publication No. US20030100524A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: DEPENDENT) EXPRESSION

TITLE OF INVENTION: DEPENDENT) EXPRESSION

FILE REFERENCE: RTs-0325

CURRENT APPLICATION NUMBER: US/10/016,149

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 84

LENGTH: 20
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APPLICANT: Tal-Singer, Ruth
APPLICANT: Tal-Singer, Ruth
APPLICANT: Tal-Singer, Ruth
TITLE OF INVENTION: Compounds And Methods For Treating And
TITLE OF INVENTION: Screening Viral Reactivation
FILE REFERENCE: P506821
CURRENT APPLICATION NUMBER: US/10/108,164
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 09/424,348
PRIOR APPLICATION NUMBER: 09/424,348
PRIOR APPLICATION NUMBER: 60/051,633
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
SPRIOR FILING DATE: 1998-44-01
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FEALSEQ FOR Windows Version 4.0
                                                           Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 127, Application US/10108164
Publication No. US20030104356A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                           Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
; OTHER INFORMATION: PRIMER 353
US-10-216-373-30
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;. ORGANISM: Mus musculus
US-10-108-164-127
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Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
FILLE REPERENCE: ISPH-0617
CURRENT APPLICATION NUMBER: US/10/001,844
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 20
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Pred. No. 9.1e+02;
0; Mismatches 3;
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Sequence 133, Application US/10149352

GENERAL INFORMATION:

APPLICANT BET., Rajinder

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES

FILE REFERENCE: 06275-254US1

CURRENT APPLICATION NUMBER: US/10/149,352

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: GB 9929487.8

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-15

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 4.0

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                         US-10-001-844-11
; Sequence 11, Application US/10001844
; Publication No. US20030105041A1
; GENEAL INFORMATION:
APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsert
                                                                                            2000 AGCAGCTGGTGGAGGACCT 2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2323 GTGTGTGTGTGTGTGTG 2341
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                                                                                                                                     20 AGCTGCTGGTGGAGGTCAT 2
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Best Local Similarity 84.2%;
Matches 16; Conservative
    0.4%;
Similarity 84.2%;
.6; Conservative
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Best Local Similarity
Matches 16; Conserv
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Sequence 32, Application US/10017621
Publication No. US20030138952A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
  Gaps
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; Sequence 25, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REPREBNCE: RT-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
                                                                                                                                                                                                     Sequence 11, Application US/10007010;
Publication No. US20030125275A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
FILE REFERENCE: RTS-034
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT APPLICATION STEEL S001-12-04
; NUMBER OF SEQ ID NOS: 87
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indel8
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-11
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Mismatches
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                                                                                 1 CCCCATCGCCTGCAGATGC 19
                                                46 CCCCAGCGGCTGCAGGTGC 64
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Matches 16; Conservative
  16; Conservative
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Matches 16; Conserv
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US-10-017-621-32/c
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  Matches
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                                Sequence 20, Application US/10269501
Publication No. US20030113347A1
Publication No. US20030113347A1
ABPLICANT: Schweiz. Serum- & Impfinstitut Bern
APPLICANT: Gluck, Reinhard
APPLICANT: Gluck, Reinhard
APPLICANT: Malti, Enst
TITLE OF INVENTION: Immunostimulating and Immunopotentiating Reconstituted Influenza
TITLE OF INVENTION: Virosomes and Vaccines Containing Them
FILE REFERENCE: 009848-0290189
CURRENT FILING DATE: 2003-02-28
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i Sequence 75, Application US/10309362

j Redulication No. US20303114412A1

GENERAL INFORMATION:
I GENERAL SOUND T. Ward

APPLICANT: DOING T. Ward

ITILE OF INVENTION: ANISENSE MODULATION OF RECQLS EXPRESSION

TITLE OF INVENTION: ANISENSE US/10/309,362

CURRENT APPLICATION NUMBER: US/10/309,362

CURRENT FILING DATE: 2002-12-03

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 92

SEQ ID NO 75

LENGTH: 20
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                             CURKENT FILLING DAIE: 2003-002-28

PRIOR APPLICATION NUMBER: 09/264,551

PRIOR PILLING DATE: 1999-03-08

PRIOR FILLING DATE: 1999-03-08

PRIOR FILLING DATE: 1994-04-11

PRIOR PLING DAIE: 1998-05-03-03

PRIOR PILLING DATE: 1998-05-03-03

PRIOR PILLING DATE: 1998-05-22

PRIOR PILLING DATE: 1998-05-23

PRIOR PILLING DATE: 1997-05-08

PRIOR PILLING DATE: 1997-05-08

PRIOR PILLING DATE: 1997-05-08

PRIOR PILLING DATE: 1991-05-08

PRIOR PILLING DATE: 1991-05-10

NUMBER OF SEQ ID NOS: 20

SOFTWARR: PARLENT NET: 1991-05-10

SOFTWARR: PARLENT NET: 1991-05-10
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%
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Best Local Similarity
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Sequence 76, Application US/10029517
Publication No. US20030148969A1
CENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Susan J. Myers
TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
FILE REFERENCE: RTS-0352
CURRENT APPLICATION NUMBER: US/10/029,517
CURRENT PILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-024-396-52

| Sequence 5.2, Application US/10024396
| Publication No. US20030147864A1
| GENERAL INFORMATION:
| APPLICANT: Kenneth W. Dobie
| TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
| TITLE OF INVENTION: NUMBER: US/10/024,396
| CURRENT APPLICATION NUMBER: US/10/024,396
| WUMBER OF SEQ ID NOS: 91
| SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide US-10-024-396-52
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,049
FILING DATE: 28-Jun-2002
CLASSIPICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                      TELEFAX: 206-442-6674
                                                                                                                           APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2415 CCCCGCTGCTGTGCAACGG 2433
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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STRANDEDNESS: single
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Sublication No. US20030138952A1
GREEAL INFORMATION:
GREEAL INFORMATION:
APPLICANT: SUSAN MARK P. ROSCH
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
TITLE OF INVENTION: ANTISENSE WOOULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
CURRENT APPLICATION WINBER: US/10/017,621
CURRENT FILING DATE: 2001-12-07
SEQ ID NO 46
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOSTER, DOBAGE C.
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
PAR4 (ZCHEMR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:

, OTHER INFORMATION: Antisense Oligonucleotide
US-10-017-621-46
                                                                                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide US-10-017-621-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
             CURRENT APPLICATION NUMBER: US/10/017,621
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 32
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1360
US-10-187-049-10/C
; Sequence 10, Application US/10187049
; Publication No. US20030143218A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; Presentl, Scott R.
Yee, David P.
Donald C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                  2729 ACGGGTACCTGAAGATGGG 2747
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                                                                                                                                                                                                                                                                                                                                                                                             20 ACGAGGACTTGAAGATGGG 2
                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.23
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle STATE: WA
FILE REFERENCE: RTS-0350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-017-621-46
                                                                                                                                                                         FEATURE:
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Sequence 67, Application US/10376566

Publication No. US20030158144A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mark P. Roach
APPLICANT: Erich Koller
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR BETA EXPRESSION FILE REFERENCE: RTS-0347
CURRENT APPLICATION NUMBER: US/10/376,566
CURRENT PILING DATE: 2003-02-27
PRIOR PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 67
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/10197927
Publication No. US20030166138A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kinsella. Todd
APPLICANT: Obashi, Cara
APPLICANT: Anderson, Dave
TITLE OF INVENTION: Cyclic Peptides and Analogs Useful to Treat Allergies
FILE REFERENCE: RIGL-002/01US
CURRENT APPLICATION NUMBER: US/10/197,927
CURRENT FILING DATE: 2003-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Antisense Oligonucleotide US-10-376-566-67
                       CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US/09/722,319
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1996-12-06
PRIOR FILING DATE: 1996-12-06
PRIOR PILING DATE: 1996-06-09
PRIOR APPLICATION NUMBER: EP 94870093.5
PRIOR FILING DATE: 1994-06-09
NUMBER OF SEQ ID NOS: 73
SOOTWARE: PATENTIN VETSION 3.1
     CURRENT APPLICATION NUMBER: US/10/339,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2608 CAAAGCTGAGCCTGCAGGG 2626
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1366
US-10-197-927-53/c
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US-10-376-566-67
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| Sequence 66, Application US/10339604
| Sequence 66, Application US/10339604
| Sequence 66, Application No. US20030152982A1
| Sequence 66, Application No. US20030152982A1
| SEENHOUWER, HANS
| APPLICANT: DETABLE, FRANCOISE
| APPLICANT: MACHTELINCKX, LIEVE
| APPLICANT: MACHTELINCKX, LIEVE
| APPLICANT: ANDI
| APPLICANT: OSSSAU, RUDI
| TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
| TITLE OF INVENTION: Antibiotic Resistance
| FILE REFERENCE: 1657.0010001
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-1948-48-8-8-9.

US-10-1948-48-8-9.

Sequence 83, Application US/10348485

Publication No. US20030148989A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Bennett, C. Frank

APPLICANT: Holmlund, Jon T.

PRIOR PLING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/10/025,139

PRIOR FILING DATE: 1997-03-31

PRIOR PILING DATE: 1997-03-31

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1993-07-09

PRIOR APPLICATION NUMBER: US 08/089,996

PRIOR APPLICATION NUMBER: US 08/089,996

PRIOR APPLICATION NUMBER: US 07/852,852

PRIOR PILING DATE: 1993-07-09

PRIOR APPLICATION NUMBER: US 07/852,852

PRIOR PILING DATE: 1992-03-16

NUMBER OF SEQ ID NOS: 121

SEQ ID NO 83

LENGTH: 20
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                                                                                                                                               , OTHER INFORMATION: Antisense Oligonucleotide
US-10-029-517-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-83
                                                                                                                                                                                                                                                                                                                                                               2380 CATCTTGCCTCCAGGTGCA 2398
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                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 76
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US-10-032-555-4348
US-10-032-555-4348
US-10-032-555-4348
i Sequence 4348, Application US/10032585
j Publication No. US2003180953A1
j GENERAL INFORMATION:
j APPLICANT: Terry, Roemer D.
j APPLICANT: Bo, Jiang
j APPLICANT: Howard, Bussey
j TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
j TURE REPRENCE: 10.182-005-999
j CURRENT APPLICANTON UNGBER: US/10/032,585
j CURRENT PILING DATE: 2001-12-20
j NUMBER OF SEQ ID NOS: 8000
j SOFTWARE: PatentIn version 3.1
j EMEGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## Sequence 5557, Application US/10032585

## Sequence 5557, Application US/10032585

## Sequence 5557, Application US/10032585

## Sequence 5557, Application US/20030180953A1

## Sequence 5557, Application US/20030180953A1

## SET INFORMATION:

## APPLICANT: Terry, Roemer D.

## APPLICANT: Howard, Bussey

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

## TITLE OF INVENTION: Gene Dis
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APPLICANT: Shepard, Peter J.
TILLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS
FILE REFERENCE: ISPH-0660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1638 CAATGTGCTGGTGACCGAG 1656
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   20 AGGACCTGCCTGACAGCA
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Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; Candida albicans US-10-032-585-5557
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; Publication No. US20030170636A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TILLE OF INVENTION. ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
; FILE REFRENCE: RTS-0244
; CURRENT APPLICATION NUMBER: US/10/091,625
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Publication No. US20030170636A1
GENERAL INFORMATION:
APPLICANT: SHERENCE TTILE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION CURRENT APPLICATION UNMER: US/10/091,625
CURRENT FILING DATE: 2002-03-05
SEQ ID NO 72
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-091-625-72
PRIOR APPLICATION NUMBER: 60/358,827
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 20
                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic primer US-10-197-927-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3048 GGGCCCTGGCACTCTTGT 3066
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                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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FEATURE:

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Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-321-856-243
                                                                                                                                                                                                                                              SEQ ID NO 2531
LENGTH: 20
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LENGTH: 20
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APPLICANT: Koller, Erich
APPLICANT: Koller, Erich
APPLICANT: Shepard, Peter J.

TITLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS
FILE REPERENCE: ISPH-0660
CURRENT APPLICATION NUMBER: 2002-03-12
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 72
LENGTH: 20
                                                                                                                                                                                                                           Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                    ; OTHER INFORMATION: Antisense oligonucleotide
US-10-096-399A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Antisense oligonucleotide
CURRENT APPLICATION NUMBER: US/10/096,399A
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 91
SEQ TWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 20
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Kaiser, Michael
Kwiatkowski, Jr., Robert W.
Lukowiak, Andrew A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allawi, Hatim
Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
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APPLICANT: Third Wave Technologies
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Sequence 72, Application US/10096399A
Publication No. US20030185829A1
                                                                                                                                                                                                                                                                                                       3048 GGCCCCTGCCACTCTTGT 3066
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ORGANISM: Artificial Sequence
                                                                                                                                 ORGANISM: Artificial Sequence
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Hall, Jeff G.
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hes 16; Conserve
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                                                                                                                 TYPE: DNA
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APPLICANT:
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Sequence 243, Application US/10321856; Publication No. US20030194393A1; GENERAL INFORMATION:
A PPLICANT: Milhausen, Michael James; TITLE OF INVENTION:
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER; FILE REFERENCE: TX-1-C2-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MICHAELES, MICHAELS OF APPLICANT: APPLICANT: GRASSO, Luigh
APPLICANT: Sass, Philip M
TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
TITLE OF INVENTION: MPPERMUTABLE CELLS
FILE REFERENCE: MOR-0005
FILE REFERENCE: MOR-0005
CURRENT APPLICATION NUMBER: US/09/708,200
PRIOR APPLICATION NUMBER: US/09/708,200
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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ilarity 84.2%; Pred. No. 9.1e+02;
Conservative 0; Mismatches 3; Indels
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                                                     APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Teteka Y.
APPLICANT: Takova, Teteka Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Todovik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
TITLE OF INVENTION: RNA Detection Assays
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
lson, Sarah M.
lson-Munoz, Marilyn C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1777 GACCGAGTCTACACTCACC 1795
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Publication No. US20030186441A1
GENERAL INFORMATION:
APPLICANT: Nicolaides, Nicholas C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 ACAAGTTTGGCAGCATCCG 488
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic US-10-084-839-2531
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Matches 16; Conservative
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS V
TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4, I
TITLE OF INVENTION: THEREOF
FILE REFERENCE: D0153 NP
CURRENT APPLICATION NUMBER: US/10/193,477
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US 60/304,888
PRIOR PILING DATE: 2001-07-11
PRIOR PLING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 229
SOFTWARE PRESE PRECEIL VERSION 3.1
SEQ ID NO 113
LENGTH: 20
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APPLICANT: Damela Nero
APPLICANT: Pamela Nero
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brich Koller
APPLICANT: Brich Koller
APPLICANT: Mano Manolaran
TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
FILE REFERENCE: ISPH-0623.
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 09/048,810
PRIOR APPLICATION NUMBER: US 09/280,805
PRIOR PLING DATE: 1999-03-26
NUMBER OF SED ID NOS: 379
SOFTWARE FEASTER FEASTER OF WINDOWS VERSION 4.0
                                                                                                                                         Score 14.2; DB 1; Length 20; Pred. No. 9.1e+02;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                  0; Mismatches
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Publication No. US20030195163A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     2340 TGTGTGTGTGTGCACATCC 2358
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-477-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-477-113
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DO153 NP
CURRENT APPLICATION NUMBER: US/10/193,477
CURRENT FILING DATE: 2002-07-11
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 2002-04-12
NUMBER: US 60/372,147
PRIOR FILING DATE: 2002-04-12
NUMBER: OF SEQ ID NOS: 229
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 105
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US-10-311-886-45
                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 14.2; DB 1; Length 20;
llarity 84.2%; Pred. No. 9.1e+02;
Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: K.U. LEUVEN Research and Development et al. TITLE OF INVENTION: Biocatalyst inhibitors FILE REFERENCE: PCT/BE 01/00106 CURRENT APPLICATION NUMBER: US/10/311,886 CURRENT FLING DATE: 2002-12-23 NUMBER OF SEQ ID NOS: 45 SOFTWARE: Patentin version 3.0 SEQ ID NO 45 LENGTH: 20
     CURRENT APPLICATION NUMBER: US/10/321,856
                         CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 243
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                            ), OTHER INFORMATION: Synthetic Primer US-10-321-856-243
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; Sequence 45, Application US/10311886
; Publication No. US20030195151A1
; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 16; Conserva
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Query Match
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US-10-461-668-53
; Sequence 53, Application US/10461668
; Publication No. US20030207839A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Fraier;
; TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
; FILE REFERENCE: RTS-0244
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/10/091,625
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 53
; LENGTH: 20
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Sequence 72, Application US/10461668

Subblication No. US20030207839A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
FILE REFERENCE: RTS-0244

CURRENT APPLICATION NUMBER: US/10/461,668

CURRENT APPLICATION NUMBER: US/10/091,625

PRIOR PILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                    Length 20;
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
                                                                                                                              3; Indels
                                                                                  Query Match

O.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                    , OTHER INFORMATION: Antisense Oligonucleotide US-10-005-344-338
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-10-461-668-72/c
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FEATURE:
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Sequence 57, Application US/10144488
Publication No. US20030212017A1
Publication No. US20030212017A1
Publication No. US20030212017A1
Publication No. US20030212017A1
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF FARNESYL TRANSFERASE BETA SUBUNIT EXPRESS FILE REFERENCE: RTS-0363
CURRENT APPLICATION NUMBER: US/10/144,488
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 20
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APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION
FILE REFERENCE: RTSP-034E 105/101,873A
CURRENT APPLICATION NUMBER: US/10/101,873A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: 09/489,868
PRIOR PILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-20
PRIOR PILING DATE: 2000-01-20
SEQ ID NOS: 89
SEQ ID NO 78
LENGTH: 20
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Publication No. US20030215854A1
GENERAL INFORMATION:
TITLE OF INVENTION: DETECTION OF DNA-BINDING PROTEINS
FILE REPERBNCE: 39147-0013
CURRENT APPLICATION UNMBER: US/10/400,670
CURRENT FILING DATE: 2003-06-28
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/10181873A Publication No. US20030212019A1 GENERAL INFORMATION:
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Matches 16; Conservative
-10-144-488-57/c
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US-10-181-873A-78
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APPLICANT: Becker, Kenneth David
APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bartram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Saunders, Aleister J.
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-110-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR PILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-12-04
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20030224380A1
GENERAL INFORMATION:
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      573 GCTGGGCAGCGACGTGGAG 591
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                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: hairpin oligonucleotide
US-10-400-670-4
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Sequence 14, Application US/10438075

Publication No. US20030216345A1

Publication No. US20030216345A1

APPLICANT: Schering Aktiengesellschaft

TILLE OF INVENTION: Histone deacetylase inhibitor and use thereof

FILE REFERENCE: 1023370

CURRENT APPLICATION UNMBER: US/10/438,075

CURRENT FILING DATE: 2003-05-15

NUMBER OF SEQ ID NOS: 31

LENGTH: 20
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Publication No. US20030219742A1
GENERAL INFORMATION:
APPLICANT: Sanjay Bhanot
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HMGI-C EXPRESSION
FILE REPERENCE: RTS-0236
CURRENT APPLICATION NUMBER: US/10/114,279
CURRENT FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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; OTHER INFORMATION: Antisense oligonucleotide no.12
US-10-438-075-14
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-279-68
                                                                                                                                                                                                                                                                                                                                                                                                                               1193 CCCTGGGCAAGCCCCTTGG 1211
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                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 84.2
Matches 16; Conservative
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                            SEQ ID NO 4
LENGTH: 20
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LENGTH: 20
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NAME/KEY:
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Sequence 80, Application US/10159266
Sequence 80, Application US/10159266
Sequence 80, Application Wo. US2030224511A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF CATHEPSIN Z EXPRESSION
TITLE OF INVENTION NUMBER: US/10/159,266
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 158
SEQ ID NO 80
LENGTH: 20
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Length 20;
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TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME EXPRESSION FILE REFERENCE: RTS-0383
CURRENT APPLICATION NUMBER: US/10/159,942
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 133
SEQ ID NO 100
LENGTH: 20
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APPLICANT: Wystt, Jacqueline R.
APPLICANT: Wystt, Jacqueline R.
APPLICANT: Vincely A.
Tille OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
FILE REFERENCE: ISIS-4503
CURRENT FILING DATE: 2003-031-12
NUMBER OF SEQ ID NOS: 947
SEQ ID NO 423
LENGTH: 20
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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Publication No. US20030228597A1
GENERAL INFORMATION:
APPLICANT: COWSERT, Lex M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 423, Application US/10388263
Publication No. US20030228597A1
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Henri M.
Douglas G.
Cara
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Sasmor, Henri M.
Brooks, Douglas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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McNeil, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker, Brenda F.
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                       TYPE: DNA
ORGANISM: H. sapiens
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US-10-388-263-442/c
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US-10-159-942-28

Sequence 28, Application US/10159942

Publication No. US20030224512A1

GENERAL INFORMATION:

ATTLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME EXPRESSION

TITLE OF INVENTION NUMBER: US/10/159,942

CURRENT APPLICATION NUMBER: US/10/159,942

CURRENT FILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 133

SEQ ID NOS: 133

LENGTH: 20
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                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                         Sequence 152. Application US/10159266

Publication No. US20030224511A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION ANTISENSE MODULATION OF CATHEPSIN Z EXPRESSION
FILE REFERENCE: RTS-0398
CURRENT APPLICATION NUMBER: US/10/159,266
CURRENT PILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 158
SEQ ID NO 152
LENGTH: 20
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                         Length 20;
                                                                       0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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US-10-159-942-28
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-266-80
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GENERAL INFORMATION: APPLICANT: Kenneth W. Dobie
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
                                                                                          Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: H. sapiens
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Preier
APPLICANT: Susan M. Dobie
TITLE OP INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES
FILE REPERBNCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT APPLICATION DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 130
                                                                                                                                                                                                          Gaps
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APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie.
TITLE OF INVENTION: ANYISENSE MODULATION OF E2-EPF EXPRESSION
FILE REFERENCE: HTS-0021
CURRENT APPLICATION NUMBER: US/10/173,240
CURRENT FILING DATE: 2002-06-14
NUMBER OF SQ ID NOS: 80
LENGTH: 20
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                        Length 20;
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Pred. No. 9.1e+02;
0; Mismatches 3;
                                                                                                                                    Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3;
                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-159-856-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 130, Application US/10159856
Publication No. US20030228689A1
GENERAL INFORMATION:
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Publication No. US20030232436A1
GENERAL INFORMATION:
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US-10-173-240-39/c
; Sequence 39, Application US/10173240
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: H. sapiens
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; FEATURE:
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US-10-159-856-80/c
| Sequence 80, Application US/10159856
| Publication No. US20030228689A1
| GENERAL INFORWATION:
| APPLICANT: Susan M. Freier
| APPLICANT: Kenneth W. Dobie
| TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
| FILE REFERENCE: RTS-03365
| CURRENT FILING DATE: 2002-05-31
| NUMBER OF SEQ ID NOS: 134
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US-10-159-866-83/c

US-10-159-866-83/c

Squares 83, Application US/10159856

Publication No. US20030228689A1

GENERAL INFORMATION:

APPLICANT: Susan M. Freier

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE

FILE REFERENCE: RTS-0365

CURRENT APPLICATION NUMBER: US/10/159,856

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 83

LENGTH: 20

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                                 APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timochy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: MODULATION BY OLIGONUCLECTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLECTIDES FOR GENE MODULATION
TITLE OF INVENTION: GENERATION OF OLIGONUCLECTIDES FOR GENE MODULATION
TITLE OF INVENTION: GENERATION OF OLIGONUCLECTIDES FOR GENE MODULATION
CURRENT APPLICATION NUMBER: 105/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SEQ ID NO 442
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Antisense Oligonucleotide US-10-388-263-442
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   Wyatt, Jacqueline R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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LENGTH: 20
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Publication No. US20030232436A1
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
FILE REPERENCE: HTS-0021
CURRENT APPLICATION NUMBER: US/10/173,240
CURRENT PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITILE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
FILE REFERENCE: HTS-0021
CURRENT APPLICATION NUMBER: US/10/173,240
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 72
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 62, Application US/10173240;
; Publication No. US20030232436A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
; FILE REFERENCE: HTS-0021
                                                                                                                                                                                                                                                                                                                                              0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-10-173-240-39
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CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 62
LENGTH: 20
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                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: H. sapiens
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US-10-173-240-72
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                                                                                                                                                                                                                                                                     FEATURE:
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Sequence 29, Application US/10174465
Publication No. US20030232772A1
Publication No. US20030232772A1
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF EXTRACELLULAR-SIGNAL-REGULATED KINASE-6 E)
TITLE OF INVENTION ANTISENSE MODULATION OF EXTRACELLULAR-SIGNAL-REGULATED KINASE-6 E)
CURRENT APPLICATION NUMBER: US/10/174,465
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 70
ILENGTH: 20
                                                                                                                                                                                                                                             Sequence 61, Application US/10174460

| Sequence 61, Application NG US2003023441A1
| GENERAL INFORMATION:
| APPLICANT: Brett P. Monia
| APPLICANT: C. Frank Bennett
| APPLICANT: Kenneth W. Dobie
| TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION FILE REFERENCE: PTS-0014
| CURRENT APPLICATION NUMBER: US/10/174,460
| CURRENT FLING DATE: 2002-06-17
| NUMBER OF SEQ ID NOS: 109
| LENGTH: 20
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Length 20;
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Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-174-465-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-10-174-460-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 29, Application US/10348431; Publication No. US20030232778A1
                                                                                                 1821 CCTGCTCTGGGAGATCTTC 1839
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ORGANISM: Artificial Sequence
FEATURE:
Query Match

0.4%;

Best Local Similarity 84.2%;

Matches 16; Conservative
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US-10-174-465-29/c
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NAME/KEY: primer_bind
LOCATION: 1..20
; OTHER INCRAMITION: downstream amplification primer 99-11206 for SEQ 3752, in compleme
US-10-349-143-11617
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Sequence 1841, Application US/20040006218A1

Publication No. US20040006218A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT PILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1841
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11617, Application US/10349143
; Sequence 11617, Application US/10349143
; Publication No. US20040005584A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; TITLE REPERENCE: GENSET. 0200CP1
CURRENT PILLING DATE: 2003-01-21
CURRENT PILLING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US/09/422.978
PRIOR PILING DATE: BARLIER PILING DATE: 1999-04-21
PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21
PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21
; PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21
; PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21
; RIOR PILING DATE: EARLIER PILING DATE: 1999-04-21
; ROWNERS OF SEQ ID NOS: 11796
; SEQ ID NO 11617
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                                                                                                                                                      Query Match
0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                       663 CAAGGTGGGCCCGGACGGC 681
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ORGANISM: Chlamydia pneumoniae
US-10-289-762-1841
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Best Local Similarity 84.2%
Matches 16; Conservative
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US-10-349-143-11617
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**APPLICANT: C. Frank Bennett

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: EXTRACELULAR-SIGNAL-REGULATED KINASE-6 INHIBITING

TITLE OF INVENTION: ANGIOGENESIS

TITLE OF INVENTION: ANGIOGENESIS

TITLE OF INVENTION: ANGIOGENESIS

CURRENT APPLICATION

NUMBER OF SEQ ID NOS: 71

LENGTH: 20

TYPE: nv.
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US-10-188-646-64/C
Sequence 64, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
ITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 64
LENGTH: 20
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; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT FILING DATE: 2002-07-02
; SEQ ID NO 134
; SEQ ID NO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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US-10-348-431-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-10-188-646-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: H. sapiens
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FEATURE:
US-10-188-646-134
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1644 GCTGGTGACCGAGGACAAC 1662
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                                                                                                                                                                                                                                                                                                                                          931 TTCATCCTGGTGGTGGCGG 949
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                                                                                         ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ), ORGANISM: Chlamydia pneumoniae US-10-289-762-4985
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5790
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NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 4798
LENGTH: 20
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Matches 16; Conserv
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APPLICANT: GITIFIAIS, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT SEPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849
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Sequence 4798, Application US/10289762

Sequence 4798, Application US/10289762

Publication No. US20040006218A1

SENERAL INFORMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering of INVENTION: and treatment of infection

TITLE OF INVENTION: 1003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27
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| Publication No. US20040006218A1
| GENERAL INFORMATION:
| TRILE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
| TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
| TITLE OF INVENTION: and treatment of infection
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                             Sequence 3458, Application US/10289762; Publication No. US20040006218A1; GENERAL INFORMATION:
   1208 TTGGGGAGGCTGCTTCGG 1226
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                                                             TTGAAGAAGGCTGCTTCGG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Chlamydia pneumoniae US-10-289-762-3458
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4668
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Best Local Similarity 84.2
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US-10-289-762-4668/c
                                                                                                                                                                                   US-10-289-762-3458
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US-10-199-199-107
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Sequence 696, Application US/10289762
Sequence 6696, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
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Publication No. US20040014047A1
GENERAL INFORMATION
APPLICANT: Lex M: Cowsert
APPLICANT: Lex M: Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
FILE REPERRENCE: RTS. 2002-07-18
CURRENT FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 32
LENGTH: 20
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Publication No. US20040014047A1
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOWAIN KINASE 1 EXPRESSION
FILE REPERENCE: RIS-0375
CURRENT APPLICATION NUMBER: US/10/199,199
CURRENT FILING DATE: 2002-07-18
NUMBER OF EQ ID NOS: 148
SEQ ID NO 107
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Antisense Oligonucleotide US-10-199-199-32
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA CRGANISM: Chlamydia pneumoniae US-10-289-762-6696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
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  US-10-289-762-6696
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US-10-199-199-107
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FULLIANT INFORMATION:

APPLICANT: MASUDA, Esteban
APPLICANT: MINSELLA, Todd M.
APPLICANT: MINSELLA, Todd M.
APPLICANT: MINSELLA, Todd M.
APPLICANT: MINSELLA, Todd M.
APPLICANT: MINSELLA, Taisei
APPLICANT: MERRE, Visein B.
APPLICANT: MINSERSON, David C.
TITLE OF INVENTION: SYNTHESIS UTILIZING AN ADENOSINE KINASE
TITLE OF INVENTION: SYNTHESIS UTILIZING AN ADENOSINE KINASE
TILE REPERBNCE: RIGL-099/0002
CURRENT APPLICATION NUMBER: US/10/197,381
CURRENT PILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 20
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APPLICANT: Kinsella, Todd M

APPLICANT: Kinsella, Todd M

APPLICANT: Kinsella, Todd M

APPLICANT: Kinsella, Todd M

APPLICANT: Kinsella, Taisei

APPLICANT: Anderson, David C

TITLE OF INVENTION: Methods of Identifying Compounds that Modulate IL-4 Receptor-N

TITLE OF INVENTION: Synthesis Utilizing a Chloride Intracellular Channel 1 Prote

FILE REFERENCE: RIGL-013/00US

CURRENT APPLICATION NUMBER: US/10/197,945A

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO 14

LENGTH: 20
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  Length 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
  Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: synthetic primer US-10-197-381-7
                                                                                                      1874 TGGAGGAGCTCTTCAAGCT 1892
                                                                                                                                                                                                                                                                             Sequence 7, Application US/10197381
Publication No. US20040014147A1
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0.4%;
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ORGANISM: Artificial Sequence
FEATURE:
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  Query Match 0.45
Best Local Similarity 84.25
Matches 16; Conservative
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APPLICANT: MASUDA, Esteban
APPLICANT: MISSILA, Todd M.
APPLICANT: KINOSHITA, Todd M.
APPLICANT: KINOSHITA, Taisei
APPLICANT: MARNET, Mark
K.
APPLICANT: BENNETT, Mark
K.
APPLICANT: MISSISSON MARCON TO TITLE OF INVENTION: SYNTHESIS UTILIZING A B-CELL ASSOCIATED PROTEIN
TITLE OF INVENTION: SYNTHESIS UTILIZING A B-CELL ASSOCIATED PROTEIN
TITLE OF INVENTION: WUMBER: US/10/197,919
CURRENT APPLICATION NUMBER: 2002-07-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 20
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
FILE REFERENCE: RTS-0367
CURRENT APPLICATION NUMBER: US/10/210,290
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic primer
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Publication No. US20040023378A1
GENERAL INFORMATION:
APPLICANT: Ming-Yi Chiang
                                                                                                                                                                                                                                        Sequence 8, Application US/10197919
Publication No. US20040014649A1
GENERAL INFORMATION:
          866 TGGAGGCTGACGAGGCGGG 884
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                                                                            20 TGGAGGCTGAAGCGCCGGG
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ORGANISM: Artificial Sequence
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Publication No. US20040014638A1

GENERAL INFORMATION:
APPLICANT: MASUDA, Esteban
APPLICANT: WARNER, Justin E.
APPLICANT: WARNER, Justin E.
APPLICANT: WARNER, Justin E.
APPLICANT: MANDERSON, David C.
ITILE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE IL-4 RECEPTOR-MEDI
ITILE OF INVENTION: SYNTHESIS UTILIZING A CLLD8 PROTEIN
FILE REFERRINCE: RIGL-007/00US
CURRENT FILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
IENGTH: 20
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APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Warner, Justin B
APPLICANT: Warner, Justin B
APPLICANT: Warner, Justin B
APPLICANT: Annoshta, Taisei
APPLICANT: Annoshta, Taisei
APPLICANT: Annoshta, Mark K
APPLICANT: Mark K
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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   84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                      US-10-197-962B-9/c
; Sequence 9, Application US/10197962B
; Publication No. US20040014149A1
                                                                                                        866 TGGAGGCTGACGAGGCGGG 884
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
Best Local Similarity 84.2
Matches 16; Conservative
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US-10-197-368-13/c
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Gaps

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Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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US-10-211-908-55/c
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             US-10-210-589-98
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Publication No. US20040023378A1
GENERAL INFORMATION:
APPLICANT: Mingery1 Chiang
APPLICANT: Mingery1 Chiang
APPLICANT: Exic G. Marcusson
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAALS31 PROTEIN EXPRESSION
FILE REFERENCE: RTS-0367
CURRENT APPLICATION NUMBER: US/10/210,290
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 111
LENGTH: 20
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US-10-210-589-48/C

i Sequence 48, Application US/10210589
i Publication No. US20040023381A1
i GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
    APPLICANT: Nicholas M. Dean
    TITLE OF INVENTION: ANTISENSE MODULATION OF PPPZRIA EXPRESSION
    TILLE OF INVENTION: ANTISENSE WOULLATION OF PPPZRIA EXPRESSION
    CURRENT APPLICATION NUMBER: US/10/210,589
    CURRENT FILING DATE: 2002-07-30
    NUMBER OF SEQ ID NOS: 122
    SEQ ID NO 48
    LENGTH: 20
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Sequence 98, Application US/10210589

Publication Vo. US20040023381A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dean
APPLICANT: Nicholas M. Dean
APPLICANT: Nicholas M. Dean
APPLICANT: Nicholas M. Dean
APPLICANT: Fenneth W. Doin
CTITLE OF INVENTION: ANTISENSE MODULATION OF PPPZRIA EXPRESSION
CURRENT APPLICATION NUMBER: US/10/210,589
CURRENT FILING DATE: 2002-07-30

NUMBER OF SEQ ID NOS: 122
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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Matches 16; Conservative
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TYPE: DNA
ORGANISM: H. sapiens
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ORGANISM: H. sapiens
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LENGTH: 20
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Sequence 55, Application US/10211908
Faguence 55, Application US/10211908
Fublication No. US20040023384A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Renneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 12 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/211,908
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 55
LENGTH: 20
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US-10-210-833-67/c

| Sequence 67, Application US/10210833 |
| Publication No. US20040023383A1 |
| GENERAL INFORMATION: APPLICANT: Sanjay Bhanot |
| APPLICANT: Sanjay Bhanot |
| TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION |
| TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION |
| TITLE OF INVENTION NUMBER: US/10/210,833 |
| CURRENT APPLICATION NUMBER: US/10/210,833 |
| NUMBER OF SEQ ID NOS: 165 |
| SEQ ID NO 67 |
| LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-833-67
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ORGANISM: Artificial Sequence
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HAPPLICANT: KINSELLA, TODD M

HAPPLICANT: WINNER, UUSTIN E

HAPPLICANT: WARNER, UUSTIN E

HAPPLICANT: BENNET, WARK K

HAPPLICANT: BENNET, MARK

HAPPLICANT: BENNET, MARK

HAPPLICANT: MARRESON, DAVID C

HITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE IL-4 RECEPTOR-MEDIJ

TITLE OF INVENTION: SYNTHESIS UTILIZING A C-MYC PROTEIN

FILE REFERENCE: RIGIOLS

CURRENT PELING DAVE: 2002-08-16

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.1

SEQ TUD NO 15
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APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: Brett P. Monia
APPLICANT: William A. Gaarde
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Wolia
APPLICANT: Brett P. Wyatt
TILLE OF INVENTION: ANTERNSE MODULATION OF MEKK3 EXPRESSION
FILE REFERENCE: RTSP-0174
CURRENT APPLICATION NUMBER: US/10/380,127A
CURRENT APPLICATION NUMBER: 09/658,688
PRIOR PLILING DATE: 2000-09-08
FRIOR PLILING DATE: 2000-09-08
FRIOR PLILING DATE: 2000-09-08
SEQ ID NO 83
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; CTHER INFORMATION: synthetic primer
US-10-222-729-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-380-127A-83/c; Sequence 83, Application US/10380127A; Publication No. US20040033976A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2°
Matches 16; Conservative
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; Sequence 61, Application US/1034544B
; Publication No. US20040029823A1
; Publication No. US20040029823A1
; Publication No. US20040029823A1
; APPLICANT: MorKay, Robert A.
; APPLICANT: Deach, Nicholas M.
; APPLICANT: Nero, Pam
; APPLICANT: Brett
; APPLICANT: OP JUK PROTEINS
; TITLE OF INVENTION: OF JUK PROTEINS
; TITLE OF INVENTION: OP JUK PROTEINS
; PRIOR PELING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: US 09/130,616
; PRIOR PILING DATE: 1999-04-07
; PRIOR PILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 61
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                                                                              Publication No. US20040029273A1
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: WAITSENSE MODULATION OF EDG1 EXPRESSION
FILE REPERRINCE: RTS-0179
CURRENT APPLICATION NUMBER: US/10/215,448
CURRENT FILING DATE: 2002-08-09
NUMBER OF EQ ID NOS: 105
SEQ ID NO 55
LENGTH: 20
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Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Antisense Oligonucleotide US-10-215-448-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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; Sequence 15, Application US/10222729
; Publication No US20040033538A1
; GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Sequence 11, Application US/10380195A

Sequence 11, Application US/10380195A

Publication No US20040072776A1

SEDERAL INFORMATION:
APPLICANT: Kiyama, Satoshi
APPLICANT: Kiyama, Satoshi
APPLICANT: Rennie, Paul
TITLE OF INVENTION: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy
FILE REFERENCE: UBC.P-023

CURRENT APPLICATION NUMBER: US/10/380,195A

CURRENT APPLICATION NUMBER: PCT/US01/28748

FRIOR FILING DATE: 2000-09-13

FRIOR APPLICATION NUMBER: US 60/232,641

FRIOR PILING DATE: 2000-09-14

FRIOR FILING DATE: 2000-09-14

FRIOR FILING DATE: 2000-09-14

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2

SEQ ID NO 11

LENGTH: 20
                                                                                                                                                                 APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE RTS-01156
CURRENT APPLICATION NUMBER: US/10/380,124
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 40
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1435
US-10-380-195A-54
Sequence 54, Application US/10380195A
; Publication No. US20040072776A1
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                                                                                                Sequence 40, Application US/10380124 Publication No. US20040053874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2696 CACTTCCCACCCTGCCCCT 2714
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gage, Freed
APPLICANT: Gage, Freed
APPLICANT: Ray, Jasodhara
ITILE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
FILE REFERENCE: REGENIA 60-5
CURRENT APPLICATION NUMBER: US/10/622,206
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/09/915,229
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: 08/445,075
PRIOR FILING DATE: 1995-06-19
PRIOR FILING DATE: 1993-01-03
PRIOR FILING DATE: 1993-01-06
PRIOR FILING DATE: 1993-01-06
SEQ ID NO SEQ ID NOS: 4
SOFTWARE: FASTEER for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
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'Sequence 3, Application US/10622206
'Sequence No. US20040048373A1
'GENERAL INFORMATION:
'APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-454-663-62
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; OTHER INFORMATION: Forward primer for PCR
US-10-622-206-3
CURRENT APPLICATION NUMBER: US/10/454,663 CURRENT FILING DATE: 2003-06-04
                  CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: 09/982,262

PRIOR PILING DATE: 2001-10-18

PRIOR PILING DATE: 2001-10-18

PRIOR PILING DATE: 2000-09-12

PRIOR FILING DATE: 1998-08-03

PRIOR PILING DATE: 1998-08-03

PRIOR PILING DATE: 1998-08-03

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1993-06-17

PRIOR FILING DATE: 1993-06-17

PRIOR FILING DATE: 1993-02-17

PRIOR PILING DATE: 1993-01-21

NUMBER OF SEQ ID NOS: 89

LENGTH: 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/10274387
Publication No. US20040077085A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CDC14A EXPRESSION FILE REPRENCE: RTS-0172
CURRENT APPLICATION NUMBER: US/10/274,387
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 14
LENGTH: 20
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APPLICANT: Thomas McGonigal
TITLE OF INVENTION: WANTSENSE MODULATION OF CDC14A EXPRESSION
FILE REPERENCE: RTS-0262
CURRENT APPLICATION NUMBER: US/10/274,311
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 14
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3;
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Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Sco...
84.2%; Pred. No. >...
                                                                                                                                                      ) OTHER INFORMATION: Antisense Oligonucleotide US-10-274-347-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-10-274-311-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Antisense Oligonucleotide
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                                                                                                                                                                                                                                                                                                                  2632 CCACATGTCCAGCACCTTG 2650
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CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 16
LENGTH: 20
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ORGANISM: Artificial Sequence
                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                      FEATURE:
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                                                                                 TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
TITLE OF INVENTION: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy
FILE REPERROCE: UBC.P-023
CURRENT APPLICATION NUMBER: US/10/380,195A
CURRENT APPLICATION NUMBER: PCT/US01/28748
PRIOR APPLICATION NUMBER: PCT/US01/28748
PRIOR APPLICATION NUMBER: US 60/232,641
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
NUMBER OF SEC ID NOS: 63
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10273826
Publication No. US20040077083A1
GENERAL INFORMATION:
ADPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 4 EXPRESSION
FILE REFRERENCE: RTS-0161
CURRENT APPLICATION NUMBER: US/10/273,826
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 87
LENGTH: 20
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US-10-274-347-16/c
Sequence 16, Application US/10274347
Publication No. US-20040077084A1
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
APPLICANT: Junling Li
APPLICANT: Junling Li
APPLICANT: Junling Li
APPLICANT: Wath Glaser
TITLE OF INVERTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 4 EXPRESSION
FILE REFERENCE: RTS-0264
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: IGFBP2 antisense US-10-380-195A-54
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ORGANISM: Artificial Sequence
                                            Kiyama, Satoshi
Nelson, Colleen
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Matches 16; Conservative
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LENGTH: 20
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Sequence 528, Application US/10280183A Publication No. US20040081964A1 GENERAL INFORMATION:
APPLICANT: Pfizer Inc. APPLICANT: Bachmanov, Alexander A
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                                                                                                                                                                                              Beauchamp, Gary K.
Chatterjee, Aurobindo
De Jong, Pieter J.
Li, Shanru
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Best Local Similarity 84.23
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-210-802-111/c
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ORGANISM: Mouse
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                                                                                                  WS-10-728-509-26

Sequence 26, Application US/10728509

Sequence 26, Application US/10728509

Publication No. US20040077583A1

GENERAL INFORMATION:

APPLICANT: Hong Zhang

APPLICANT: Hong Zhang

APPLICANT: APPLICANT: APPLICATION UNMBER: US/10/728,509

CURRENT APPLICATION NUMBER: US/10/728,509

CURRENT FILING DATE: 2001-07-17

PRIOR FILING DATE: 2001-07-17

SEQ ID NO 26

LENGTH: 20

LENGTH: 20
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APPLICANT: Read, Danielle R.
APPLICANT: Reed, Danielle R.
APPLICANT: Reed, Danielle R.
APPLICANT: Rober, Danielle R.
APPLICANT: Tordoff, Michael G.
APPLICANT: Tordoff, Michael G.
TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETINERS
FILE REPERENCE: PC18306A
CURRENT APPLICANTON NUMBER: US/10/280,183A
CURRENT APPLICANTON NUMBER: 60/200,794
PRIOR FILING DATE: 2002-10-25
PRIOR PAPLICANTON NUMBER: 60/200,794
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US-10-280-183A-230/c
Sequence 230, Application US/10280183A
Publication No. US20040081964A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bachmanov, Alexander A
Beauchamp, Gary K.
Chatteriee, Aurobindo
De Jong, Pieter J.
Li, Shanru
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20 GCCGAGTCCAAATAGGAGC 2
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 230
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ORGANISM: Mouse
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APPLICANT:
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APPLICANT:
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APPLICANT: Li, Xia
APPLICANT: Li, Xia
APPLICANT: Cohmen, Jeffrey D
APPLICANT: Reed, Danielle R.
APPLICANT: Rese, David
APPLICANT: Ross, David
APPLICANT: Ross, David
APPLICANT: Tordoff, Michael G.
TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
FILE REFERENCE: PC18306A
CURRENT APPLICATION NUMBER: US/10/280,183A
CURRENT APPLICATION NUMBER: 60/200,794
PRIOR APPLICATION NUMBER: 60/200,794
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PALENTIN OF: 3.1
SEQ ID NO 528
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Publication No. US20040087523A1

GENERAL INFORMATION:

APPLICANT: Ming-Yi Chiang

TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

TITLE TOF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

FILE REPERENCE: RTS-036

CURRENT APPLICATION UNMER: US/10/210,802

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 47

LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 3; Indels
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Gaps

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                                                                                                                                                                                                                                                              3; Indels
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US-10-300-424-94

$ Gaquence 94, Application US/10300424

$ Publication No. US20040096835A1

$ GENERAL INFORMATION:

$ APPLICANT: Kenneth W. Dobie

$ TITLE OF INVENTION: MODULATION OF THESF14 EXPRESSION

$ FILE REFERENCE: RTS-0437

$ CURRENT FILING DATE: 2002-11-19

$ NUMBER OF SEQ ID NOS: 129

$ SEQ ID NO 94

$ LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kenneth W. Dobie
TITLE OF INFORMATION: MODULATION OF THESF14 EXPRESSION
FILE REFERENCE: RTS-0437
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 129
LENGTH: 20
                                                                                                                                                                                                     Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                     ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-81
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-424-25
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0.4%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
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US-10-300-424-25/c
Sequence 25, Application US/10300424
; Publication No. US20040096835A1
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  SEQ ID NO 81
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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ORGANISM: H. sapiens
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| Publication No. US20040091920A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: TSUJI, Toru
| APPLICANT: TSUJI, Toru
| TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
| TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
| TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
| TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
| TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
| TITLE OF INVENTION: MUMBER: US/10/637,009
| PRIOR PILING DATE: 2000-10-17
| PRIOR PILING DATE: 2000-10-17
| PRIOR PILING DATE: 2003-03-26
| PRIOR FILING DATE: 2001-02-06
| NUMBER OF SEQ. ID NOS: 50
| SOFTWARE: PatentIn version 3.2
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Publication No. US20040092465A1
GENERAL INFORMATION:
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
TITLE OF INVENTION: WOULD OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
TITLE OF INVENTION: WOULD TO HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
CURRENT APPLICATION UNMERR: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
                                                                     APPLICANT: Ming-Yi Chiang
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAAL531 PROTEIN EXPRESSION
FILE REPERENCE: RTS-035 (10) 10/210, 802
CURRENT APPLICATION NUMBER: US/10/210, 802
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Sequence 111, Application US/10210802
Publication No. US20040087523A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                           US-10-210-802-111
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US-10-293-864-81
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                                                                                                                                                                                                                                                              SEQ ID NO 111
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LENGTH: 20
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Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
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TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-10-17
SOFTWARE: PACHICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
SOFTWARE: PACHICIN VERSION 3.2
SEQ ID NO 3049
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Broschat, KAY
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01399/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
LENGTH: 20
                                                                                                                                                                                                                     0.4%; Sco. No. 84.2%; Pred. No. ...
CURRENT APPLICATION NUMBER: US/10/303,329
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 59
LENGTH: 20
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; OTHER INFORMATION: human GFAT antisense
US-10-688-706-3049
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Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Parmacia Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73, Application US/10688706 Publication No. US20040102412A1 GENERAL INFORMATION: APPLICANT: Pharmacia Corp.
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                     TYPE: DNA
ORGANISM: H. sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-688-706-3049/c
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US-10-688-706-73
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US-10-303-329-31
US-10-303-329-31
Sequence 31, Application US/10303329
Publication No. US20040101850A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobien
TITLE OF INVENTION: MODULATION OF C-SRC TYROSINE KINASE EXPRESSION
FILE REPRENCE: HTS-0005
CURRENT APPLICATION NUMBER: US/10/303,329
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 70
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Publication No. US20040101850A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
APPLICANT: ROUPLAITION OF C-SRC TYROSINE KINASE EXPRESSION
FILE REPERENCE: HTS-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                           APPLICANT: Uniderery, Richard A. APPLICANT: Lindberg, Richard A. APPLICANT: Shutter, John R. TITLE OF INVENTION: MODULATION OF FORKHEAD BOX OIA EXPRESSION FILE REPERENCE: AMGNO001-10.1 CURRENT APPLICATION NUMBER: US/10/671,074 CURRENT FILING DATE: 2003-09-25 PRIOR APPLICATION NUMBER: US 10/260,203 PRIOR FILING DATE: 2002-09-26 LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                       APPLICANT: Bhanot, Sanjay
APPLICANT: Veniant-Ellison, Murielle
                          Sequence 36, Application US/10671074 Publication No. US20040097459A1 GENERAL INFORMATION: APPLICANT: Dobie, Kenneth W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 TGCTGGGCAGCGACGTGGA 590
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Best Local Similarity 84.2%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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         US-10-671-074-36
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LENGTH: 20
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Publication Wo. US20040110139A1
General Information
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REFERENCE: RTS-0338
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
IENGTH: 20
                                                                                                                                                                                                             APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REFERENCE: RTS-0338
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
EBQ ID NO 37
LENGTH: 20
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Publication No. US20040110150A1
GENERAL INFORMATION:
APPLICANT: Erich Koller
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: WODULATION OF EPHRIN-B2 EXPRESSION
FILE REFERENCE: PTS-0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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Pred. No. 9.1e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/316,516
  1288 GIAGCCGTGAAGATGCTGA 1306
                                                                                                                                                  ; Sequence 37, Application US/10315474 ; Publication No. US20040110139A1
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                              US-10-315-474-37/c
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Sequence 10, Application US/10332406A

Publication No. US20040103453A1

GENERAL INFORMATION:
APPLICANT: Robert Dudler
APPLICANT: Robert Dudler
TITLE OF INVENTION: Lipoxygenase Genes, Promoters, Transit Peptides and Proteins Ther
FILE REFERENCE: 3144405PCT:
CURRENT APPLICATION NUMBER: US/10/332,406A
CURRENT FILING DATE: 2003-06-19
PRIOR FILING DATE: 2003-06-19
PRIOR PRILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1
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US-10-688-706-3054/C

Sequence 3054, Application US/10688706

Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Broschat, Kay.

ITTLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

FILE REPERENCE: 10393/1

CURRENT APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION VUMBER: 5002-10-17

PRIOR PILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: PatentIn version 3.2
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  Length 20;
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                                             3; Indels
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Pred. No. 9.1e+02;
0; Mismatches 3;
  Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                          0; Mismatches
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; OTHER INFORMATION: human GFAT antisense
US-10-688-706-3054
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; OTHER INFORMATION: oligonucleotide US-10-332-406A-10
                                                                                   3269 TTTGCTTTGTCCTTTTCA 3287
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Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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LOCATION: (1)..(20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3054
LENGTH: 20
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LENGTH: 20
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US-10-671-395-122

Sequence 122, Application US/10671395

SEQUENCE 122, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

SAPPLICANT: Pharmacia Corp.

APPLICANT: Gieres, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: SAPERSSATON

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT PILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

FRIOR FILING DATE: 2002-09-25
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Publication No. US20040132063A1;
GENERAL INFORMATION:
A PAPLICANT: Pharmacia Corp.
APPLICANT: Gieree, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                 Sequence 19, Application US/10317279
Publication No. US20040110703A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ming-Yi Chiang
APPLICANT: Mang-Yi Chiang
APPLICANT: Memerh W. Dobie
TITLE OF INVENTION: MODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
TITLE OF INVENTION: MODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
CURRENT APPLICATION UNDRER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
SEQ ID NO 19
IENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-10-317-279-19
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               2 CTGAGCCTGCCGGGGATCC 20
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SOFWHARB: PatentIn version 3.2
SEQ ID NO 122
LENGTH: 20
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Matches 16; Conservative
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                                                                                       RESULT 1461
US-10-317-279-19/c
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US-10-671-395-309
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US-10-317-270-12/C
US-10-317-270-12/C
Sequence 12, Application US/10317270
Publication No. US20040110701A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
FILE REFRENCE: RTS-0479
CURRENT APPLICATION UNMER: US/10/317,270
CURRENT PILING DATE: 2002-12-10
SEQ ID NO 12
LENGTH: 20
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Publication No. US20040110701A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
FILE REPERENCE: RTS-0479
CURRENT APPLICATION UNDEER: US/10/317,270
CURRENT APPLICATION UNDEER: US/10/317,270
UNDEER OF SEQ ID NOS: 160
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-516-23
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NUMBER OF SEQ ID NOS: 134
SEQ ID NO 23
LENGTH: 20
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: H. sapiens
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US-10-317-270-90
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                                                                                                                   TYPE: DNA
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Sequence 1117, Application US/10671395
; Sequence 1117, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: EXPRESSION
; FILLE OF INVENTION: EXPRESSION
; FILLE OF INVENTION: LEXPRESSION
; FILLE OF INVENTION: LOOP 25
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: 06/413,549
; PRIOR APPLICATION NUMBER: 06/413,549
; RIGHT PRIOR PILLING DATE: 2002-09-25
; SEQ ID NOS: 1809
; SEQ ID NO 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 966, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
    TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 966
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3; Indels
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                                                                                                                                          OTHER INFORMATION: Human PGE2 antisense
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 574
LENGTH: 20
TYPE: DNA
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Matches 16; Conservative
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Matches 16; Conservative
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                                                                                           ORGANISM: artificial FEATURE:
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US-10-671-395-966
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WS-10-671-395-501

Sequence 501, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN EZ SYNTHASE
TITLE OF INVENTION: AND EXPRESSION
FILE REFERENCE: 1179/1/US

CURRENT FILING DATE: 2003-09-25

PRIOR APPLICATION UNMBER: 2002-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFWRARE: Patentin Version 3.2

SEQ ID NO 501

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Sequence 574, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT PPLICATION NUMBER: US/10/671, 395

CURRENT PPLICATION NUMBER: 06/413, 549

PRIOR FILING DATE: 2002-09-25
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                      FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 60/413,549
FRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
LENGTH: 20
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Human PGE2 antisense US-10-671-395-309
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       EXPRESSION
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Best Local Similarity 84.2
Matches 16; Conservative
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       TITLE OF INVENTION:
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Sequence 1450, Application US/10671395

Sequence 1450, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE WOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;
TITLE OF INVENTION: ANTISENSE WOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;
TITLE OF INVENTION: 1179/1/US
CURRENT FILING DATE: 2003-09-25

CURRENT FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 1450

LENGTH: 20
                                                                                                                                                                                                   APPLICANT: Pharmacia Corp.
APPLICANT: Bramacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
FRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1180
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1180
                                                                                                                               Sequence 1180, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
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Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conservative
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                                                                                                              US-10-671-395-1180/c
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                                                                                                                                                                                                                                                                                        Sequence 1140, Application US/10671395

Fublication No. US20040132063A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLEANT: Pharmacia Corp.
FILLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
FILLE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
FRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PATCHIN VORSION 3.2
SEQ ID NO 1140
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1469
US-10-671-395-1174/c
is gequence 1174, Application US/10671395
is publication No. US20040132063A1
is gequence 1174, Application No. US20040132063A1
is gequence 1174, Application No. US20040132063A1
is gequence 1174, Application No. US20040132063A1
is APPLICANT: Pharmacia Corp.
is APPLICANT: Gierse, James K
i TITLE OF INVENTION: EXPRESSION
is TITLE OF INVENTION: EXPRESSION
is TITLE OF INVENTION: LATISTENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
is TITLE OF INVENTION: LATISTENSE (1771)
is RILING DATE: 2003-09-25
is NUMBER OF SEQ ID NOS: 1809
is SOFTWARE: Patentin version 3.2
is SEQ ID NO 1174
illength: 20
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                                     Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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Pred. No. 9.1e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1174
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                                                                                                                                         2007 GGTGGAGGACCTGGACCGT 2025
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: artificial
                                          Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-671-395-1140/c
US-10-671-395-1117
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; Sequence 1499, Application US/10671395

2362 TGTGCCTGTGTGCGTGCGC 2380

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Sequence 1788, Application US/10671395

Sequence 1788, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE WOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

TITLE 
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Publication No. US20040132682A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REPRESENTED BY THE UNITED STATES OF AMERICA AS
APPLICANT: HUMAN SERVICES
APPLICANT: Klinman, Dennis M.
APPLICANT: Xamada, Hiroshi
TITLE OF INVENTION: METHOD OF TREATING INFLAMMATORY LUNG DISEASE WITH SUPPRESSORS OF
TITLE OF INVENTION: CDG OLIGONUCLEOTIDES
FILE REFERENCE: 4239-66902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 9.1e+02;
0; Mismatches 3;
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Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
LENGTH: 20
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CURRENT FILING DATE: 2003-10-07
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1788
                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1769
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PRIOR FILING DATE: 2002-10-08
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1 Similarity 84.2%;
16; Conservative
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Best Local Similarity 84.2'
Matches 16; Conservative
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ORGANISM: artificial
FEATURE:
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Best Local Similarity
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ORGANISM: artificial
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                                                                                                   APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/05
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1499
LENGTH: 20
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APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: 05/10/671,395
CURRENT PLING DATE: 2003-09-25
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PALENTIN Version 3.2
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Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Flaarmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1499
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Publication No. US20040132063A1
GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative (
      Publication No. US20040132063A1
GENERAL INFORMATION:
                                                                    APPLICANT: Pharmacia Corp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: artificial
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US-10-671-395-1662/c
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US-10-671-395-1769
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LENGTH: 20
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Sequence 105, Application US/10476962
; Sequence 105, Application US/10476962
; Publication No. US20040191904A1
; GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
    APPLICANT: C. Frank Bennett
    TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
    FILE REPRENENT
    PRIOR REPERING DATE: 2003-11-05
    PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
; PRIOR PILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 105
    LENGTH: 20
                                                                                                                                                                                            Sequence 104, Application US/10476962
; Sequence 104, Application US/10476962
; Publication No. US20040191904A1
; CENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
    TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
    TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
    TITLE OF INVENTION: ANTISENSE NOT 11-05
    PRIOR PAPLICATION NUMBER: US/10/476,962
    CURRENT FILING DATE: 2003-11-05
    PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
    PRIOR PILING DATE: 2001-05-18
    NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 104
    LENGTH:: 20
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3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Antisense Oligonucleotide US-10-476-962-104
0; Mismatches
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; Publication No. US20040191904A1
                                                      2290 GGAGACAGCTACACAGA 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1533 GGAGCAGCTCACCTTCAAG 1551
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                                                                                                            2 GAAGAACAGCTACCCAGA 20
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
Matches 16; Conservative
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US-10-476-962-150/c
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15 Sequence 12, Application US/10766185

15 Sequence 12, Application US/10766185

15 Sequence 12, Application US/10766185

16 Sequence 12, Application US/10766185

17 Sequence 12, Application US/10766185

18 APPLICANT: Abn, Chang Ho

19 APPLICANT: Abn, Chang Bok

10 APPLICANT: Mao, Lingjun

10 APPLICANT: Mao, Lingjun

11 APPLICANT: Mao, Lingjun

12 SEPERROKE: REX 7034

13 CURRENT APPLICATION NUMBER: US/10/766,185

14 CURRENT FILING DATE: 2004-01-28

15 NUMBER OF SEQ ID NOS: 130

16 SOSTWARE: PatentIn version 3.1
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US-10-741-601-26226
Sequence 26226, Application US/10741601
Fublication No. US20040166519A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, WETHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
FERSIOL NO 26226
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                      , OTHER INFORMATION: Suppressive oligonucleotide sequence.
US-10-682-130-23
                                                                                                                                                                                                                                                                             Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 20
                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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CRGANISM: Homo sapiens
US-10-741-601-26226
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Best Local Similarity
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LENGTH: 20
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Gaps

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vivlemore401-10.rnpb

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GENERAL INFORMATION:
APPLICANT: Keene, Jack D.
APPLICANT: Tenenbaum, Scott A.
APPLICANT: Tenenbaum, Scott A.
APPLICANT: Tenenbaum, Scott A.
APPLICANT: Tenenbaum, Scott A.
APPLICANT: Phelps, William C.
TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Targets;
FILE REFERENCE: RBN-001CP
CURRENT APPLICATION NUMBER: US 10/309,788
CURRENT APPLICATION NUMBER: US 60/173,338
PRIOR PILING DATE: 2009-12-28
PRIOR APPLICATION NUMBER: US 90/750,401
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 23
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APPLICANT: Keene, Jack D.

APPLICANT: Tenenbaum, Scott A.

APPLICANT: Carson, Craig C.

TITLE OF INVENTION: Complexes
FILE REFERENCE: RBN-001CN
CURRENT FILING DATE: 2002-09-10
PRIOR PAPLICATION NUMBER: US 09/750,401
PRIOR PILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/173,338
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US-10-309-788-20
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                                                                                                                                                                                                                                                                                              0.4%; Score 14.2; DB 1;
15.8%; Pred. No. 1e+03;
tive 13; Mismatches 3;
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PRIOR APPLICATION NUMBER: US 60/173,338
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 23
TYPE: NAA
TYPE: NAA
ORGANISM: Artificial Sequence
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Publication No. US20030211466A1
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Best Local Similarity
Matches 3; Conserva
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Best Local Similarity
Matches 3; Conserva
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Sequence 20, Application US/09750401
Sequence 20, Application US/09750401
Sequence 20, Application US/09750401
Sequence 20, Application US-09-04211A1
GENERAL INFORMATION:
APPLICANT: Keene, Jack D.
APPLICANT: Tenenbaum, Scott A.
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein TITLE OF INVENTION: complexes
FILE REPRENCE: RBN-001
CURRENT APPLICATION NUMBER: US/09/750,401
CURRENT FILING DATE: 2000-12-28
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TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
FILE REFERENCE: DX.7003 CON
CURRENT APPLICATION NUMBER: US/09/988,899
CURRENT FILING DATE: 2000-11-19
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 1999-05-18
PRIOR PILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 17
LENGTH: 23
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                                                APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
FILE REFERENCE: RTS-0222
CURRENT APPLICATION NUMBER: US/10/476,962
CURRENT APPLICATION NUMBER: DRIOP APPLICATION NUMBER: US/09/860,473
PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
PRIOR FILING APPLICATION NUMBER: US/09/860,473
PRIOR FILING APPLICATION NUMBER: US/09/860,473
SEQ ID NOS: 169
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-476-962-150
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
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Patent No. US20020102613A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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       GENERAL INFORMATION:
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US-09-988-899-17/c
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APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGANATA, YOLCHI
APPLICANT: TARAMATA, WASAXI
APPLICANT: TARAMADA, KASUTAKA
APPLICANT: YAMADA, KASUTAKA
APPLICANT: YAMADA, KASUTAKA
APPLICANT: YAMADA, KASUTAKA
APPLICANT: YAMADA, KASUTAKA
APPLICANT: YOKOWAKU, TOYOKAZU
TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS (
TITLE OF INVENTION: METHOD
FILE REPERENCE: 210352US-1994-163-0-X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.2; DB 1; Length 30; 70.4%; Pred. No. 1.3e+03; tive 0; Mismatches 8; Indels
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CURRENT FILING DATE: 2001-06-27
PRIOR PRIOR PRILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
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                                   PRIOR PEDILICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFWARE: Patentin version 3.1
LENGTH: 30
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Publication No. US20030082592A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09891517 Patent No. US20020106653A1
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
SORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-13
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ORGANISM: Artificial Sequence
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es 19; Conserva
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US-09-891-517-13
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Best Local S:
Matches 19
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Sequence 20, Application US/10629453

Sequence 20, Application No. US20040096878A1

SEQUENCE 20, Application No. US20040096878A1

SEQUENCE CASE OF CAS
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Publication No. US20010000175A1
GENERAL INFORMATION:
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: YAMAGAMA, YOUNGHI
APPLICANT: YAMAGAMA, YOUNGHI
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, YENTA
APPLICANT: FUNUSHO, KENTA
APPLICANT: FUNUSHO, KENTA
APPLICANT: FUNUSHOR: NUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: USE OF THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: USE OF THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: USE OF THE METHOD FOR ANALYZING DAT
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TITLE OF THE METHOD FOR THE METHOD FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 2
Best Local Similarity 15.8%; Pred. No. 1e+03;
Matches 3; Conservative 13; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of Neuronal-Cadherin
US-10-238-306B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THER INFORMATION: 3 -UTR sequence of Neuronal-Cadherin
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PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 23
                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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US-09-725-265-13
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105-10-108-969-8

Sequence 8, Application US/10108969

Sequence 8, Application US/20030198959A1

Publication No US20030198959A1

GENERAL INFORMATION:

APPLICANT: Kurnit, David M.

TITLE OF INVENTION: Methods and Compositions for Analysis of Urine Samples in the Diacy

TITLE OF INVENTION: and Treatment of Kidney Diseases

TITLE OF INVENTION: and Treatment of Kidney Diseases

FILE REFERENCE: 6598-0001

CURRENT APPLICATION NUMBER: US/10/108,969

CURRENT PILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 9

SOFFWARE: Patentin version 3.1

SEQ ID NO 8

LENGTH: 32
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                                                                                                                                                                  Sequence 558, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Human beta-actin reverse primer
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0.4%; Score 14.2; DB 1;
Best Local Similarity 70.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 65.5%; Pred. No. 1.3e+03; Matches 19; Conservative 1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR PELING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 958
LENGTH: 31
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3259 AGATATTTTATTTGCTTTGTCCTTTTT 3285
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                                               Sequence 2, Application US/10208357
Publication No. US20020182687A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-801-274-958
                                                                                                                                                             US-09-801-274-958/c
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APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
APPLICANT: FURUSHO, KENTA
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: NUMBER: US/10/683,386
CURRENT APPLICATION NUMBER: US/10/683,386
CURRENT APPLICATION NUMBER: US/9/556,127
PRIOR APPLICATION NUMBER: US/9/556,127
PRIOR APPLICATION NUMBER: US/99-111601
PRIOR APPLICATION NUMBER: J99-04-20
NUMBER OF SEQ ID NOS: 70
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VETSION 3.1
                                       APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: UNGLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE REPRENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US/10/209,608
CURRENT APPLICATION DATE: 2002-08-01
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                                                                                                                                                                                                                                                                                                               PRIOR PELICATION NUMBER: US/09/725,265
PRIOR PILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 1999-04-20
PRIOR PILING DATE: 1999-04-20
NUMBER OF SEC ID NOS: 70
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/10683386
Publication No. US20040063137A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: SYNTHETIC DNA US-10-209-608-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3259 AGATATTTTATTGCTT
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LENGTH: 30
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LENGTH: 30
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Sequence 479, Application US/09263959

Patent No. US20020150891A1

Patent No. US20020150891A1

PAPELICANT: Hood, Leroy E. APPLICANT: Rowen, Lee

APPLICANT: Rowen, Lee

APPLICANT: ROWEN, Lee

APPLICANT: NOOP, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , DB 1; be...
n. 6.7e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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CURRENT APPLICATION DATA: 15.25
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-WAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                            10.4%; Score 14; DB 1; Lu ilarity 100.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 1; Pred. No. 6.7e
                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-15
CURRENT APPLICATION NUMBER: US/09/735,363A
                    CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 60/228,925
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION:
ATTORNEY/ACENT INFORMATION:
NAME: MCMASICERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 479:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
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Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTG 2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 14, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-263-959-479/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-263-959-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Sequence 6, Application US/10289921

Sublication No. US20030113337A1

GENERAL INFORMATION:

APPLICANT: MENUELO. Daniel

APPLICANT: LEVIN, Brandi A.

TITLE OF INVENTION: HIGH EFFICIENCY TISSUE SPECIFIC COMPOUND

TITLE OF INVENTION: DELIVERY SYSTEM USING STREPTAVIDIN-PROTEIN A FUSION PROTEIN

FILE REFERENCE: 5986/11123-US1

CURRENT APPLICATION NUMBER: US/10/289,921

CURRENT APPLICATION NUMBER: US/10/289,921

CURRENT FILING DATE: 1995-11-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FESTERSE (for Windows Version 3.0

SEQ ID NO 6

LENTH: 39
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APPLICANT: Philip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02891-0181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.4%; Score 14.2; DB 1; Length 38; Best Local Similarity 62.9%; Pred. No. 1.5e+03; Matches 22; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
0.4%; Score 14.2; DB 1; Length 39;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: biotinylated poly(dT) oligonucleotide US-10-289-921-6
                  APPLICANT: Lobie, Peter
APPLICANT: Magner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT APPLICATION NUMBER: US/10/619,103
PRIOR APPLICATION NUMBER: 00/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FRSEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: designed sequence to act as a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3307 GGATTTTTTTAGGAGATTTTATTTTTGGACTTC 3341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3262 TATTTTATTTGCTTTGTCCTTTTTCAG 3288
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                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
     APPLICANT: Kurz, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1495
US-09-735-363A-15
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                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Gaps

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Sequence 562, Application US/09263959
Patent No. US20020150831A1
BENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ACO, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14; DB 1;
                                                               FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMBaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEFORMINICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 632-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MCMAGLERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEFONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3466 ATATATCTATATAT 3479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%
Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-263-959-562
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US-09-263-559-532
US-09-263-559-532
Sequence 532, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESCONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Lee
APPLICANT: ROSOP, Ben P.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104-7092

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 06-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
RELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CLARACTERISTICS:
LENGTH: LA base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Le
. 6.7e+02;
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                                                                                              Sequence 530, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
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STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Sc
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                    Washington
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US-09-263-959-530
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                             US-09-263-959-530/c
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GENERAL INFORMATION:
APPLICANT: Rowen, Leeroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lip
ADDRESSEE: Seed and Berry Lip
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
COMPUTE: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 6.7 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMSaters, David D.
REJETRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-263-959-726/c
; Sequence 726, Application US/09263959
; Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 726:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTG 2331
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STATE: Washington
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Lercy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hood, Lerry E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14; DB 1; Ld
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 592:
INFORMATION FOR SEQ ID NO: 592:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                           Sequence 592, Application US/09263959; Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 100.0%; P.
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2826 ATATACATATAT 2839
                                   3466 ATATATCTATATAT 3479
                                                                            1 ATATATCTATATAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle STATE: Washingto COUNTRY: 110
                                                                                                                                         RESULT 1500
US-09-263-959-592/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-09-263-959-592
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US-09-263-959-658
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Sequence 111, Application US/10292198
; Publication No. US20030157654A1
; GENERAL INFORMATION:
    APPLICANT: SHEN, BEN
; APPLICANT: SHEN, BEN
; TITLE OF INVENTION: BATHWAY
; FILE OF INVENTION: BATHWAY
; FILE OF INVENTION: BATHWAY
; FILE REFERENCE: 054030-0007
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/10/292,198
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 09/478,188
; PRIOR APPLICATION NUMBER: US 60/115,434
; PRIOR APPLICATION NUMBER: US 60/115,434
; PRIOR APPLICATION NUMBER: US 60/115,434
; PRIOR ELING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 111
; LENGTH: 15
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100.0%; Pred. No. 7.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLIGATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 14; DB 1; L
100.0%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 822:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Streptomyces globisporus
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100.08; L1.
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Seattle
Washington
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                                                               98104-7092
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Matches
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
WUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESPONDENCES: 1279
CORRESPONDENCE ADDRESS:
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     DB 1; ле...
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0; Indels
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARKETERS DAVID DAVID:
REGISTRATION NUMBER: 33,963
REPRENCE/DOCKET NUMBER: 33,963
REPRENCE/DOCKET NUMBER: 33,963
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 752:
SEQUENCE CRARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                      Query Match 0.4%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 6.7 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 822, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              US-09-263-959-752
; Sequence 752, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
                                                                                                                 2824 ATATATACATATAT 2837
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-263-959-822/c
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US-09-263-959-752
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APPLICANT: MCSwiggen, Jim
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Method and Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEHBOD-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2748, Application US/10156306
| Publication No. US20030119017A1
| GENERAL INPORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: McSwiggen, James
| TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related;
| TITLE OF INVENTION: Levels of IRK-Gamma and PKR
| FILE REPERENCE: MBHB01-664-A (400/050)
| CURRENT APPLICATION NUMBER: US/10/156,306
| CURRENT PILING DATE: 2002-05-28
| NUMBER OF SEQ ID NOS: 8013
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 2748
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
PILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: PatentIn version 3.0
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100.0%; Pred. No. 8.2e+02;
Ative 0; Mismatches 0; Indels
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50.0%; Pred. No. 7.7e+02;
ive 7; Mismatches 0; Indels
Ribozyme Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3576, Application US/10156306
; Publication No. US20030119017A1
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Best Local Similarity 50.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
US-10-156-306-2748
                                                                                                                                                                                                                                                                                                                                                LENGTH: 16
TYPE: RNA
CRGANISM: Homo sapiens
US-10-287-949A-6067
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Best Local Similarity
Matches 14; Conserva
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US-10-156-306-2748/c
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LENGTH: 17
TYPE: RNA
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Publication No. US20040077565A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escopedo, Jaime
APPLICANT: Escopedo, Jaime
APPLICANT: Escopedo, Jaime
APPLICANT: Part APPLICANTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
           Sequence 111, Application US/10159257A

Publication No. US20040161828A1

GENERAL INFORMATION:
APPLICANT: SHEN, BEN

APPLICANT: CHRISTENSON, STEVEN D.
APPLICANT: CHRISTENSON, STEVEN D.
TITLE OF INVENTION: ANTIBIOTIC C-1027

TITLE OF INVENTION: ANTIBIOTIC C-1027

FILE REFERENCE: 4077-896020US

CURRENT APPLICATION NUMBER: US/10/159,257A

CURRENT FILING DATE: 2002-05-31

PRIOR PPLICATION NUMBER: 09/478,188

PRIOR PPLICATION NUMBER: 60/115,434

PRIOR PILING DATE: 1999-01-06

NUMBER OF SEQ ID NOS: 207

SEQ ID NOS: 207

SEQ ID NO 11
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-159-257A-111
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Pred. No. 7.7e+02;
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CURRENT PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PATENTIN VEFFION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-287-949A-6067
Sequence 6067, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 50.0%;
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US-10-138-674-6067
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US-10-138-674-6067
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LENGTH: 16
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rowsyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Mayorigen, Jim
APPLICANT: Service of Vincential Company of C
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                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                            0; Indels
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US-10-676-154-523

Sequence 523, Application US/10676154

Publication No. US20040081996A1

GENERAL INFORMATION:

APPLICANT: John Landers

APPLICANT: David Houseman

APPLICANT: Alain Charest

TITLE OF INVENTION: Methods and Products Related to

TITLE OF INVENTION: Methods and Products Related to

TITLE OF INVENTION: Methods and Products Related to

TITLE OF INVENTION: Mossell 100 NA Analysis

FILE REFERENCE: NO656/7045 (HCL/MAT)

CURRENT FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/101,757

PRIOR APPLICATION NUMBER: PCT/US99/22283

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 691

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH:: 17
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. 8.2e+02;
                                        Query Match 0.4%; Score 14; DB 1; I
Best Local Similarity 78.6%; Pred. No. 8.2e+02;
Matches 11; Conservative 3; Mismatches 0;
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Pred. No.
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Local Similarity 100.0%; Pi
hes 14; Conservative 0;
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                                                                                                                                                                                                                 1794 CCAGAGTGACGTCT 1807
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Best Local Similarity 78.6%;
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-10-287-949A-8982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-676-154-523
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...drmaceuticals, Inc.

...drmaceuticals, Inc.

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases

FILE REFERENCE: MBHB00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin version 3.0

SEQ ID NO 8982

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                                                                                Score 14; DB 1; Length 1., Pred. No. 8.2e+02;
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100.0%; Pred. No. 8.2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Box, Neil F
APPLICANT: Duffy, David L
APPLICANT: Hayward, Nicholas K
APPLICANT: Hayward, Nicholas G
APPLICANT: Sturm, Richard A
APPLICANT: Sturm, Richard A
APPLICANT: Gruis, Nelleke A
APPLICANT: Van Der Velden, Pieter
APPLICANT: Prants, Nima
APPLICANT: Prants, Rune R
TITLE OF INVENTION: MELANOMA RISK DETECTION
FILE REFERENCE: 8795-2701
CURRENT APPLICATION NUMBER: US/10/108,732
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/279,515
PRIOR APPLICATION NUMBER: US 60/279,515
PRIOR APPLICATION NUMBER: US 60/279,515
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10108732
Publication No. US20030175721A1
GENERAL INFORMATION:
                                                                                                                        Query Match 0.4%; SG
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                     798 GGGCAATTCTATTG 811
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Best Local Similarity 100.
Matches 14; Conservative
; ORGANISM: Homo sapiens
US-10-156-306-3576
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US-10-138-674-8982
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LENGTH: 17
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Sequence 15, Application US/09953562
Publication No. US20030096241A1
GENERAL INFORMATION:
APPLICANT: ZERIA PHARACEUTICALS CO., LTD.
TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
TITLE OF INVENTION: CELL CARCINOMA
FILE REPERRACE: B6114-01
CURRENT APPLICATION NUMBER: US/09/953,562
CURRENT APPLICATION NUMBER: US 2001-083352
PRIOR APPLICATION NUMBER: US 2001-08352
PRIOR FILING DATE: 2001-03-22
SEQ ID NOS: 27
SEQ ID NO 15
LENGTH: 19
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0.4%; Score 14; DB 1; Lu
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                      APPLICANT: Syngente Participations AG
APPLICANT: Cornell Research Foundation, Inc.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Lu, Shen-wen
TITLE OF INVENTION: Furgal Iron Reductase Gene
FILE PEFERENCE: 1360.017W01
CURRENT APPLICATION NUMBER: US/10/432,422
CURRENT APPLICATION NUMBER: US 60/252,732
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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; Sequence 86, Application US/09733294A
; Patent No. US20020045588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Sc.
100.0%; Pre
                                                              Sequence 27, Application US/10432422
Publication No. US20040076981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 14; Conservative
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                                                                                                           GENERAL INFORMATION:
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                                            US-10-432-422-27
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                                                                                                               Sequence 260', Application US/10712672

Sequence 260', Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Bloozyme Pharmaceuticals, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: Stinchcomb, Dan

TILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

FILE REPERENCE: MBHB00-882-C (400/019).

CURRENT APPLICATION NUMBER: US/10/712,672

CURRENT APPLICATION NUMBER: US/09/653,225

PRIOR PILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SEQ ID NO 2607
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US-10-416-110-12

US-10-416-110-12

Sequence 12, Application US/10416110

Publication No. US20040072198A1

GENERAL INFORMATION:

APPLICANT: DIEK, Alexander

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Cdk4

TITLE OF INVENTION: Diagnosis of Diseases Associated with Cdk4

TITLE OF TWENTION: Diagnosis of Diseases Associated with Cdk4

FILE REFERENCE: 5013.1018

CURRENT APPLICATION NUMBER: US/10/416,110

FRIOR APPLICATION NUMBER: DE 10054974.8

PRIOR APPLICATION NUMBER: DE 10054974.8

PRIOR APPLICATION NUMBER: DE 10054974.8

SEQ ID NO 12

LENGTH: 18
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-416-110-12
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0; Indels
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100.0%; Pred. No. 8.7e+02;
tive 0; Mismatches 0; Indels
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Pred. No.
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Best Local Similarity 100.0%; P:
Matches 14; Conservative 0;
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-712-672-2607
                                                                                                               US-10-712-672-2607
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Gaps

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Sequence 1. Application US/10362010

Publication No. US20040038247A1

GENERAL INFORMATION:
APPLICANT: Branner, Sidney
APPLICANT: Tan, Yin, Hwee
TITLE OF INVENTION: AND PHARMACEUTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR TITLE OF INVENTION: AND PHARMACEUTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR TITLE OF INVENTION: REGULATING T-CELL MEDIATED IMMUNE RESPONSE
FILE REFERENCE: 01/22004
CURRENT APPLICATION NUMBER: US/10/362,010
CURRENT FILING DATE: 2003-08-19
NUMBER OF SEQ 1D NOS: 27

SOFTWARE: PATENTINE VERSION 3.2
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i Sequence 60, Application US/10126355

i Sequence 60, Application No. US20030198965A1

j CENERAL INFORMATION:

APPLICANT: SUBSOMM. Freier

i TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID

TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION

FILE REFERENCE: RTS-0428

CURRENT APPLICATION NUMBER: US/10/126,355

CURRENT FILING DATE: 2002-04-19

NUMBER OF SEQ ID NOS: 122

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 60

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-181-846-66
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CURRENT APPLICATION NUMBER: US/10/181,846
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: PCT/US01/01416
PRIOR FILING DATE: 2001-01-16
PRIOR PLLING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
LENGTH: 20
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Matches 14; Conservative
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LENGTH: 20
                                                                                                                                                                                                                                                                                                              TYPE: DNA
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| Sequence 5, Application US/09969037
| Publication No. US20030022247A1
| GENERAL INFORMATION:
| APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
| TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
| TITLE OF INVENTION: Gor 1175-tyrosine phosphorylated KDR/Flk-1 and usages of the sammer of the properties of the same of the properties of the properties of the same price and the properties of the pr
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US-09-969-037-5
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GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: William Gaarde

APPLICANT: Susan M. Freier

APPLICANT: Susan M. Freier

APPLICANT: Edward V. Wancewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION

FILE REFERENCE: ISPH-0527

CURRENT APPLICATION NUMBER: 08/09/733,294A

CURRENT FILING DATE: 2000-12-07

FRIOR APPLICATION NUMBER: 09/572,423

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 108

SEQ ID NOS: 108
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TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTSP-0363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
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100.0%; Pred. No. 9.7e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.7e+02;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-86
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Publication No. US20030083297A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 14; Conservative
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US-09-969-037-5/c
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Query Match

0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 70.6%; Pred. No. 9.7e+02;
Matches 12; Conservative 4; Mismatches 1; Indels
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12) - (12)
; OTHER INFORMATION: Any nucleotide
US-10-362-010-1
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0; Gaps

Search completed: October 28, 2004, 12:21:44 Job time : 110 secs 1669 AAGATCGCAGACTTCGG 1685 ||:||:||:||:||:|| 4 AARATHGCNGAYTTYGG 20 g

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GenCore version 5 Copyright (c) 1993 - 2004 C	OM nucleic - nucleic search, using sw model	Run on: October 28, 2004, 12:01:21 ; S(wi) 3.7.	US core: 37		Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 0.5	Searched: 3741 segs, 81979 residues	Total number of hits satisfying chosen parameters	Minimum DB seq length: 8 Maximum DB seq length: 50	ייים איניים איני	Post-processing: Minimum Match 1008	malo com:	: bee confirm	Pred. No. is the number of results predic score greater than or equal to the score and is derived by analysis of the total is	Mus	* Ouerv	No. Score Match Length DB ID	36.4 1.0 48 1 36.4 1.0 49 1	3 35.6 0.9 50 1	35.6 0.9 50 1	7 35.6 0.9 50	35.2 0.9 48 1 34.8 0.9 48 1	34.6 0.9 46 1 34.4 0.9 44 1	12 34.4 0.9 44 1 13 34.2 0.9 42 1	14 34.2 0.9 47 1	34.2 0.9 47 1	17 34.2 0.9 47 1 18 34.2 0.9 47 1	19 33.8 0.9 37 1	21 33.8 0.9 38 I	33.8 0.9 38 1	24 33.8 0.9 39 1	33.8 0.9 39 1 33.8 0.9 39 1	33.8 0.9 39 1	33.8 0.9 39 1 33.8 0.9 40 1	30 33.8 0.9 40 1	C 31 33.8 0.9 40 1 AAT65/25 C 32 33.8 0.9 40 1 AAT665/51 C 33 33.8 0.9 40 1 AASG1373	33 53.8 C.9 40 I

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ппентипп					28 1 AALSO672 28 1 AALSO672 28 1 ADK61709 28 1 ADK61709 25 1 ACIS658 25 1 ACIS658 25 1 AAX34894 20 1 AAAS4426 20 1 AADS5442 20 1 AADS5440 20 1 AADS5440 20 1 AADS5440

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Human microarray D Human microarray D Sequence of a micr Microsatellite seq Microsatellite seq Antitumoural phosp	Oligonucleotide Wil 20-mer oligonucleo Human MCIR gene re	Human MC1R gene re Simple sequence re	Simple sequence re Mrell related prob	Human PEPCK-cytoso	Antibody binding o	SSR motif #5. Uni SSR motif #9. Uni	Human uridine diph	Oligonucleotide sy	Oligonucleotide SE	Oligonucleotide (C	Oligonucleotide (T	Polynucleotide (ds	Single nucleotide	Human mPGES-1 chim	Human mPGES-1 chim Himan mPGES-1 chim	mPGES-1	mPGES-1	mPGES-1	mPGES-1	mPGES-1	mPGES-1	Human mPGES-1 chim	mPGES-1	mPGES-1	Human mPGES-1 chim Himan mPGES-1 chim	mPGES-1	Human mPGES-1 Cittii Human mPGES-1 Chim	mPGES-1	Human mPGES-1 chim	mPGES-1	rion pro	ο. ε	Human myosin heavy		Phosphorothioate 2	Human F1k-1/KDR DN	5, anchored (ISSR)	Human IL-3 recepto	Human IL3 receptor	Human IL3 receptor	Human kelch protei	microar	Single chain antib	
ABS75681 AC144270 AAQ34170 AAQ33672 AAQ33672	AAV06824 AAA39091	AAA73096 AAS13762	AAS13705	AAF62932	AAF28355 AAH48201	AA164445	AAL50667	AAL50667 AAL45125	ABA96307	ABA96306 ABZ24438	ABZ24439	AAD55436 ADD26665	ADF88088	ADF88505 ADM13954	ADM14466	ADM14546 ADM13955	ADM14167	ADM14413 ADM14345	ADM14426	ADM13951 ADM14130		ADM13989 ADM14297	ADM14346	ADM14132 ADM13953	ADM14129	ADM14134 ADM14296	1 ADM14298	ADM14133	ADM14295	ADM13988	ADM14427	AD081097	L ADP74230	L ADQ26959 L ABN88973	1 ABN88972	1 ADJ97603	1 ADD69446	1 AAT76174 1 AAX53971	1 AAF19538	1 ABZ95232	1 AAH43222	1 ABK99282	1 ADL99557.	
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Chimeric phosphoro Chimeric phosphoro Chimeric phosphoro Human Jun N-termin PlGF PCR primer # Human mpGES-1 chim Human glucose tran Human glucose tran Human DR1-associat Novel human CD25 a Human BAF53 antise Novel human Pootein Cow prion protein HLA DRB345 gene PC Antitumoural phosp Yeast DGG2 stress Rice semi-dwarf (8 Synthetic deoxyrib Poly h nucleotide Probe poly h for a Human single nucle Normalised library Probe APC 1-MUT. Polymorphism detect Human oligonucleot Human oligonucleot AA497002-darived o	AA49/DOZ-GARAGO O Human tryptase a o Human Tryptase a o Human Tryptase a d Oligonucleotide as Human oligonucleot chromosome 9; detection;
0.4 20 1 ADK79910 0.4 20 1 ADK79910 0.4 20 1 ADK79286 0.4 20 1 ADK89289 0.4 20 1 ADK89289 0.4 20 1 ADK892143 0.4 20 1 ADK82143 0.4 20 1 ADK82169 0.4 20 1 ADK95895 0.4 25 1 AAK9866 0.4 25 1 AAK9866 0.4 26 1 AAK98819 0.4 26 1 AAK98819 0.4 30 1 ABK96894 0.4 30 1 ABK96894 0.4 30 1 ABK96894 0.4 30 1 ABK97619 0.4 20 1 ABK97619 0.4 20 1 ABK97619 0.5 30 1 ABK97619 0.6 30 1 ABK97619 0.7 30 1 ABK97619 0.8 30 1 ABK97619 0.9 30 1 ABK97619	0.4 20 1 ABD29562 0.4 20 1 ABD29663 0.4 20 1 ABD31693 0.4 1 Location/Qualifiers replace(26,A) 7*tag= a 13-A2. 00. 00. 04. 1 Location/Qualifiers replace(26,A) 7*tag= a 13-A2. 06. 07. 08. 99WG-US027293. 09. 99US-00443199. 09. 138786633.
C 2 2 0 0 7 8 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2108 14:2 0.2110 14:2 0.2111 14:2 0.2112 14:2 0.2111 14:2 0.2112 14:2 0.2112 14:2 0.2112 14:2 0.2112 14:2 0.2112 14:2 0.2112 14:2 0.2212 1
Primer for the det Human MDC PCR prim Amino labelled oli Amino labelled oli Human gene signatu Probe for PZA-real Phosphorothiate ol PCR primer used to Human ABO DNA PCR JNK1-specific prob Primer for RT-PCR PCR primer for RT-PCR PCR primer for pea Reverse PCR primer for pea Reverse PCR primer for pea Reverse PCR primer for pea Human mtisense IGFBP-5 Human protein kina Human CYPLAI RT-PC Cancer cells detected Human CYPLAI RT-PC Cancer cells detected Human APC primer # Xenobiotic respons Human antibody 146 Primer XDYP-415AT PCR primer used to Sphingosine-1-pos Human Jun N-termin	thuman Interfility Chicken ALASI gene Human TNFRSF6 seque 5-Aminolevulinic a Variant detecting Human oligonucleot Human noryopyrin cD Human RT-PCR rever Human noryopyrin cD Human myosin X-der ALG72565-derived oli Human stanniocalci Human stanniocalci Human glucocortico Chimeric phosphoro Chimeric phosphoro Chimeric phosphoro
- е е е е е е е е е е е е е е е е е е е	20 1 ADD942845 20 1 ADD942845 20 1 ADD942845 20 1 ADD964297 20 1 ABZ89454 20 1 ABZ894315 20 1 ABZ894315 20 1 ABZ894315 20 1 ABZ89496 20 1 ABZ89496 20 1 ABZ89496 20 1 ABZ89496 20 1 ABZ8948 20 1 ABZ8948 20 1 ABZ8948 20 1 ABZ8948 20 1 ABZ8948 20 1 ABZ8948 20 1 ADM63499 20 1 ADM63499 20 1 ADM63499 20 1 ADM63499 20 1 ADM63499 20 1 ADM63693 20 1
	C2033 C2033 C2033 C20033 C20033 C20033 C20040 C20040 C20040 C20040 C20040 C20040 C20040 C20040 C20040 C20040 C20040 C20050 C

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which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 (AAA74219) are consecutive pairs of nucleotides which contain callent SNPs. Sequences 1113 to 1122 (AAA7430-AA7509) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAA7430-AA7509) are consecutive casquences 1113 to 1128 (AAA7445) lead to conservative amino acid sequences 1113 to 1128 (AAA7745) lead to conservative amino acid sequences 1113 to 1128 (AAA77430-A77509) are 1192 changes, while those in Sequences 1129 to 1186 (AAA7746-A77503) result in on- conservative changes. The SNPs in sequences 1187 to 1192 changes to a method of detecting a polymorphic site in a nucleic acid and a method of detecting polymorphic sites, antibodies raised against such peptides containing polymorphic sites, antibodies raised against such peptides containing polymorphic sites, antibodies raised against such peptides containing polymorphic sites, antibodies raised cagainst such peptides und a method of detecting polymorphic cagainst such peptides und antibodies. The nucleic acids are useful for gene therappy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence colymorphism. Such treatment would comprise administration of the wild-
      Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Response element; Z-DNA; neoplasia; hexokinase II; glycolysis; cancer;
gene therapy; diabetes; tumour; rat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transcription regulating fragments of hexokinase II DNA contg. response element - and methods for diagnosis or treatment of neople that over-express hexokinase II and for regulating glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatoma AS-30D Type II hexokinase promoter fragment from -3843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2314 GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCG 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 36.4; DB 1; Length 48; 37.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48 BP; 1 A; 2 C; 25 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pedersen PL, Mathupala SP, Rempel A;
                                                                                               Claim 1; Page 465; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 11; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9704104-A2.
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hexokinase promoter region. Response elements (transcription factor binding site) in this fragment may consist of all or part of the present chinding site) in this fragment may consist of all or part of the present caequence. AS-30D is a new isolated hexokinase II. The present DNA cragment is capable of regulating transcription of a downstream open creading frame and contains at least one response element. The present DNA cragment may be coupled to a reporter gene and used to screen for it alternatively it may be coupled to a toxic gene and used to treat or it hat over-express hexokinase II, such as those present in patients with cancer. It may also be used in gene therapy to treat diabetes. The With cancer it may also be used in gene therapy to treat diabetes. The the concerning an element are used in the method the caigmosting a neoplasia that over-expresses hexokinase. The new for diagnosing a neoplasia that over-expresses hexokinase. The new concepts are active only in tumours, not in normal cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific
     present sequence represents a segment of the hepatoma AS-30D Type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      2320 TGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                                             DB 1; Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd46.
                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 3 A; 5 C; 20 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               1.0%; Score 36.4; D
87.0%; Pred. No. 15;
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation; chromosome; ds.
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91US-00754351.
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(first entry)
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Best Local Similarity 87.0°
Matches 40, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1994;
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05-SEP-1991;
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17-JUN-1997
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Gaps

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having the sequence (GC-dA)n (GG-dT)n which can be used as genetic markers. Primers based on these sequences can be used as genetic repeats. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those clones where the repeat sequence has been determined are shown in AATGS704-797. This repeat sequence is from the marker clone Mdf15 which contains the repeat sequence is from the marker clone Mdf15 which contains the repeat sequence is from
phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-777. This repeat sequence is from the marker clone Mdf46 which contains the repeat sequence having the formula: (AC)25. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymorase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromsome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                      2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
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                                                                                                                                                                                                                                                                              formula: (AC)25. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                        Score 35.6; DB 1; Length 50;
Pred. No. 20;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat seguence from polymorphic marker clone Mfd15.
                                                                                                                                    Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                        0.9%;
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91US-00754351
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                                                                                                                                                                                            Local Similarity 82.0 tes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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DB 1; Length 50;

0.9%; Score 35.6;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ99483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of satellite sequences from genomic DNA for use as DNA markers isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                           DNA fragmentation; microsatellite DNA; DNA marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.6; DB 1; Length 50;
Pred. No. 20;
                Indels
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  Pred. No. 20;
0; Mismatches
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                                                                                                                                                                                                                                H. discus derived sequence #10.
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                                                                                                                                             BP.
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 82.0%;
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Best Local Similarity 82.0%;
Matches 41; Conservative
                                                                                                                                             AAZ98492 standard; DNA; 50
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                                                                                                                                                                                                  19-JUN-2000 (first entry)
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              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takahashi H, Sekino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-224692/19.
                                                                                                                                                                                                                                                              sednence;
                                                                                                                                                                                                                                                                          Haliotis discus; ss.
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                                                                                                                                                                                                                                                                   Haliotis discus
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                                                                                                                                                                                                                                                                                                                                                             02-MAR-2000
                                                                                                                                                                                                                                                           Satellite
                                                                                                                                                                       AAZ98492;
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AAZ98512/C
LD AAZ985:
XX
AC AAZ985:
XX
XX
DT 19-JUN
VX
DE H. diss
                                                                                                                RESULT 5
AAZ98492/c
                                                                                                               RESULT
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The invention provides a novel method for isolation of satellite sequences from ganomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA298483-514 represent sequences from Haliotis discus, used in the method of the invention
                                                                                                                                                                                                                                                                     Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
          Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide used to test inhibition of cylindrical formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capsid protein; HIV; protein cavity; capsid maturation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                         MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                    Example 5; Page 15; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang H, Hill CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001; 2001US-0307998P.
26-NOV-2001; 2001US-0333553P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2002; 2002WO-US023875
                                                                                                                                      99WO-JP003551
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                                                                                                                                                                98JP-00232153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ77520 standard; DNA; 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                       Sekino M;
                                                                                                                                                                                                                                              WPI; 2000-224692/19.
                           Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                     Haliotis discus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sundquist WI,
                                                                                WO200011156-A1
                                                                                                                                                                                         (NORQ ) JAPAN
                                                                                                                                                                                                                       rakahashi H,
                                                                                                                                                                 18-AUG-1998;
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                                                                                                                                       01-JUL-1999;
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                                                                                                           02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ö The specification describes a composition for assaying conformational change of a capsid protein. The composition comprises a Human farmunodesficiency virus (HIV) capsid protein which has a modification, and comprises a cavity of about 600 Angstrom cubed. The composition is useful for screening molecules that inhibit capsid carboxy terminal domain dimerisation. The composition is also useful in in vitro maturation assays, for inhibiting capsid maturation, in in vitro assembly assay, to assembly assay, to assembly to inhibit to maturation of the capsid protein. The present sequence represents an oligonucleotide used to test the inhibition of cylindrical formation of capsid proteins by compounds of the Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss. of capsid proteins, sing a 600 cubic angstrom Gaps 2316 rerererererererecererererererererececerere 2365 ö The invention relates to a method of identifying or detecting M. DB 1; Length 50; 9; Indels Giffard Human microsatellite D1S191 detection PCR primer #12. conformational change of cap capsid protein comprising a Sequence 50 BP; 0 A; 0 C; 25 G; 25 T; 0 U; 0 Other; ъ, Barnard Score 35.6; DE Pred. No. 20; 0; Mismatches Example 10; Page 55; 89pp; English. Wolter L, Claim 106; Page 60; 127pp; English assisted spacer addition assay. ВР 09-MAY-2001; 2001WO-AU000526. 09-MAY-2000; 2000US-0202771P. 10-MAY-2000; 2000US-0202559P. 0.9%; ABK24304 standard; DNA; 48 (first entry) Composition for assaying comprises a modified HIV 41; Conservative Timms P, (DIAT-) DIATECH PTY LTD. WPI; 2002-121948/16. WPI; 2003-268130/26 Query Match Best Local Similarity WO200185987-A1. Brockhurst V, Homo sapiens. 15-NOV-2001. 09-APR-2002 invention Matches ABK24304/ 8 8

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Gaps

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Indels

6 DB 1;

Score 35.6; DE Pred. No. 20; 0; Mismatches

82.0%;

BP

Length 50;

Alam S;

Davis DR,

Stemmler TL,

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CC nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (CC (LASA) assaay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, thurtington's disease, or muscular dystrophy. Furthermore, the method may be used for identifing and/or typing microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genotyping subjects including humans. The method can be used to provide markers for use in microorganisms, to ascertain cancers and other malignancies. Moreover, the method can be used to provide markers for use in dentification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, dentification of human and non-human individuals, plants and conditor responses to therapies including the possibility of microorganisms, to ascertain parentage of human or non-human individual, condition responses to therapies including the possibility of crime, in gene mapping and population studies. LASA may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crime. In gene mapping and population studies. LASA method such as a nucleotide length polymorphism in a enkaryotic genome. The LASA method avoids the time and cost required by prior art methods using gel electrophoresis and southern transfer analysis. In midting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primes used to human in detection or human in the method of the human or microsatellites as described in the metericular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.2; DB 1; Length 48; Pred. No. 21; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48 BP; 24 A; 24 C; 0 G; 0 T; 0 U; 0 Other;
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replace(26,G)
/*tag= a
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99US-00443199.
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Best Local Similarity 83.3%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA77335 standard; cDNA; 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-1998;
16-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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which contain single nucleotide polymorphisms (SNPS). Sequences 1 to 1112

(AAA76318-A77429) are consecutive pairs of nucleotides which contain

CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain

CC sequences 1131 to 1128 (AAA77430-A77489) are consecutive

CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in

CC changes, while those in sequences (AAB11749-B11828). The SNPs in

CC changes, while those in sequences 1129 to 1186 (AAA77440-A77503) result

CC in non-conservative changes. The SNPs in sequences 1187 to 1192

CC (AAA77504-A77509) generate frameshift mutations. The invention also

CC relates to a method of detecting a polymorphic site in a nucleic acid and

CC amethod of determining the relatenses of two nucleic acids. It also

CC compasses peptides containing polymorphic sites, antibodies raised

CC against such peptides, and a method of detecting polymorphic

CC against such peptides using the antibodies. The nucleic acids are useful for

CC gene therapy of an individual having, suspected of having, or at risk of

CC developing a pathological condition due to the presence of a sequence

CC polymorphism. Such treatment would comprise administration of the wild-
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                                                    Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                      Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              septides can also be used in the treatment of such individuals
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Pred. No. 23;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequence. Antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat sequence from polymorphic marker clone Mfd109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48 BP; 2 A; 2 C; 24 G; 20 T; 0 U; 0 Other;
                                                                       for treating a subject suffering, or
presence of a sequence polymorphism.
                                                                                                                                  Claim 1, Page 466; 543pp; English.
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91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.3%;
Best Local Similarity 84.8%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                WPI; 2000-387826/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-042299/04.
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05-SEP-1991;
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17-JUN-1997
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04-APR-1994;
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05-SEP-1991;
                                                                          25-MAR-2003
17-JUN-1997
                                                                                                  JS5582979-A.
                                                                                                      10-DEC-1996
                                                                      AAT65763;
                                                                                                                         Weber JL;
                                                        46
                                            Query Match
                                                Matches
                                                              RESULT
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ö The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone MdIIO9 which contains the repeat sequence is from formula; GGGAAATAGG(CA)18. (Updated on 25-MAR-2003 to correct PF field.) Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds. Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers. Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers. Gaps ; DB 1; Length 46; 4; Indels 2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 2356 rerererererererererererererererererecenar 6 Repeat sequence from polymorphic marker clone Mfd69. Sequence 46 BP; 22 A; 18 C; 5 G; 1 T; 0 U; 0 Other; Pred. No. 23; 0; Mismatches Score 34.6; Pred. No. 23 Claim 1; Col 11-12; 186pp; English. Claim 1; Col 13-14; 186pp; English AAT65763 standard; DNA; 44 BP 89US-00341562. 91US-00754351. 94US-00222177 0.9%; Local Similarity 90.2%; les 37; Conservative (first entry) (MARS-) MARSHFIELD CLINIC (revised) WPI; 1997-042299/04.

Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences which contain single nucleotide polymorphisms (SNRs). Sequences 1 to 1112 AAA76318-A77429) are consecutive pairs of nucleotides which contain silent SNRs. Sequences 1113 to 1192 (AAA7430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the sequences 1113 to 128 (AAA77449-B1828). The SNPs in sequences 1113 to 1128 (AAA77445) lead to conservative amino acid sequences 1129 to 1186 (AAA77446-A77503) result in non- conservative changes. The SNPs in sequences 1187 to 1192 (AAA77509-A77509) generate frameshift mutations. The invention also relates to a method of detecting a polymorphic site in a nucleic acid and a method of determining the relatedness of two nucleic acides. It also ö Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism. genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf69 which contains the repeat sequence is from formula: (AC)18.5A(AC)3. (Updated on 25-MAR-2003 to correct PF field.) Human; single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; ss. Gaps ö Score 34.4; DB 1; Length 44; Pred. No. 23; 0; Mismatches 6; Indels 2307 GAGCTITGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350 Human clone cg44024536 polymorphic site, SEQ ID NO:1019. Sequence 44 BP; 23 A; 21 C; 0 G; 0 T; 0 U; 0 Other; Location/Qualifiers Claim 1; Page 466; 543pp; English. 98US-0109024P. 0.9%; 99WO-US027293 AAA77336 standard; cDNA; 44 (first entry) Query Match 0.9 Best Local Similarity 86.4 Matches 38; Conservative /*tag= Shimkets RA, Leach MD; (CURA-) CURAGEN CORP. WPI; 2000-387826/33. WO200029623-A2 Homo sapiens 17-NOV-1998; 16-NOV-1999; 17-NOV-1999; 16-NOV-2000 25-MAY-2000 variation AAA77336; 44 RESULT 12 Key AAA77336 8.83333333333 ઠ 셤

Gaps

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Indels

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Length 42;

DB 1;

Score 34.2; Pred. No. 23; 0; Mismatches

Query Match 0.9%; Best Local Similarity 92.3%; Matches 36; Conservative

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf1 which contains the repeat sequence having the marker clone Mdf1 which contains the repeat sequence having the cormula: CATA(CA)19. (Updated on 25-MAR-2003 to correct PF field.)
              against such peptides, and a method of detecting polymorphic proteins/peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence bolymorphism. Such treatment would comprise administration of the wild-type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
encompasses peptides containing polymorphic sites, antibodies raised
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                  DB 1; Length 44;
                                                                                                                                                                                                                                                                                              rGTGTGTGTGTGCACATCCG 2359
                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                     Sequence 44 BP; 0 A; 2 C; 22 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfdl.
                                                                                                                                                                                                              Score 34,4; DE Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                2316 TCTGTGTGTGTGTGTGTGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT65797 standard; DNA; 42 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00341562.
91US-00754351.
                                                                                                                                                                                                                Query Match

Best Local Similarity 86.4%;
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
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05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT65797;
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT65797,
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selection; primers; OPTIPRIM; breeding; cattle; parentage;

genetic mapping; traits; amplification; ss

WO9213102-A1

Bos taurus.

06-AUG-1992.

92WO-US000340. 91US-00642342.

(GENM-) GENMARK 15-JAN-1991; 15-JAN-1992;

Microsatellite sequence from clone TGLA245.

(revised)
(first entry)

02-FEB-1993

25-MAR-2003

AAQ33834;

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AAQ33834 standard; DNA; 47

RESULT 14

g

AAQ3383

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
constant an (AF)15 and an (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
constant and Mbol sites, the frequency of (TG)n >9 microsatellites
constant and one persone is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence usetrate and
constream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
controsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
conomically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
conomically see also AAQ33501-34437. (Updated on 25-WAR-2001 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47 BP; 0 A; 0 C; 23 G; 24 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 263; 517pp; English.
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Best Local Similarity 83.0%;
Matches 39; Conservative
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Seguence 42 BP; 21 A; 20 C; 0 G; 1 T; 0 U; 0 Other;

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Homo sapiens
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17-JUN-1997
                                                                                                                             14-APR-1994;
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05-SEP-1991;
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                                                               Homo sapiens
                                                                                   JS5582979-A.
                                                                                                         10-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of Genetic disease, commercial enepast sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clomes were amplified by primers Arte7394-R6647. Those clomes where the repeat sequence has been determined are shown in AAAT65704-797. This repeat sequence is from the marker clone Mdf11 which contains the repeat sequence is formula: (AC)23A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 34.2; DB 1; Length 47; 83.0%; Pred. No. 27; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd14.
                                                                                               Repeat sequence from polymorphic marker clone Mfdll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47 BP; 24 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                             91US-00754351.
                          AAT65713 standard; DNA; 47 BP
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                                                                               (first entry)
                                                                                                                                                                                                                                                                                                  (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Conservative
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                                                                    (revised)
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                          WPI; 1997-042299/04
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17-JUN-1997
                                                                    25-MAR-2003
17-JUN-1997
                                                                                                                                                                                Homo sapiens
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05-SEP-1991;
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                                                                                                                                                                                                                                                                                                                         Weber JL;
                                                AAT65713;
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     RESULT 15
              AAT65713,
                           BXHHXH
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PCR; polymerase chain reaction; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           formula: (AC)23A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 34.2; E
83.0%; Pred. No: 27;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 9-10; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00222177.
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nes 39; Conservative
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vivlemore401-10.rng

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15-JAN-1991;
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                                                                                                                                                                                                                              The invention relates to the isolation of polymorphic repeat sequences having the sequence (dG-dA)n (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AT6579-766047. Those clones where the repeat sequence has been determined are shown in AAT65704-799. This repeat sequence is from the marker clone Mdf59 which contains the repeat sequence is from the marker clone Mdf59 which contains the repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; hypersensitivity disease; neoplastic disease; atlanta disease; multiple sclerosis; alsease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                           formula: (AC)23.5. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 34.2; DB 1; Length 47; 13.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47 BP; 24 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Vbeta gene repeat sequence #167.
                                                                                                                                                                                                         Disclosure; Col 11-12; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH70377 standard; DNA; 47 BP
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                        94US-00222177
                                                 89US-00341562
91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.0%;
                                                                                       (MARS-) MARSHFIELD CLINIC.
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Matches 39; Conservative
                                                                                                                                         WPI; 1997-042299/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast cancer;
                        04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999;
                                                 21-APR-1989;
05-SEP-1991;
10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH70377;
                                                                                                                 Weber JL;
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ADH70377
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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, vbetaRNA or cDNA. The kit is useful for diagnosing organ transplant respection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, infectious diseases arophic gastritis. Degenerative nervous system diseases include multiple arrophic gastritis. Degenerative nervous system diseases include multiple arrophic gastritis begenerative nervous system diseases include multiple arrophic gastritis begenerative nervous system diseases include multiple arrophic gastritis. Degenerative nervous system diseases include multiple of allergies. Type II hypersensitivities such as those present in allergies, Type II hypersensitivities such as those present in coodpasture's syndrome and Type IV hypersensitivities such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include as those caused by Mycobacterium. Neoplastic diseases include as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                        Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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83.0%; Pred. No. 2.,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 571; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ34178 standard; DNA; 37 BP.
   94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                        WPI; 2004-059052/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                         Rowen L;
                                                                                                  (HOOD/) HOOD L E. (ROWE/) ROWEN L.
19-SEP-1994;
19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vbeta gene
                                                                                                                                                                                                         Hood LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ34178;
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91US-00642342.

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                                                                                                                                                                                       The sequence is a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is settinated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for general extentions and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 33.8; DB 1; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfd50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2315 Grengrengrengrengrecergrengrengren 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37 BP; 0 A; 0 C; 19 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crerererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003 to correct PN field.)
                                                                                                                                                             rable 7; Page 402; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-00341562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%;
Best Local Similarity 94.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT65750 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                маввеу ЛМ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-042299/04.
                                                                            WPI; 1992-284684/34.
             (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JUN-1997
                                              Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT65750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT65750,
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                                                                                                The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybrid sation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers ANT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the contains the repeat sequence is from the contains the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              formula: (CA)19. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2315 GICTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (dC-dA)n.(dG-dT)n polymorphic repeat sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 grandrererererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.8; i
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
using novel nucleic acid mols. as primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Col 57-58; 186pp; English.
                                                          Disclosure, Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT66048 standard; DNA; 38 BP.
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91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.9
Best Local Similarity 94.6
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1991;
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18-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
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such as pig selected for having desired genotypic or potential phenotypic properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its fragment is useful for selecting an animal estimed for slaughter or a breeding animal having desired genotypic or potential phenotypic properties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in breeding animals destined for slaughter. The

present sequence represents a microsatellite oligonucleotide, which is given in an example from the present invention for the identification of DNA sequence polymorphisms in the IGF2 (insulin-like growth factor 2) and

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Gaps ö

Indels

2351

GCGTGTGTGTGTGTGTGTG

2315 GTCTGTGTGTGTGTGTG

8

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DB 1; Length 38;

Score 33.8; DE Pred. No. 23; 0; Mismatches

Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;

flanking loci

88888888888888888

0.9%;

ilarity 94.6%; Conservative

Local Similarity les 35; Conserv

Query Match Matches

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analysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence; 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dG-dA)n. (dG-dT)n, or from at least 10 uninterrupted monomucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats except that the runs of CA are interrupted. The sequence presented here is an example of a perfect repeat sequence of structure: (AC)19. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine; pig; wild boar; quantitative trait locus; QTL; chromosome 2; mapping; 2p1.7; select breeding; genotype; phenotype; muscle mass; fat deposition; IGF2; insulin-like growth factor 2; microsatellite; ds.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                             Score 33.8; DB 1; Length 38; Pred. No. 23; 0; Mismatches 2; Indels
                                                                                                                                                                                                     Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                        Porcine microsatellite PIGQTL3 oligonucleotide #31
                                                                                                                                                                                                                                                                                                                 38 Grererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                             94.68;
                                                                                                                                                                                                                                                                                                                                                                                         AAA65562 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                             Local Similarity 94.6
les 35, Conservative
                                                                                                                                                                         to correct PF field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200036143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAA65562;
                                                                                                                                                                                                                                   Query Match
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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition [LASA] assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, thuntington's disease, or muscular dystrophy. Purthermore, the method may be used for identifying and/or typhng microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                  Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giffard PM
                                                                                                                                                   Human microsatellite D1S191 detection PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnard R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10; Page 55; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wolter L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assisted spacer addition assay.
                                     멺
                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2001; 2001WO-AU000526
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2000; 2000US-0202771P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2000; 2000US-0202559P
                                     ABK24299 standard; DNA; 38
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Timms P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DIAT-) DIATECH PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-121948/16.
                                                                                                                                                                                                                                                                                                                        WO200185987-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brockhurst V,
                                                                                                                                                                                                                                                                                                                                                           15-NOV-2001.
                                                                                                              09-APR-2002
                                                                        ABK24299;
                                                                                                                                                                                                                                                                                   Ношо
RESULT 23
                 ABK24299,
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derived

The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises testing the animal for the presence of a parentally imprinted quantitative trait locus (CTL). The pig QTL is located at chromosome 2, mapping at around position 2pl.7. Also described are: (1) an isolated and/or recombinant nucleic acid (N1) comprising a parentally imprinted QTL or its functional fragment, (2) an isolated and/or recombinant nucleic acid (N2) comprising a synthetic parentally imprinted QTL derive from at least one chromosome or its functional fragment; (3) an animal

Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat

Example 4; Fig 10; 107pp; English

deposition

Spincemaille G;

Georges M,

Andersson L,

WPI; 2000-431612/37

MELICA HB. SEGHERSGENTEC NV

(MELI-)

(UYLI-) UNIV LIEGE.

98EP-00204291

16-DEC-1998;

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microorganisms; and for genotyping subjects including humans. The method is also useful for detecting certain cancers and other malignancies.

C is also useful for detecting certain cancers and other malignancies.

C identification of human and non-human individuals, plants and individuals, plants and complication of human and non-human individuals, plants and to monitor responses to therapies including the possibility of and to monitor responses to therapies including the possibility of conclaic acid damage. The nucleotide polymorphisms may be used in forensic crime, in gene mapping and population studies. LASA may also be used in crime, in gene mapping and population studies. LASA may also be used in crepast regions such as a nucleotide length polymorphism in a eukaryotic genome. The LASA method avoids the time and cost required by prior art comparticular, current diagnosis of fluntington's disease relies heavily upon the use of gel electrophoresis and Southern transfer analysis. In particular, current diagnosis of fluntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to the use of gel electrophoresis, a process that has proved difficult to the unintaurise. The LASA method allows total avoidance of this and laboratory procedures. ABK24276-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol eites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grererererererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone MTGT4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.8;
Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Table 7; Page 189; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%;
Local Similarity 94.6%;
Les 35; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33648 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENM-) GENMARK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33648;
                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33648
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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

creening a library of bovine Mbol DNA fragments of between 250 and 500

clones cross-hybridised. Assuming independent distribution of

clones cross-hybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100,000. The sequence information

con 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream

constructed PCR primers for in vitro amplification of the corresp.

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite individuals, for parantage testing, and in the genetic

sapping of economic trait loci, or genes involved the determinism of

connect pN approximat traits esp. in cattle, to allow selective

the connection of the correct PN action of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits sp. in cattle, to allow selective by the determinism of the content of the content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 0 A; 0 C; 19 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2315 grergrergrergrergregegrergrergre 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone TGLA227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.8;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 7; Page 259; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33825 standard; DNA; 39 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9
Best Local Similarity 94.6
Matches 35, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9213102-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33825;
                                                                                                                                                                                                                                                                                                                                                               field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33825
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field.)

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The sequence is that of a bovine microsatellite sequence obtd. by

creening a library of bovine Mbol DNA fragments of between 250 and 500

CC bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50

CC clones cross-hybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

cn in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

cspecification and indexed herein (see below). The sequences upstream and

constrained PCR primers for in vitro amplification of the corresp.

crequired PCR primers for in vitro amplification of the corresp.

cused to identify individuals, for parentage testing, and in the genetic

cused to identify individuals, for genes involved the determinism of

cenomonically important traits esp. in cattle, to allow selective

checking. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN

field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                             ö
                                        Score 33.8; DB 1; Length 39; Pred. No. 24; 0; Mismatches 2; Indels
                                                                                                           Sequence 39 BP; 0 A; 0 C; 19 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39 BP; 0 A; 0 C; 20 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 252; 517pp; English.
                                                                                                                                                                                                                          AAQ33807 standard; DNA; 39 BP
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                                                          Local Similarity 94.6%;
es 35; Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massey JM;
                                                                                                                                                                                                                                                                                          (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
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                                                                                                                                                                                                                                                                                       25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges M,
                                                                                                                                                                                                                                                        AAQ33807;
                                             Query Match
                                                                             Matches
                                                                                                                                                                                          RESULT 26
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XS
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Md£29 which contains the repeat sequence is from the marker clone Md£29 which contains the repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                             PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ormula: (AC)19.5. (Updated on 25-MAR-2003 to correct PF field.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 33.8; DB 1; Length 39;
14.6%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                primer;
                                                                                                                               Repeat sequence from polymorphic marker clone Mfd29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 20 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                              repeat sequence, genetic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 9-10; 186pp; English.
                 BP.
                                                                                                                                                                                                                                                                                                                                                                              89US-00341562.
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               AAT65731 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH70484 Btandard; DNA; 39
                                                                                (revised)
(first entry)
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Matches 35; Conserv
                                                                                                                                                                Polymorphism;
                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                              21-APR-1989;
05-SEP-1991;
                                                                              25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                               JS5582979-A.
                                                                                                                                                                                                                                                                                                               10-DEC-1996
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                                               AAT65731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weber JL;
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AAT65731/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
ADH70484
ID ADH70-
XX
AC ADH70-
DT 25-MAI
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Gaps

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Score 33.8; DB 1; Length 39; Pred. No. 24; 0; Mismatches 2; Indels

0.9%;

Query Match Best Local Similarity

35; Conservative

Matches

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers consociated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, consociated by the specifically priming and allowing amplification of acat Vbeta gene, consociated diseases and diseases and diseases and diseases including autoimmune diseases, degenerative nervous system diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's diseases are propried astritis. Degenerative nervous system diseases include multiple atrophic gastritis. Degenerative nervous system diseases include multiple controphic gastritis and percentivities such as those contact with allergens that lead to allergies, Type II Mypersensitivities such as those contact contact with allergens that lead to consisted in leprosy. Infections diseases include viral infections caused by viruses such as HUV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases contact between and bacterial infections such as those caused by hopeastic filtaria and bacterial infections such as those caused by hycobacterium. Neoplastic diseases include lymphoproliferative diseases include as those caused by breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a Vbeta gene.
                                                                                                 Addison's disease, atrophic gastritis;
Addison's disease, atrophic gastritis;
degenerative nervous system disease; multiple sclerosis;
Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
allergy; type II hypersensitivity; Goodpasture's syndrome;
type IV hypersensitivity; leprosy; infectious disease; viral infection;
HIV; fungal infection; Candida; parasitic infection; schistosome;
filaria; bacterial infection; Mycobacterium; neoplastic disease;
lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                          degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 33.8; DB 1; Length 39;
94.6%; Pred. No. 24;
ive 0; Mismatches 2; Indels
                                      human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39 BP; 0 A; 0 C; 20 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 678; 164pp; English.
Human Vbeta gene repeat sequence #274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00263959
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Best Local Similarity
Matches 35; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                           US2002150891-A1.
                                                                                                                                                                                                                                                                                                         preast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1995;
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

91US-00642342. 92WO-US000340

15-JAN-1992; .5-JAN-1991;

409213102-A1

Bos taurus.

36-AUG-1992.

Georges M, Massey JM; WPI; 1992-284684/34.

(GENM-) GENMARK.

Table 7; Page 368; 517pp; English.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Sequence of a microsatellite from clone TGLA52.

(revised)
(first entry)

25-MAR-2003 02-FEB-1993

AAQ34091;

AAQ34091 standard; DNA; 40 BP.

4AQ34091

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

CC olones cross-hybridised. Assuming independent distribution of for an icrosatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC domicrosatellites and mboI sites, the frequency of (T6)n >9 microsatellites

CC ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and specification and indexed herein (see below). The sequences upstream and commistream of the microsatellite sequence were used to generate the commistream of the microsatellite sequence were used to generate the microsatellite (using the program OPITREM). The microsatellites may be microsatellite (using the program OPITREM). The microsatellites may be consected to identify individuals, for parentage testing, and in the genetic mapping of economically important traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN first)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40 BP; 0 A; 0 C; 20 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Gregergregrererererererererere 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (dC-dA)n.(dG-dT)n polymorphic repeat sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT66054 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%;
ilarity 94.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Les 35; Conserv
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18-JUN-1997
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1D AAT660

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DT 25-MAR

DT 18-JUN

XX
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Gaps

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2315 GICTGIGIGIGIGIGIGGGGGGGGGGGGGGGGGG 2351

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94.68;

Conservative

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21-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences

having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
markers bramers based on these sequences can be used to detect these

repeats, especially for use in e.g paternity or maternity testing, human

genetic analysis such as linkage analysis of genetic disease, commercial
analysed, fall into 4 categories: 1) perfect repeats which are
alternating tandem CA repeats with no interruptions and without adjacent

crepeats of another sequence; 2) imperfect repeats which are

consecutive non-repeat bases; 3) compound perfect repeats which are

consecutive non-repeat bases; 3) compound perfect repeats which are

consecutive non-repeat bases; 3) compound perfect repeats which are

consecutive non-repeat bases; 5 innerrupted dinuclective on-

repeat bases from a run of at least 5 uninterrupted dinuclection

crepeat bases from a run of at least 5 uninterrupted dinuclection

crepeat bases from a run of at least 5 uninterrupted dinuclection

crepeats of a sequence other than (dC-dA)n. (dG-dT)n, or from at

least 10 uninterrupted mononuclectides; and 4) imperfect compound repeats

which are defined as for the perfect compound repeats

cross a perfect repeat sequence of structure: (CA)20. (Updated on 25-MAR-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 33.8; DB 1; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 Grererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                Example 8; Col 57-58; 186pp; English.
                                                                                                                                                                                   89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT65725 standard; DNA; 40 BP
                                                                                                                                                           94US-00222177
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35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                           (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                              WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                             Homo sapiens
                                                                                                                                                           04-APR-1994;
                                                                                                                                                                                     21-APR-1989;
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                                                                                                      US5582979-A.
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf23 which contains the repeat sequence is from formula: (AC)20. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism, repeat sequence, genetic marker, primer, amplification, PCR; polymerase chain reaction, paternity, maternity, human, pedigree, linkage analysis, genetic disease, animal, plant, breeding, locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n(dG\text{-}dT)\,n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2315 GICTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 9-10; 186pp; English
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                                                                                                                                                                                                94US-00222177.
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                                                                                                                                                                                                                                                                                                                                                                    (MARS-) MARSHFIELD CLINIC.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-042299/04.
Homo sapiens.
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                                                                                                                                                                                                04-APR-1994;
                                                                                                                                                                                                                                                                                                       05-SEP-1991;
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18-JUN-1997
                                                            US5582979-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber JL;
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Forster JW, Jones ES;
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ABK24300/
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                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences

Ca having the sequence (dc-dA)n. (dg-dT)n which can be used as genetic

markers. Primers based on these sequences can be used to detect these

crepeats, especially for use in e.g paternity or maternity testing, human

crepeats, especially for use in e.g paternity or maternity testing, human

contained or plant breeding or pedigree analysis of genetic disease, commercial

analysed, fall into 4 categories: 1) perfect repeats which are

alternating tandem CA repeats analysis of genetic disease, commercial

alternating tandem CA repeats separated by no more drian 3

cor more runs of uninterrupted CA repeats separated by no more than 3

consecutive non-repeat bases; 3) imperfect repeats which are

consecutive non-repeat bases; 4) compound perfect repeats which are

consecutive non-repeat bases; 5) compound perfect repeats which are

consecutive non-repeat bases; 5) minimerrupted dinucleotide or

consecutive on a run of at least 5 uninterrupted dinucleotide or

conger repeat bases from a run of at least 5 uninterrupted dinucleotide or

conger repeats of a sequence other than (dc-dA)n. (dd-dT)n, or from at

consecutive non-repeat sequence congound repeats except that the

consecutive non-repeated monouncleotides; and 4) imperfect compound repeats

consecutive non-repeat sequence of structure; (AC)20. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; profiling; grass profiling; seed batch purity testing.
                                                                                               Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.8; DB 1; Length 40;
Pred. No. 24;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2315 GICTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS. STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INT: MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                       Example 8; Col 57-58; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simple sequence repeat, SSR, #44.
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04-MAY-2000; 2000AU-00007310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%;
       91US-00754351.
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hes 35; Conservative
                                (MARS-) MARSHFIELD CLINIC
                                                                             WPI; 1997-042299/04
       05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002
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(VICT-)
(UYAD-)
(ITMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                       Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements core repeat (SSR), having 2 or more tandemly repeated nucleotide core elements core includes in length. Also included are a nucleic acid primer a uitable for amplifying an SSR, identifying (M1) an SSR by preparing a core include for amplifying an SSR, identifying SSRs by prepared by the M1, selecting for referred genomic DNA enriched for SSRs and the gene are associated with the gene such that the SSR and the gene are speciated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, and thod for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal ceed batches by assessing variation within seed batch of an SSR. The SSRs or profiling grass or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the creating the purity of grass or cereal seed as profiles, and for DNA profiling to establish the sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                             New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite, ligase-assisted spacer addition assay; LASA, cancer, nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human microsatellite D1S191 detection PCR primer #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 33.8; I
Best Local Similarity 94.6%; Pred. No. 24;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                          Claim 13; Page 53; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2000; 2000US-0202771P.
10-MAY-2000; 2000US-0202559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2315 GTCTGTGTGTGTGTGTGT
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WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200185987-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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vivlemore401-10.rng

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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, the funtington's disease, or muscular dystrosphy. Purthermore, the method may be used for identification of purpose or muscular dystrosphy. Purthermore, the method may be used for identifying and/or typing microorganisms including yeasts and clower uni- and multi-cellular organisms, as well as prokaryotic is also useful for detecting certain cancers and other malignancies. Moreover, the method can be used to provide markers for use in dentification of human and non-human individuals, plants and confortable including the possibility of microorganisms, to ascertain parentage of human or non-human individual, and to monitor responses to therapies including the possibility of and confication of human and non-human individuals, plants and confort in gene mapping and population studies. LASA may also be used in forensic crime, in gene mapping and population studies. LASA may also be used in crepeat regions such as a nucleotide length polymorphism in a eukaryotic genome. The LASA method avoids the time and cost required by prior art marticular virtular populative defentify and current diarmore is also be used in mathor mathorical and mucleotide length polymorphism is a eukaryotic genome. The LASA method avoids the time and cost required by prior art matricular virtular virtular sequence is an allocation such as an eucleotide length polymorphism in a eukaryotic genome. The LASA method avoids the time and cost required by prior art mathoricallar polymorphism and an enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to automate or minitatirise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24216-ABK24313 represent primers used to
                                                          Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detect polymorphisms or microsatellites as described in the method of
                                                                                                                                                                                                                                                  Example 10; Page 55; 89pp; English.
WPI; 2002-121948/16.
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                                                             Gaps
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                             Score 33.8; DB 1; Length 40; Pred. No. 24;
                                                            2; Indels
Seguence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                          2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                        39 energrererererererererererererere
                                                            0; Mismatches
                           ch 0.9%;
1 Similarity 94.6%;
35; Conservative
                                             Local Similarity
                              Query Match
                                                             Matches
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Repeat sequence from polymorphic marker clone Mfd8.
                    AAT65710 standard; DNA; 41 BP
                                                            (revised)
(first entry)
                                                            25-MAR-2003
                                                                      17-JUN-1997
                                        AAT65710;
RESULT 35
AAT65710/C
ID AAT65X
X
AC AAT65
DT 25-MA
DT 17-JU
XX
DE Repea
XX
RW PCR;
KW PCR;
KW PCR;
KW hybri
XX
COS HOMO
XX
OS HOMO
XX
OS HOMO
XX
DE REPEA
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PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds. Polymorphism; repeat sequence; genetic marker; primer; amplification;

JS5582979-A 10-DEC-1996

Homo sapiens

Weber JL;

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The invention relates to the isolation of polymorphic repeat sequences markers. Primers based on these sequences can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AATGS79-166047. Those clones where the repeat sequence has been determined are shown in AATGS704-797. This repeat sequence is from the marker clone Mdf8 which contains the repeat sequence is from the marker clone Mdf8 which contains the repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formula: (AC)20A. (Updated on 25-MAR-2003 to correct PF field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.8; DB 1; Length 41;
Pred, No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41 BP; 21 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTG 2351
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                                                                                                                                                                                                                                               Claim 1; Col 9-10; 186pp; English.
                                            89US-00341562.
91US-00754351.
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91US-00754351.
               94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.9%;
Best Local Similarity 94.6%;
Matches 35; Conservative
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                                                                                              (MARS-) MARSHFIELD CLINIC
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                                                                                                                                                              WPI; 1997-042299/04.
                                                               05-SEP-1991;
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                                                21-APR-1989;
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17-JUN-1997
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RESULT 38
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                                                                                The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the animal or plant breeding or pedigree analysis. Glones containing the phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(GC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf45 which contains the repeat sequence is from formula: (CA)20.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of polymorphic genetic markers of the form (dG\text{-}dA)\,n\,(dG\text{-}dT)\,n using novel nucleic acid mols. as primers.
                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                    DB 1; Length 41;
                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd63.
                                                                                                                                                                                                                                                                                                                                   2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                            Sequence 41 BP; 20 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                    0.9%; Score 33.8; D
94.6%; Pred. No. 25;
ve 0; Mismatches
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                                                               Disclosure; Col 9-10; 186pp; English.
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91US-00754351.
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nes 35; Conservative
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      WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1994;
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05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                     Matches
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Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises mucleic acid primers specifically priming and allowing amplification of a
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repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers ART65798-766047. Those clones where the repeat sequence has been determined are shown in ART65704-797. This repeat sequence is from the marker clone Mdf63 which contains the repeat sequence is from the marker clone Mdf63 which contains the repeat sequence having the formula: (CA)20.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; Goodpasture's syndrome; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41 BP; 20 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33.8;
Pred. No. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Vbeta gene repeat sequence #91.
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95US-00531241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.6'
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002150891-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH70301;
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CC vbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases.
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease.
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those contact with allergens include Type
CC allergies, Type II hypersensitivities such as those caused by viruses such as HIV, fungal infections such as those caused by sepast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by such as leukaemias, lymphomas and cancers such as cancer of the brain, because the present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bow with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41 BP; 0 A; 0 C; 21 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 erdiérérérérérérérérérérérérérérére 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 238; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33770 standard; DNA; 42 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9213102-A1
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required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective by receding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf62 which contains the repeat sequence is from formula: (AC)21. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                  DB 1; Length 42;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd62.
                                                                                                                                                                                                                                                                               2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                           Sequence 42 BP; 0 A; 0 C; 21 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                Query Match 0.9%; Score 33.8; E
Best Local Similarity 94.6%; Pred. No. 26;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                  AAT65757 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1994;
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17-JUN-1997
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                                                                                                                        field.)
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ID AAT657
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Gaps ö

2; Indels

0; Mismatches Pred. No.

Best Local Similarity 94.6 Matches 35; Conservative

GTGTGTGTGTGTG 2351

2315 GTCTGTGTGTGTGTGTGCGT

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence acid (I) from ryegrass or fescue species including a simple sequence or repeat (SSR), having 2 or more tandemly repeated nucleic dore elements 2.6 nucleotides in length. Also included are a nucleic acid primer or interpretation of fescue genomic DNA enriched for SSRs and fescue genomic DNA enriched for SSRs and fescue genomic DNA enriched for SSRs and fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely caspociated with the gene act and that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, a cereal species variaties by assessing variation between SSR variation within seed batch of an SSR. The SSRs seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species variation the purity of grass or cereal season or cereal section of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                          tandem repeat;
                                     Gaps
                                     ö
                                                                                                                                                                                                                                                                                                                                                        Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tan
cereal profiling; grass profiling; seed batch purity testing.
Length 42;
                                     2; Indels
                                                                        2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE VICTORIA DEPT NATURAL RES & ENVIRO.
DB 1;
                                                                                                              42 cherchercherchercherchercherchercher
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                                     Mismatches
                     26;
Score 33.8;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                        Simple sequence repeat, SSR, #32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 51; 72pp; English.
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                                                                                                                                                                                                            BP.
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04-MAY-2000; 2000AU-00007310.
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 Query Match
Best Local Similarity 94.6%;
Matches 35; Conservative
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AAS13735 standard; DNA; 42
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones ES;
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                                                                                                                                                                                                                                                                                       08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          varieties
                                                                                                                                                                                                                                                  AAS13735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SAUS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (VICT-)
(UYAD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ITMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (nxsc-)
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                                                                                                                                                                           RESULT 41
AAS13735/c
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0.9%; Score 33.8; DB 1; Length 42;

BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;

Sequence 42

Query Match

sequence is a ryegrass or feacue SSR

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The invention relates to a method of identifying or detecting a mucleotide regeat region in a nucleic acid molecule characterised by a mucleotide regeat region in a nucleic acid molecule characterised by a comprising employing ligase-sasisted spacer addition classed assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide length polymorphism in animals or humans, which is a sesciated with a neurodegenerative disease including fragile X syndrome, a useciated with a neurodegenerative disease including fragile X syndrome, be used for identifying and/or typing microorganisms including yeasts and cover uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genocryping subjects including humans. The method can be used to provide markers for use in Moreover, the method can be used to provide markers for use in identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, crime, in gene mapping and population studies including the possibility of science to identify a particular victim or an alleged perpetrator of a crime, in gene mapping and population studies lass may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crime and complex mapping and population studies lass may also be used in the methods using gelelectrophoresis and Southern transfer analysis. In methods using gelelectrophoresis and Southern transfer analysis. In parented diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                         Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giffard PM;
                                                                                                                                                                                                                                                   Human microsatellite D18191 detection PCR primer #9.
41 crererererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnard R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 55; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Timms P, Wolter L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assisted spacer addition assay.
                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001; 2001WO-AU000526.
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10-MAY-2000; 2000US-0202559P.
                                                                                                                   ABK24301 standard; DNA; 42
                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-121948/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200185987-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                               09-APR-2002
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automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n - using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                                                                                   DB 1; Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd123
                                                                                                                                                                                                              Sequence 42 BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
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                                                                                                                                                                                                                                                                            Score 33.8; DE
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                   0.9%;
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AAT65794 standard; DNA; 43
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                                                                                                                                                                                                                                                                                                                                                    35; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1989;
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17-JUN-1997
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                                                                                                                                                 invention
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AAT6
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DB 1; Length 43;

Score 33.8; 1 Pred. No. 27;

0.9%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening a library of bovine Molo DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 closes cross-hybridised. Assuming independent distribution of microsatellites and Mbo! sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for a. 230 such bovine microsatellites is summarised in the sequence information for an expecification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

In vitro amplied (using the program OPTIPRIM). The microsatellites may be used to identify individuals for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - used in genetic identification, gene
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a bovine microsatellite sequence obtd. by
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                                                                                                                                                                                                                                                                        PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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 Indels
                              2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
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                                                          42 ererererererererererererererererere
Mismatches
                                                                                                                                                                                                                                             Microsatellite sequence from clone MTGT11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                                                                                     AAQ33636 standard; DNA; 44
                                                                                                                                                                                                                (first entry)
 35; Conservative
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                                                                                                                                                                                                  (revised)
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02-FEB-1993
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Best Local
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Matches
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Bos taurus.

AAQ33983;

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The sequence is that of a bovine microsatellite sequence obtd. by

creening a library of bovine MboI DNA fragments of between 250 and 500

creening a library of bovine MboI DNA fragments of between 250 and 500

creening a cross-hybridised. Assuming independent distribution of

creening a genome is estimated at >100, 000. The sequence information

crossatellites and MboI sites, the frequency of (T6)n >9 microsatellites

crossatellites approach fries, the frequency of (T6)n >9 microsatellites

crossatellites and midexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream and

crossatellite sequence ware used to generate the

crossatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

credited to identify individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

connecting. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 33.8; DB 1; Length 44; 94.6%; Pred. No. 27; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Table 7; Page 376; 517pp; English.
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                                                                                                                                                                                                                                                                                      Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                15-JAN-1991;
                                                                 WO9213102-A1
                                                                                                                                                      LS-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
screening a library of bovine Mbol DNA fragments of between 250 and 500
clones cross-bybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence water used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
cused to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
connomically important traits epp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
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0
                                                                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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94.6%; Pred. No. 27;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44 BP; 0 A; 0 C; 22 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of a microsatellite from clone TGLA61.
                                                                                                                                        Microsatellite sequence from clone TGLA381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Table 7; Page 323; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping, and selective breeding.
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35; Conservative
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(first entry)
                                                                                                   (first entry)
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                                                                              (revised)
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Matches 35; Conserv
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02-FEB-1993
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                06-AUG-1992
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AAQ34113;

XXXEEXEXXXX

AAQ34113

Query Match

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Gaps .,

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                                                                                                                                                                                                                             The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf66 which contains the repeat sequence is from formula: (AC)22. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.8; DB 1; Length 44;
Pred. No. 27;
0; Mismatches 2; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat sequence from polymorphic marker clone Mfd49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44 BP; 22 A; 22 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                    Disclosure; Col 11-12; 186pp; English
             89US-00341562.
91US-00754351.
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                                                          (MARS-) MARSHFIELD CLINIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Conservative
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                                                                                                                      WPI; 1997-042299/04
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              21-APR-1989;
05-SEP-1991;
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                                                                                         Weber JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf49 which contains the repeat sequence is from formula: (CA)22. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nuclectide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (IASA) assay. The method is useful in the identifying or detecting a
Detection of polymorphic genetic markers of the form (dG-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                                                                            markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                  genetic
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                                                                                           The invention relates to the isolation of polymorphic repeat having the sequence (dC-dA)n.(dG-dT)n which can be used as ge
                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 33.8; DB 1; Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human microsatellite D1S191 detection PCR primer #10.
                                                                                                                                                                                                                                                                                                                                                         Sequence 44 BP; 22 A; 22 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barnard R,
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 27;
0; Mismatches
                                                      Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 55; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assisted spacer addition assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2000; 2000US-0202771P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2001; 2001WO-AU000526.
                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 94.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK24302 standard; DNA; 44
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                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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cc nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, thurtington's disease, or muscular dystrophy. Furthermore, the method may thurtington's disease, or muscular dystrophy. Furthermore, the method may be used for identifing and/or typing microorganisms including yeasts and concern and multi-cellular organisms, as well as prokaryotic microorganisms, and for genotyping subjects including humans. The method is also useful for detecting certain cancers and other malignancies.

Cc microorganisms, to ascertain parentage of human or non-human individual, identification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, crime of and to monitor responses to therapies including the possibility of mucleic acid damage. The nucleotide polymorphisms may be used in forensic crime, in gene mapping and population studies. LASA may also be used in crime and population studies. LASA may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crime to identify upon the use of gel electrophoresis and Southern transfer analysis. In methods using gel electrophoresis and Southern transfer analysis. In particular, current diagnosis, a process that has proved difficult to the use of gel electrophoresis, a process that has proved difficult to immiting step, making it a strong candidate for future use in clinical limiting step, making it a strong candidate for future use in clinical limiting step, making it a strong candidate for future use in clinical limitant candidate for future use in clinical limitant as a nuclear candidate for future use in clinical limitant controlled to miniaturise. ABKA2476-ABK2413 represent prime to method in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.8; DB 1; Length 44; Pred. No. 27; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 44 BP; 22 A; 22 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA325.
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Best Local Similarity 94.6%;
Matches 35; Conservative (
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02-FEB-1993
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Table 7; Page 295; 517pp; English.

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CC general properation and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence ware used to generate the

CC downstream of the microsatellite sequence ware used to generate the

Microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellity individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved the determinism of

CC contract traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 210 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
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                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2315 GICTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                            Sequence 45 BP; 0 A; 0 C; 22 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 Grerererererererereres 38
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Score 33.8; Pred. No. 28;
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Best Local Similarity 94.6'
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                      field.)
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Length 46;

DB 1;

Query Match

Gaps

vivlemore401-10.rng

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required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                               DB 1; Length 45;
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                                                                                                                                                           Sequence 45 BP; 0 A; 0 C; 23 G; 22 T; 0 U; 0 Other;
                                                                                                              Score 33.8; DE
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA254.
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                                                                                                                                                                                                                                        AAQ33840 standard; DNA; 46 BP.
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                                                                                                            Query Match 0.9%;
Best Local Similarity 94.6%;
Matches 35; Conservative
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(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                              AAQ33840;
                                                                     field.)
                                                                                                                                                                                                                  RESULT 52
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC1)5 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequence information of commistream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The equired PCR primers for in vitro amplification of the corresp.

The increase little (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 46 BP; 0 A; 0 C; 23 G; 23 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp with an (AC115 and a (TC1)5 oligonucleotide probe. One out of 50 closes cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites is summarised to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conomically important traits esp. in cattle, to allow selective reeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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    used in genetic identification, gene

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genetic mapping; traits; amplification; ss.
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                                Indels
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                                                                  Score 33.8; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA340.
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0.9%;
llarity 94.6%;
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             Local Similarity
les 35; Conserv
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                                                                                                                                                                                                                                                  25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1992
                                                                                                                                                                                                                   AAQ33939;
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                  Best Loca
Matches
                                                                                                                                                 RESULT 53
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Homo sapiens
                                                                                                                        04-APR-1994;
                                                                                                                                             21-APR-1989;
05-SEP-1991;
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17-JUN-1997
                                                      Homo sapiens
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                                                                           US5582979-A.
                                                                                                10-DEC-1996
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                                                                                                                                                                                                     Weber JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those close where the repeat sequence has been determined are shown in AATG5704-797. This repeat sequence has been determined are shown in AATG5704-797. This repeat sequence is from the marker close Mdf17 which contains the repeat sequence is from the marker close Mdf17 which contains the repeat sequence having the formula: (AC)23. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                           Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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14.6%; Pred. No. 29;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd61.
                                                                                       Repeat sequence from polymorphic marker clone Mfd17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 9-10; 186pp; English
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              BP.
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(first entry)
              AAT65719 standard; DNA; 46
                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                               (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042299/04.
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                        04-APR-1994;
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                                                       25-MAR-2003
17-JUN-1997
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17-JUN-1997
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                                    AAT65719;
  Matches
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the phage libraries which a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AMES798-f6647. Those clones where the repeat sequence has been determined are shown in AATGS704-797. This repeat sequence has been determined are shown in AATGS704-797. This repeat sequence is from the marker clone Mdf61 which contains the repeat sequence is from the marker clone Mdf61 which contains the repeat sequence having the formula: (CA)23. (Updated on 25-MAR-2003 to correct PF field.)
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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC_-dA_)\,n\,(dG_-dT)\,n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2315 Grerererererererererererererererere 2351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-00222177.
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AAT65709 standard; DNA; 46
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Best Local Similarity 94.6
Matches 35; Conservative
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704.797. This repeat sequence is from
                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the marker clone Mdf7 which contains the repeat sequence having the formula: (CA)20TA(CA)2. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46 BP; 23 A; 22 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         Claim 1; Col 9-10; 186pp; English.
                      94US-00222177
                                                               89US-00341562
                                                                                     91US-00754351
                                                                                                                           (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                 WPI; 1997-042299/04.
                      04-APR-1994;
                                                               21-APR-1989;
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Gaps
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0
     Score 33.8; DB 1; Length 46; Pred. No. 29; O; Mismatches 2; Indels
                                                              2315 GrenGrenGrenGrenGrenGrenGrenGrenG 2351
                                                                            Ouery Match
Best Local Similarity 94.6%;
Marches 35; Conservative
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BP

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Human microsatellite D1S191 detection PCR primer #11.
      ABK24303 standard; DNA; 46
                      (first entry)
                                                       Homo sapiens.
                      09-APR-2002
              ABK24303;
RESULT 57
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Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.

15-NOV-2001

WO200185987-A1

09-MAY-2000; 2000US-0202771P.

09-MAY-2001; 2001WO-AU000526

(DIAT-) DIATECH PTY LTD.

Barnard R, Giffard PM; Wolter L, Brockhurst V, Timms P, WPI; 2002-121948/16,

breast cancer; ds.

The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, Huntington's disease, or muscular dystrophy. Furthermore, the method may consist and for genotyping microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genotyping subjects including humans. The method can be used to provide markers for use in dentification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, and to response to therapies including the possibility of microorganisms, to ascertain parentage of human or non-human individual, and to cidentify a particular victim or an alleged perpetrator of a crime, in gene mapping and population studies. LASA may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crepeat regions such as a nucleotide length polymorphism in a enkaryotic crepeat regions such as a nucleotide length polymorphism in a enkaryotic genome. The LASA method avoids the time and cost required at at Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-Example 10; Page 55; 89pp; English. assisted spacer addition assay.

Sequence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;

methods using gel electrophoresis and Southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to

detect polymorphisms or microsatellites as described in the method of

invention

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Gaps ô 0.9%; Score 33.8; DB 1; Length 46; 94.6%; Pred. No. 29; ve 0; Mismatches 2; Indels llarity 94.6%; Conservative Local Similarity nes 35; Conserv Query Match Best Loca Matches

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2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351 45 crererererererererererererererere

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human; T-cell associated disease; Wheta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; addison a disease; attophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; allergy; type II hypersensitivity; Goodpasture's syndrome; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer; Human Vbeta gene repeat sequence #371. ВР ADH70581 standard; DNA; 48 (first entry) 25-MAR-2004 ADH70581; RESULT 58 ADH70581, Homo sapiens

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including autoimmune diseases, degenerative nervous system diseases, including autoimmune diseases, thereses, infectious diseases, graft versus host diseases, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease, and neoplastic diseases. Autoimmune diseases include Addison's disease, arrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type clerosis and Alzheimer's disease. Hypersensitivity diseases include Type allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Che yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases include as cancer of the brain, such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2321 GTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 33.8; DB 1; Length 48; Best Local Similarity 84.4%; Pred. No. 31; Matches 38; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfd115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48 BP; 23 A; 23 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 775; 164pp; English
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                                                                                                                                           99US-00263959
                                                                                                                                                                                 94US-00309335.
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                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-059052/06
                                                                                                                                                                                                                                                                                                             Hood LE, Rowen L;
                                                                                                                                                                                                                                                (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                        (ROWE/) ROWEN L.
                                                           US2002150891-A1.
                     Homo sapiens.
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17-JUN-1997
                                                                                                                                           05-MAR-1999;
                                                                                                                                                                                     19-SEP-1994;
                                                                                                                                                                                                             19-SEP-1995;
                                                                                                    .7-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vbeta gene
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of Genetic disease, commercial repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdflis which contains the repeat sequence is from the marker clone Mdflis which contains the repeat sequence by primer ATAGGAG(AC)17.5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dG-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analyais; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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1 Similarity 90.0%; Pred. No. 30;
36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                         91US-00754351.
                                                                                                        94US-00222177.
                                                                                                                                        89US-00341562
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(first entry)
                                                                                                                                                                                      (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                      WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
17-JUN-1997
                                                                                                            04-APR-1994;
                                                                                                                                          21-APR-1989;
                                                                                                                                                           05-SEP-1991;
                                             US5582979-A.
                                                                            10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT65711;
                                                                                                                                                                                                                          Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT65711/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 60
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf9 which contains the repeat sequence latiom formula: (CA)17G. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35 BP; 17 A; 17 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                       Claim 1; Col 9-10; 186pp; English.
89US-00341562
91US-00754351
                                                                 (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                           WPI; 1997-042299/04.
21-APR-1989;
                       05-SEP-1991;
                                                                                                                 Weber JL;
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Gaps
                                   .
0
Score 33.4; DB 1; Length 35;
Pred. No. 23;
0; Mismatches 1; Indels
                                                               2317 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                               35 crererererererererererererererere
ch 0.9%;
il Similarity 97.1%;
34; Conservative
 Query Match
Best Local Similarity
Matches 34; Conserv
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Microsatellite sequence from clone TGLA414.
                                AAQ34006 standard; DNA; 43
                                                                                                                       (first entry)
                                                                                                     (revised)
                                                                                                   25-MAR-2003
02-FEB-1993
                                                                  AAQ34006;
RESULT 61
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BP

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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                    WO9213102-A1
                                              Bos taurus
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding. 91US-00642342 Georges M, Massey JM; WPI; 1992-284684/34. (GENM-) GENMARK. LS-JAN-1991;

92WO-US000340

15-JAN-1992;

06-AUG-1992

Table 7; Page 333; 517pp; English

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The sequence is that of a bovine microsatellite sequence obtd. by

Screening a library of bovine MboI DNA fragments of between 250 and 500

by with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

con the bovine genome is estimated at >100,000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence waset to generate the

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

used to identify individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

conomically important traits esp. in cattle, to allow selective

breding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen gatients for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron sequence variations on mRNA expression and stability. The polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a CYP3A4 sequence polymorphism of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 33.4; DB 1; Length 43;
86.0%; Pred. No. 30;
live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2320 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGT 2362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43 BP; 2 A; 0 C; 19 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated CYP3A4 polymorphic sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CYP3A4 gene polymorphism #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 35; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US018158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX28288 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 86.0
nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AXYS-) AXYS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guida M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-215070/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9913106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lichter JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX28288;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 62
AAX28288/c
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,00. The sequence information
cfor ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence upstream and
downstream of the microsatellite sequence water used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYP3A4. The nucleic acids can also be used to generate genetically modified non-human animals or site specific gene modifications in cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                          ;
                                                                                                                       Score 33; DB 1; Length 41;
Pred. No. 31;
0; Mismatches 5; Indels
                                                                                                                                                                                          41 renererererererererererererererererananaece 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                     Sequence 41 BP; 17 A; 16 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 7; Page 319; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00642342
                                                                                                                        ch 0.9%;
(1 Similarity 87.8%;
36; Conservative
                                                                                                                                                                                                                                                                                                              AAQ33974 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
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                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9213102-A1.
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                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus,
                                                                                                                                                                                                                                                                                                                                               AAQ33974;
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                   63
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleocide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32.8; DB 1; Length 36; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2316 rergrererererererererererererer 2351
2350
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                              36
 2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGT
                               1 crererererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Table 7; Page 311; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                markers -
breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В.
                                                                                                              AAQ33953 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34068 standard; DNA; 36
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9
Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA mapping, and selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                        WO9213102-A1
                                                                                                                                                                              25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                           Bos taurus.
                                                                                                                                                AAQ33953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 65
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ID AAQ3
XX
                                                                                                  AAQ33953
                                                                                  RESULT
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Gaps

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tch 0.9%; Score 32.8; DB 1; Length 36; al Similarity 94.4%; Pred. No. 28; 34; Conservative 0; Mismatches 2; Indels

Best Local Similarity Matches 34; Conserv

Query Match

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AClis and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         economically important traits esp. in cattle, to allow selective breeding. See also AAQ33S01-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%; Score 32.8; DB 1; Length 36; Best Local Similarity 94.4%; Pred. No. 28; Matches 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA318.
                                                                                                                                                                                                                                                                                                                                                                                                                       Table 7; Page 261; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                           mapping, and selective breeding.
                                                                                                                                92WO-US000340.
                                                                                                                                                                           91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
                                                                                                                                                                                                                    GENM-) GENMARK
                                           WO9213102-A1.
                                                                                                                                                                           15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
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                                                                                                                                15-JAN-1992;
                                                                                  06-AUG-1992.
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02-FEB-1993
  Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ33906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
con the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparised of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
confounded thy indoviduals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
find.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                         Microsatellite sequence from clone TGLA445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 358; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                    92WO-US000340.
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                                         (revised)
(first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK
                                         25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                      Bos taurus.
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AAQ34068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps ö

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACLIS and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine propried herein (see below). The sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.9%; Score 32.8; D Similarity 94.4%; Pred. No. 28; 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic mapping; traits; amplification; ss.
                                                                                                                                    Table 7; Page 292; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GTCTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33819 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges M, Massey JM;
                             маввеу ЛМ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                          WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENM-) GENMARK.
(GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
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02-FEB-1993
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                             Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ33819;
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Matches
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 257; 517pp; English

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 olds one cone out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
con in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
constream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
connomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 210 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                 Score 32.8; DB 1; Length 36; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA303.
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 7; Page 282; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33882 standard; DNA; 36 BP
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%;
Best Local Similarity 94.4%;
Matches 34; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33882;
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X232322222
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Gaps

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7 DB 1;

0.9%; Score 32.8; I llarity 94.4%; Pred. No. 28; Conservative 0; Mismatches

Best Local Similarity Matches 34; Conserv

Query Match

2350

36 erererererererererererererererer

2315 GTCTGTGTGTGTGTGT

ВЪ

AAT65720 standard; DNA; 36

RESULT 71 AAT65720,

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Length 36; Indels

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required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                      Gaps
                                                                                                                                                      ö
                                                                                                                            DB 1; Length 36;
                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd113.
                                                                                                     Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                             2316 rerererererererererererererere 2351
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                                                                                                                          Score 32.8; DE
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                 AAT65784 standard; DNA; 36 BP
                                                                                                                      Query Match
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00222177
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91US-00754351
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-1991;
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17-JUN-1997
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                                                                           field.)
                                                                                                                                                                                                                                          RESULT 70
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PCR; polymerase chain reaction; paternity; maternity; human; pedigree; Linkage analysis; genetic disease; animal; plant; breeding; locus;

hybridisation; chromosome; ds

Homo sapiens

US5582979-A 10-DEC-1996. 94US-00222177.

04-APR-1994;

21-APR-1989; 05-SEP-1991;

91US-00754351.

(MARS-) MARSHFIELD CLINIC

WPI; 1997-042299/04.

Weber JL;

Polymorphism; repeat sequence; genetic marker; primer; amplification;

Repeat sequence from polymorphic marker clone Mfd18.

(revised)
(first entry)

25-MAR-2003 17-JUN-1997

AAT65720;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has been determined are shown in AAT65704 or correct sequence is from the marker clone Mdfils which contains the repeat sequence is from formula: (AC)18. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Conservative
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Claim 1; Col 13-14; 186pp; English

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

Disclosure; Col 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdfill which contains the repeat sequence having the formula: (AC)18. (Updated on 25-MAR-2003 to correct PF field.) Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

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RESULT

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New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                 Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                        STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                            INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is a ryegrass or fescue SSR
                                                                  Simple sequence repeat, SSR, #10.
                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                           24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                         03-JAN-2001; 2001NZ-00509193
                                                                                                                                                                                                                                  UNIV SOUTHERN CROSS
         AAS13713 standard; DNA; 36
                                               (first entry)
                                                                                                                                                                                                                                                                                  Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                   WPI; 2001-512563/56.
                                               08-MAY-2002
                                                                                                                                                       25-MAY-2001
                                                                                                                                     NZ509193-A.
                                                                                                                                                                                                                                                                                                                                                    varieties
                           AAS13713;
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                                                                                                                                                                                                                                   (UYSC-)
(VICT-)
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                                                                                                                   Poeae.
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence crepeat (SSR), having 2 or more tandemly repeated nucleit decree elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2-6 nucleotides in length. Also included are a nucleic acid primer controlled for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and included for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, a comethod for DNA profilling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal company be used in the selection of genes in grass or cereal breeding, for profilling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profilling to establish the control of grass or cereal breeding, for distinct identity, uniformity and/or stability of a cultivar. The present

Score 32.8; DB 1; Length 36; Pred. No. 28; 0.9%; 94.48; Query Match Best Local Similarity 94.44 Matches 34; Conservative

2316 rererererererererererererererere 2351

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Query Match
Best Local Similarity
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Gaps ö

2; Indels

0; Mismatches

ABK24298 standard; DNA; 36 BP.

ABK24298;

(first entry) 09-APR-2002 Human microsatellite D1S191 detection PCR primer #6.

Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.

Homo sapiens.

W0200185987-A1.

15-NOV-2001.

09-MAY-2001; 2001WO-AU000526

09-MAY-2000; 2000US-0202771P. 10-MAY-2000; 2000US-0202559P.

(DIAT-) DIATECH PTY LTD.

Barnard R, Giffard PM; Brockhurst V, Timms P, Wolter L,

WPI; 2002-121948/16.

Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay

Example 10; Page 55; 89pp; English

The invention relates to a method of identifying or detecting a cucleotide repeat region in a nucleic acid molecule characterised by a comprision in a nucleic acid molecule characterised by a cucleotide repeat region in a nucleic acid molecule characterised by a cucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a particular in particular, the method is useful for identification of a mucleotide length polymorphism in animals or humans, which is a necleotide length polymorphism in animals or humans, which is casociated with a neurodegenerative disease including fragile x syndrome, be used for identifying and/or typing microorganisms including yeasts and compared in the method can be used for identification of microorganisms, and expecting certain cancers and other malignancies.

CC Muntingrows, the method can be used to provide markers for use in identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and conditor responses to therapies including the possibility of microorganisms, to ascertain parentage of human or non-human individuals, and to monitor responses to therapies including the possibility of crime, in gene mapping and population studies. LASA may also be used in forensic condense; the manufacture of a kit for detecting and/or identifying mucleotide crime, in gene mapping and population studies. LASA may also be used in the methods using gel electrophoresis and Southern transfer and and cost required by prior art methods using gel electrophoresis and Southern transfer and and the contract of automate or miniaturise. The LASA method avoids the time and cost required by prior art malaturise. The LASA method avoids the time and cost required subject polymorphisms or microsatellites as described in the method of the collimation of all aboratory procedures. ABK2476-ABK24313 represent primers used to contract polymorphisms or microsatellites as described in nventior

Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

Score 32.8; DB 1; Length 36; Pred. No. 28; 0.9%;

> ABK24298/C RESULT 73

(first entry)

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highly-dormant wheat; genetic marker; high dormancy; seed; chromosome 4A;
                                                                                                                                                                                                                                                                                                                                                                                                         Selecting highly-dormant wheat using genetic marker associated with gene that provides high dormancy to seeds.
                                                                                                                              Wheat SSR containing amplification genetic marker, Xgwm637
                                                                                                                                                                                                                                                                                                                                                  (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; SEQ ID NO 7; 13pp; Japanese.
                         ADO80224/c
ID ADO80224 standard; DNA; 36 BP.
                                                                                                                                                                                                                                                                                         24-SEP-2002; 2002JP-00276822
                                                                                                                                                                                                                                                                                                                      24-SEP-2002; 2002JP-00276822
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-310662/29.
                                                                                                                                                                                                                                 JP2004113007-A.
                                                                                                 29-JUL-2004
                                                                                                                                                                                                                                                              15-APR-2004
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                                                                                                                                                                                                     Triticum.
                                                                     ADO80224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ34041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of typing (MI) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DMR region of (I) that includes PML, using as template a DMR sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, man metabolic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                  Prion protein polymorphic microsatellite marker consensus sequence #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. Th sequence represents a prion protein polymorphic microsatellite marker
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                           disease predisposition, microsatellite marker, prion disease, cystic fibrosis, malignant hyperthermia syndrome, metabolic disease, milk protein, hormone, transcription factor, pT7-blue-vector, sheep,
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2; Indels
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                            2316 TCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                               polymorphic microsatellite loci; PML;
                                           Score 32.8; DE
Pred. No. 28;
0; Mismatches
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 50; 64pp; German.
                                                                                                                              ADO81134 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cn 0.9%;
1 Similarity 94.4%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2002; 2002DE-01036711
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geldermann H, Preuss S,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYHO-) UNIV HOHENHEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-215730/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                        microsatellite; ds
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                                                                                                                                                                                                                                                gene typing;
                                                                                                                                                                                      29-JUL-2004
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34;
                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                           ADO81134;
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The invention relates to a novel method for selecting highly-dormant wheat using a genetic marker associated with a gene that provides high dormancy to the seeds. In the method of the invention, the genetic marker exists specifically in the genetic region within 44 cM from the gene associated with high dormancy in chromsoome 4A. The method is useful for selecting highly-dormant wheat. This polynucleotide sequence represents a
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                  Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone TGLA433.
                                                                                                                                                                                     Score 32.8; i
Pred. No. 28;
                                                                                                                                                                                                                           0; Mismatches
                                                                                                              wheat genetic marker of the invention.
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                                                                                                                                                                                     Query Match 0.9%;
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           AAQ34041 standard; DNA; 37
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2316 rcrGrGrGrGrGrGrGrGrGrGrGrGrGrGrG

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In crossatellite (using the program OPTIPRIM). The microsatellites may be microsatellite (using the program OPTIPRIM). The microsatellites may be applied to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits, and cattle, to allow selective.
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                                                                                                                                                                                                                                                                                                                                                                                       breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                   Table 7; Page 347; 517pp; English.
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                 91US-00642342
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Local Similarity 94.4%;
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                                                                                                   WPI; 1992-284684/34.
                                                                       Маввеу
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                                           (GENM-) GENMARK
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                  15-JAN-1991;
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02-FEB-1993
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                                                                       Georges M,
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                                                                                                                                                                                                                                                                                                                                                                                                            field.)
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The sequence is that of a bovine microsatellite sequence obtd. by

considering a library of bovine MboI DNA fragments of between 250 and 500

considering a library of bovine MboI DNA fragments of between 250 and 500

considering an (ADI)15 and and (TC)15 alignoutclectide probe. One out of 50

considering an analysis of Assuming independent distribution of

microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites

considering approach is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence waset to generate the

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

contained to identify individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

conomically important traits esp. in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.8; DB 1; Length 37; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 BP; 0 A; 0 C; 18 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                              rable 7; Page 289; 517pp; English.
mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT65732 standard; DNA; 37 BP
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91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .98;
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(first entry)
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05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65799-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf30 which contains the repeat sequence is from the marker clone Mdf30 which contains the repeat sequence having the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                             formula: (AC)18.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                          DB 1; Length 37;
                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                    Sequence 37 BP; 19 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     37 rererererererererererererererere
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA153.
                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                          Score 32.8;
                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 225; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33737 standard; DNA; 39 BP
                                                                                                                                                                                                                                                      0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340
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                                                                                                                                                                                                                                                                                              Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9213102-A1.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ33737;
                                                                                                                                                                                                                                                          Query Match
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AAQ33737
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which contain single nucleotide polymorphisms (SNPB). Sequences 1 to 1112

(AAA76318-A77429) are consecutive pairs of nucleotides which contain

Salent SNPB. Sequences 1131 to 1129 (AAA77430-A77509) are consecutive

pairs of nucleotides containing SNPS which result in changes in the

corresponding amino acid sequences (AAB1749-B11828). The SNPB in

corresponding amino acid sequences (AAB1749-B11828). The SNPB in

corresponding amino acid sequences (AAB1749-B11828). The SNPB in

corresponding amino acid sequences (AAB17446-A77503) result

corresponding amino acid sequences (AAA77446-A77503) result

corresponding amino acid detecting in sequences 1187 to 1192

changes to a method of detecting a polymorphic site in a nucleic acid and

camethod of determining the relatedness of two nucleic acids. It also

corresponding the antibodies. The nucleic acids are useful for

corresponding an individual having, suspected of having, or at risk of

developing a pathological condition due to the presence of a sequence

polymorphism. Such treatment would comprise administration of the wild-

cypetides can also be used in the treatment of such individuals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                  Human; single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; 88.
                                                                                        ;
0
                                               Query Match 0.9%; Score 32.8; DB 1; Length 39; Best Local Similarity 94.4%; Pred. No. 31; Matches 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                Human clone cg44024536 polymorphic site, SEQ ID NO:1020.
                 Sequence 39 BP; 2 A; 0 C; 17 G; 20 T; 0 U; 0 Other;
                                                                                                                          2316 rengrengrengrengrengrengrengren 2351
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                                                                                                                                                                                                                                                      AAA77337 standard; cDNA; 44 BP
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                                                                                                                                                                                                                                                                                                                               16-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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variation
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                       Microsatellite sequence from clone TGLA126.
                                 AAQ33692 standard; DNA; 34 BP.
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                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                      (GENM-) GENMARK.
                                                                                                                                                                                                                                                                     15-JAN-1992;
                                                                                                                                                                                                                                                                                             15-JAN-1991;
                                                                                                                                                                                                                   WO9213102-A1
                                                                                                                                                                                                                                           36-AUG-1992.
                                                                                      25-MAR-2003
02-FEB-1993
                                                                                                                                                                                           Bos taurus.
                                                            AAQ33692;
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          RESULT 82
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                        AAQ3369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers Anfe5799-f66047. Those clones where the repeat sequence has been determined are shown in AAT65704-777. This repeat sequence is from the marker clone Mdf52 which contains the repeat sequence is from the marker clone Mdf52 which contains the repeat sequence in first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formula: (AC)18TTG(CA)3. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 32.8; DB 1; Length 45; ilarity 94.4%; Pred. No. 37; Conservative 0; Mismatches 2; Indels
                         DB 1; Length 44;
                                                                          2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCG 2359
                                                   7; Indels
                                                                                                     1 rerererererererererererererererererece 44
                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd52.
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Sequence 44 BP; 1 A; 2 C; 21 G; 20 T; 0 U; 0 Other;
                         Score 32.8; DB
Pred. No. 36;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                             hybridisation; chromosome; ds.
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91US-00754351.
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                            94.18;
                                                                                                                                                                      AAT65751 standard; DNA; 45
                                                                                                                                                                                                                        (revised)
(first entry)
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                                     Best Local Similarity 84.1
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Ношо варіеля
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17-JUN-1997
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                                                                                                                                                                                                 AAT65751;
                             Query Match
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Matches
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92WO-US000340.

(first entry)

(revised)

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                                                                                                                                 The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTPIREM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 32.4; Dilarity 97.1%; Pred. No. 29; Conservative 0; Mismatches
                                                                                                rable 7; Page 207; 517pp; English.
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(first entry)
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Matches 33; Conserv
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02-FEB-1993
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Gaps

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2315 GICTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350

34;

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36 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGI 1

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The sequence is that of a bovine microsatellite sequence obtd. by

creening a library of bovine MboI DNA fragments of between 250 and 500

CD by with an (ACI)s and a (TC)15 oligonuclectide probe. One out of 50

CLONES cross-hybridised. Assuming independent distribution of

clones cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC in the bovine genome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

Specification and indexed herein (see below). The sequence information

CC downstream of the microsatellite sequence were used to generate the

CC downstream of the program of printerion of the corresp.

CM in vitro amplification of the corresp.

CM in crosatellite (using the program OPTIRRIW). The microsatellites may be

CM incrosatellite (using the program OPTIRRIW). The microsatellites may be

CM in apping of economic trait loci, or genes involved the determinism of

CM connected trait loci, or genes involved the determinism of

CM connected to dentify individuals. The microsatellites and the determinism of

CM connected to dentify individuals. The microsatellites are the connected trait loci, or genes involved the determinism of

CM connected the contract trait sep. in cattle, to allow selective
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                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                        Table 7; Page 279; 517pp; English.
                                                                              91US-00642342.
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91US-00754351.
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                                                                                                                                                                              Georges M, Massey JM;
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                                                                           15-JAN-1991;
                            15-JAN-1992;
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05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MooI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised Assuming independent distribution of microsatellites and MooI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and domonstream of the microsatellites sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Microsatellite sequence from clone TGLA179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Table 7; Page 240; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33873 standard; DNA; 34 BP.
                                                                                                                                                                                                                                                                               92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                  (GENM-) GENMARK.
                                                                                                                                                                                                                                                                               15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                              WO9213102-A1
                                                                                                                                                                                                                             06-AUG-1992.
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02-FEB-1993
                                                                                                                             Bos taurus.
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Gaps

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(MARS-) MARSHFIELD CLINIC.

WO9213102-A1

Bos taurus.

AAQ33873;

RESULT

Query Match

Matches

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06-AUG-1992

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WO200185987-A1.
                                                                  Homo sapiens
                                                      09-APR-2002
                                                                       15-NOV-2001.
                                                   ABK24297;
                                 Query Match
                                    Matches
                                              RESULT 86
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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a farticular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a condition of particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, thuntington's disease, or muscular dystrophy. Purthermore, the method may condition and multi-cellular organisms, Purthermore, the method may condition of human and for genotyping subjects including humans. The method is also useful for detecting certain cancers and other malignancies.

Condition of human and non-human individuals, plants and identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and identification of human and non-human individuals, cand to monitor responses to therapies including the possibility of and to monitor responses to therapies including the possibility of crime, in gene mapping and population studies lash may also be used in the manufacture of a kit for detecting and/or identifying nucleotide repeat regions such as a nucleotide length polymorphism in a eukaryotic crepeat regions such as a nucleotide length polymorphism in a eukaryotic crepeat regions such as a nucleotide length polymorphism in a eukaryotic crepeat regions such as a nucleotide length polymorphism in a eukaryotic crepeat regions such as a nucleotide length polymorphism in eukaryotic crepeat regions such as a nucleotide length polymorphism in eukaryotic crepeat regions such as a nucleotide length polymorphism in eukaryotic crepeat regions euch detecting and condition transfer analysis. In particular, current diagnosis of H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detect polymorphisms or microsatellites as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat sequence from polymorphic marker clone Mfd47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 rererererererecererererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 32.4; Interity 97.1%; Pred. No. 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT65747 standard; DNA; 35 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00341562.
91US-00754351.
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tes 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           888888888888888888888888888888888888
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                                                                                                                                                                                                                                                               The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to defect these markers. Primers based on these sequences can be used to defect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf44 which contains the repeat sequence is from formula: (CA)17. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite, ligase-assisted spacer addition assay; LASA, cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnard R, Giffard PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human microsatellite D1S191 detection PCR primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 rererererererecererererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 rererererererererererererererere
                                                                                                                                                                                                                       Disclosure; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolter L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 55; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK24297 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-2000; 2000US-0202771P.
10-MAY-2000; 2000US-0202559P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           march 0.9%;
Local Similarity 97.1%;
es 33; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DIAT-) DIATECH PTY LTD.
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                                                                                  WPI; 1997-042299/04
                                    Weber JL;
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Gaps ö

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
                                                                                                                                                                    markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dc-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has the marker clone Mdf47 which contains the repeat sequence is from the marker clone Mdf47 which contains the repeat sequence having the formula: (AC)17.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                          sednences
                                                 Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                         genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                     The invention relates to the isolation of polymorphic repeat having the sequence (dC-dA)n. (dG-dT)n which can be used as ge
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.4; DB 1; Length 35;
Pred. No. 30;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35 BP; 18 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite sequence from clone TGLA112.
                                                                                                  Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 7; Page 197; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ33669 standard; DNA; 37 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          97.18;
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Best Local Similarity 97.1
Best Local 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
              WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus.
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in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traites esp. in cattle, to allow selective by reeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis of genetic disorders associated with chromosomal abnormaliti and uniparental disomy, e.g. Prader-Willi:Angelman syndrome - using in situ hybridisation using probes spanning the IR4-3R or GABRB3 regions.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast Artificial Chromosome, YAC, polymerase chain reaction, PCR, sequence tagged site, genetic disorder, diagnosis, abnormality, Prader-Willi, Angelman, Beckwith-Wiedermann, syndrome, ds.
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                                                                                                                                                                                                                               DB 1; Length 37;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                 Sequence 37 BP; 1 A; 1 C; 18 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                               2351
                                                                                                                                                                                                                                                                                                                           2 rererererererecerererererereres
                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                              Score 32.4; 1
Pred. No. 32;
                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 64; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chromosomal repeat element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                             ВР
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                                                                                                                                                                                                                              ch 0.9%;
1 Similarity 97.1%;
33; Conservative
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(first entry)
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/*tag=
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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28-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ68850;
                                                                                                                                                                     field.)
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                                                                                                                                                                                                                                                               Matches
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PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                                                                                                                                                                Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd12.
                                                                                                                                                                                                                                                                                                                                                      hybridisation; chromosome; ds.
                                                                AAT65714 standard; DNA; 39 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1989;
05-SEP-1991;
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                                                                                                                                                             25-MAR-2003
17-JUN-1997
                                                                                                                AAT65714;
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                   RESULT 91
AAT65714/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n - using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Gaps
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                                               Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38 BP; 20 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
Seguence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd6.
                                               DB 1;
                                                                                                                                           2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
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0; Mismatches
                                                                                            0; Mismatches
                                            Score 32.4; 1
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hybridisation; chromosome; ds.
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                                          cch 0.9%;
al Similarity 97.1%;
33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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Best Local Similarity
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                               Query Match
                                                                                              Matches
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                                                                                                                                                                                                                                                                 RESULT 90
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 AAT6.

AAT7.

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94US-00222177.

(revised)
(first entry)

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91US-00754351.

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                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers: primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf12 which contains the repeat sequence is from formula: (AC)11AT(AC)8A. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39 BP; 20 A; 18 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 GTGTGTGTGTGTGTATGTGTGTGTGTGTGTGTGTG 2
Disclosure; Col 9-10; 185pp; English.
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17-JUN-1997
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ID AAT6572
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AC AAT6572
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DT 25-MAR:
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2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351

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US5582979-A.

10-DEC-1996

Weber JL;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-737. This repeat sequence is from the marker clone Mdf42 which contains the repeat sequence is from the marker clone Mdf42 which contains the repeat sequence is from formula: (CA)16T(AC)3.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 9-10; 186pp; English.
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                                                                                                                                                                 91US-00754351.
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                                                                                              94US-00222177
                                                                                                                                           89US-00341562
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                                                                                                                                                                                                                (MARS-) MARSHFIELD CLINIC.
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les 34; Conservative
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                                                                                            04-APR-1994;
                                                                                                                                             21-APR-1989;
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  US5582979-A.
                                               10-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-977. This repeat sequence has been determined are shown in AAT65704-777. This repeat sequence is from the marker clone Mdf34 which contains the repeat sequence a from formula: (AC)4AT(AC)15. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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0
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                        Repeat sequence from polymorphic marker clone Mfd34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2315 Grerererererererecerererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 U; 0 Other;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 9-10; 186pp; English.
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91US-00754351.
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Matches 34; Conservative
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                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                     04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1989;
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Gape

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3; Indels

0; Mismatches

ВЪ.

25-MAR-2003 17-JUN-1997

AAT65743;

AAT65743, RESULT

Query Match

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Score 32.2; DB 1; Length 40; Pred. No. 38;

Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.

Example 5; Page 14; 35pp; Japanese

The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA298483-514 represent sequences from Haliotis discus, used in the method of the invention

Sequence 40 BP; 19 A; 19 C; 0 G; 2 T; 0 U; 0 Other;

Gaps ö Length 40; 3; Indels 2315 GTCTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTG 2351 39 crarcrererererererererererererereres 3 DB 1; 0; Mismatches Score 32.2; 1 Pred. No. 38; 0.8%; 34; Conservative Local Similarity Query Match Best Local S tches g

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776/c AAT65776 standard; DNA; 42 BP. AAT65776;

(first entry) (revised) 25-MAR-2003 17-JUN-1997 Repeat sequence from polymorphic marker clone Mfd105.

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

Homo sapiens

US5582979-A

10-DEC-1996.

94US-00222177. 04-APR-1994;

91US-00754351 89US-00341562 21-APR-1989; 05-SEP-1991;

(MARS-) MARSHFIELD CLINIC.

Weber JL;

WPI; 1997-042299/04.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)nusing novel nucleic acid mols. as primers.

Claim 1; Col 13-14; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases ö Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a phage libraries with a synthetic poly(dc-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf105 which contains the repeat sequence is from formula: TCAAACACAA(AC)16. (Updated on 25-MAR-2003 to correct PF field.) degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity doodpasture's syndrome; type IV hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leprosy; infections disease; viral infection; HIV; fungal infection; candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukasmia; lymphoma; cancer; brain cancer; Gaps ö human; T-cell associated disease; Vbeta; autoimmune disease; 42; 3; Indels DB 1; Length Sequence 42 BP; 22 A; 19 C; 0 G; 1 T; 0 U; 0 Other; 42 grerererererererererererererererere Disclosure; SEQ ID NO 797; 164pp; English. O.8%; Score 32.2; I ilarity 91.9%; Pred. No. 40; Conservative 0; Mismatches Human Vbeta gene repeat sequence #393. BP 99US-00263959. 94US-00309335. 95US-00531241. ADH70603 standard; DNA; 44 (first entry) WPI; 2004-059052/06. Hood LE, Rowen L; Local Similarity les 34; Conser breast cancer; ds. (HOOD/) HOOD L E. (ROWE/) ROWEN L. US2002150891-A1. Homo sapiens 05-MAR-1999; 19-SEP-1994; 19-SEP-1995; 25-MAR-2004 17-0CT-2002. *N*beta gene ADH70603; Query Match Best Loc Matches ADH70603/c RESULT 96 88888888 g ઠે

been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf36 which contains the repeat sequence having the formula: (AC)15AT(AC)6A. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 45 BP; 23 A; 21 C; 0 G; 1 T; 0 U; 0 Other;

DB 1; Length 45;

43;

0.8%; Score 32.2; 91.9%; Pred. No. 43

Query Match

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                           atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type I hypersensitivities such as contact with allergens that lead to allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schicosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
   neoplastic diseases. Autoimmune diseases include Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.2; DB 1; Length 44;
Pred. No. 42;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence from polymorphic marker clone Mfd36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 44 BP; 22 A; 21 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 Grerererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT65737 standard; DNA; 45 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%;
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91US-00754351
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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05-SEP-1991;
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17-JUN-1997
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ID AAT6

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
compared by with an (AF)15 and and (TC)15 and and mboI sites, the frequency of (T6)n >9 microsatellites
and compared are setimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene
                  Gaps
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                                                                                                                                                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 37;
0; Mismatches 1; Indels
                                                      2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 0 A; 0 C; 16 G; 17 T; 0 U; 0 Other;
                                                                                        40 crererarererererererererererererere
                                                                                                                                                                                                                                                                                                          Sequence of a microsatellite from clone TGLA54
                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 370; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping, and selective breeding.
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Best Local Similarity 97.0%;
Matches 32; Conservative
                                                                                                                                                                               AAQ34097 standard; DNA; 33
                                                                                                                                                                                                                                                                           (first entry)
Best Local Similarity 91.9
Matches 34; Conservative
                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                     AAQ34097;
                                                                                                                                             RESULT 98
AAQ34097
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having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has

The invention relates to the isolation of polymorphic repeat sequences

Disclosure; Col 9-10; 186pp; English.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

WPI; 1997-042299/04.

(revised)
(first entry)

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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols, as primers.
                                               Repeat sequence from polymorphic marker clone Mfd58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
                                                                                                                                                                                                                                                    04-APR-1994;
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05-SEP-1991;
         25-MAR-2003
17-JUN-1997
                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                            JS5582979-A.
                                                                                                                                                                                                                       10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                             Weber JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a bovine microsatellite sequence obtd. by

Screening a library of bovine MboI DNA fragments of between 250 and 500

Co screening a library of bovine MboI DNA fragments of between 250 and 500

Co by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

Co can cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

co in the bovine genome is estimated at >100, 000. The sequence information

co in the bovine genome microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

coperation and indexed herein (see below). The sequences upstream and

comparteam of the microsatellite sequence were used to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite in vitro amplification of the corresp.

coused to identify individuals, for parentage testing, and in the genetic

mepping of economic trait loci, or genes involved the determinism of

connection.

connective

connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 31.4; DB 1; Length 33; 97.0%; Pred. No. 37; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33 BP; 0 A; 0 C; 16 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA415.
      2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                   1 rerererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 334; 517pp; English.
                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                     92WO-US000340.
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                                                                                                               AAQ34009 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.0
Matches 32; Conservative
                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1991;
                                                                                                                                                                                                                                                                                                                             WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                            06-AUG-1992.
                                                                                                                                                                         25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                  Bos taurus.
                                                                                                                                               AAQ34009;
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89US-00341562. 91US-00754351. 94US-00222177.

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.9 paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those clones where the repeat sequence has by primers AATG579-TG647. Those clones where the repeat sequence is from the marker clone Mdf58 which contains the repeat sequence is from the marker clone Mdf58 which contains the repeat sequence having the formula: (CA)16.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.4; DB 1; Length 33;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, Indels
                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 BP; 16 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2319 grandrardrardraccingrardrardrarg 2351
                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Scoll No. 3., 97.0%; Pred. No. 3., ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT65705 standard; DNA; 33 BP.
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17-JUN-1997 (First en
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2318 rerererererererererererererer 2350 rérerererererererererererererer

AAT65754 standard; DNA; 33 BP.

RESULT 100 AAT65754/

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AAT65754;

Weber JL;

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New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.
                                                                                                                                                                                                                                                                                                     The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-associated chondrodysplasia, particularly FGFR3 achondroplasia, e.g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect mouse FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers – used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.8%; Score 31.4; DB 1; Length 33; Best Local Similarity 97.0%; Pred. No. 37; Matches 32; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 BP; 8 A; 11 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818 CTCATCACTCTGCGTGGTGGTGCTGCCAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 cccarcacrcrcccrccrccrccrccrccrccrcca 1
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                                                                                                                                                                                                                                                                  Example, Col 14; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33921 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US000340
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(YEDA ) YEDA RES & DEV CO L'
(PROC-) PROCHON BIOTECH LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                          WPI; 2001-463946/50
                                                                   Segev 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ33921;
                                                                   Yayon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf3 which contains the repeat sequence is from formula: (CA)16C. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; chondrodysplasia; achondroplasia; transgenic mouse; therapy; fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 BP; 16 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse FGFR3 allele detecting antisense PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 9-10; 186pp; English
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                                                                                                                                                                                               89US-00341562.
91US-00754351.
                                                                                                                                                      94US-00222177
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Best Local Similarity 97.0%;
Matches 32; Conservative (
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                                                                                                                                                                                                                                                                  (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-042299/04
                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999;
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                                                                                                                                                        04-APR-1994;
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                                                                   US5582979-A.
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AAD34806;

RESULT 102

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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by

Screening a library of bovine Mool DNA fragments of between 250 and 500

Screening a library of bovine Mool DNA fragments of between 250 and 500

CC clores cross-hybridised. Assuming independent distribution of

CT can genome is estimated at >100, 000. The sequence information

CT cr ca. 230 such bovine microsatellites is summarised in the

Specification and indexed herein (see below). The sequences upstream and

CT cr ca. 230 such bovine microsatellite sequence waset to generate the

CT cr ca. 230 such point microsatellite sequence waset to generate the

CT cr ca. 240 such points microsatellite sequence waset to generate the

CT cr ca. 250 such points with a consideration of the corresp.

CT cr ca. 250 such points to vitro amplification of the corresp.

CT cr ca. 250 such points to parentage testing, and in the genetic

CT cr ca. 250 such points trait loci, or genes involved the determinism of

CT cr ca. 250 such papers of cr callow selective

CT cr ca. 250 such papers in cattle, to allow selective

CT cr ca. 250 such papers in cattle, to allow selective

CT cr ca. 250 such papers in cattle, to allow selective
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0.8%; Score 31.4; DB 1; Length 34; llarity 97.0%; Pred. No. 38; Conservative 0; Mismatches 1; Indels Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other; 2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIG 2351 Local Similarity 32; Query Match Matches

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BP

AAT65748 standard; DNA; 34

RESULT 105

AAT65748/

(first entry)

(revised)

25-MAR-2003 17-JUN-1997

AAT65748;

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Gaps . 0

> Repeat sequence from polymorphic marker clone Mfd20. ВР AAT65722 standard; DNA; 34 (revised)
> (first entry) 25-MAR-2003 17-JUN-1997 AAT65722; RESULT 104 AAT65722, 용

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

94US-00222177. 89US-00341562. 91US-00754351. 04-APR-1994; Homo sapiens 21-APR-1989; US5582979-A. 10-DEC-1996,

(MARS-) MARSHFIELD CLINIC. Weber JL;

05-SEP-1991;

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers. WPI; 1997-042299/04.

Disclosure; Col 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the

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repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA).(dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAF5798-R56047. Those clones where the repeat sequence has been determined are shown in AAF65704-797. This repeat sequence is from the marker clone Mdf20 which contains the repeat sequence is from formula: (AC)17. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                      Score 31.4; DB 1; Length 34; Pred. No. 38; 0; Mismatches 1; Indels
                                                                                                                                                                   Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                        GTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                             0.8%;
Local Similarity 97.0%;
hes 32; Conservative
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Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers. Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds. Repeat sequence from polymorphic marker clone Mfd48. 89US-00341562. 94US-00222177. 91US-00754351. (MARS-) MARSHFIELD CLINIC. WPI; 1997-042299/04. Homo sapiens. 04-APR-1994; 21-APR-1989; 05-SEP-1991; 10-DEC-1996. Weber JL;

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial page 1 ibraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those close where the repeat sequence has by primers AAT65798-T6647. Those close where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf48 which contains the repeat sequence is from formula: (AC)17. (Updated on 25-MAR-2001 to correct PF field.)

Disclosure; Col 11-12; 186pp; English.

Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

Homo sapiens

US5582979-A.

.0-DEC-1996

94US-00222177. 89US-00341562. 91US-00754351.

04-APR-1994; 21-APR-1989; 05-SEP-1991; (MARS-) MARSHFIELD CLINIC.

WPI; 1997-042299/04.

Weber JL;

Repeat sequence from polymorphic marker clone Mfd101.

(first entry)

(revised)

25-MAR-2003 17-JUN-1997

AAT65772;

BP.

AAT65772 standard; DNA; 34

AAT65772/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                               PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                       Gaps
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   Length 34;
                                   Indels
                                                                                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfd41.
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0.8%; Score 31.4; D
97.0%; Pred. No. 38;
iive 0; Mismatches
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                                                                     GTGTGTGTGTGTGCGT
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                                   Conservative
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                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1989;
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17-JUN-1997
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   Query Match
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                                   Matches
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Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
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Pred. No. 38;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 13-14; 186pp; English.
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(first entry)
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nes 32; Conservative
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17-JUN-1997
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Gaps

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Best Local Similarity 97.0 Matches 32; Conservative

Query Match

2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351

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34 crerererererererererererere

0.8%; Score 31.4; DB 1; Length 34; 97.0%; Pred. No. 38;

92WO-US000340.

15-JAN-1992;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps .
                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 1 Similarity 97.0%; Pred. No. 51; Similarity 97.0%; Pred. No. 51; 32; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43 BP; 21 A; 19 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of a microsatellite from clone TGLA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                  94US-00222177
                                                                                                                                                                                                                 89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34104 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                  (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                             WPI; 1997-042299/04
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02-FEB-1993
                                                                                                                                                                                                                    21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                    04-APR-1994;
                                                                                           Homo sapiens
                                                                                                                       US5582979-A
                                                                                                                                                       10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ34104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                  Weber JL;
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The sequence is that of a bovine microsatellite sequence obtd. by

Screening a library of bovine Mbol DNA fragments of between 250 and 500

CC by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

CC clones cross-hybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites

cc microsatellites and mborine microsatellites is summarised in the

for ca. 230 such bovine microsatellites is summarised in the

cc specification and indexed herein (see below). The sequence upstream and

downstream of the microsatellite sequence were used to generate the

cc macrosatellite using the program OPTIPRIM). The microsatellites may be

microsatellite using the program OPTIPRIM). The microsatellites way be

microsatellity individuals, for parentage testing, and in the genetic

used to identify individuals, for parentage testing, and in the genetic

cc mapping of economic trait loci, or genes involved the determinism of

preceding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

field.)
                                                                                                                                      - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; resequence; genotype; disease; forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/standard name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2330 TGTGCGTGTGTGTGTGTGTGCACATCCGCGTGTGCCTGTGTG 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 rerererererererererererere 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human single nucleotide polymorphism (SNP) FGFR3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44 BP; 4 A; 6 C; 17 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.2; 1
Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
replace(16,C)
                                                                                                                                                                                            Table 7; Page 372; 517pp; English.
                                                                                                                                               Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI30469 standard; DNA; 31 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2001; 2001WO-US007268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2000; 2000US-0187510P.
22-MAY-2000; 2000US-0206129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
ilarity 81.8%;
Conservative
                      91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                      Massey JM;
                                                                                                                   NPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
36; Conser
                                                        (GENM-) GENMARK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2001
                           15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Variation
                                                                                       Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI30469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 3
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ID AAI3
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Gaps

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particular genotype.
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      WPI; 2001-522952/57
                                                            Best Local Similarity
                                                                                                                               WO200166800-A2
                                                                                             18-OCT-2001
                                                                                                              Homo sapiens
                                                                                                                                    13-SEP-2001
                                                                                                                   Key
Variation
                                                                                         AAI30470;
                                                         Query Match
  Cargill
                                                testing
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The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resequence; genotype; disease; forensic; paternity testing; nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/standard_name= "single_nucleotide_polymorphism"
                                                                                                                                                                                                                                                                                                                DB 1; Length 31;
38;
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                                                                                                                                                                                                                                                                   Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human single nucleotide polymorphism (SNP) FGFR3 4.
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                                                                                                                                                                                                                                                                                                  0.8%; Scot.
100.0%; Pred. No. 30,
... 0; Mismatches
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Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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22-MAY-2000; 2000US-0206129P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI30472 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 31; Conservative
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Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI30472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI30472
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                                                                                                                                                                                                                                                                                        (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.
                                                                                                                                 sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a
                                                                                                                                                                                                                                                                     The invention relates to the identification of nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, resequence, genotype, disease, forensic, paternity testing, single nucleotide polymorphism, SNP, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "single_nucleotide_polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                            molecules from the human genome which include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 31; 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human single nucleotide polymorphism (SNP) FGFR3 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31 BP; 9 A; 10 C; 6 G; 6 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1928 ACTGCACACACCACCTGTACATGATCATGCG 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Scor.
100.0%; Pred. No. Ju.
... 0; Mismatches
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                                                                                                                                                                                                                         Claim 1; Page 87; 145pp; English.
                       Lander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI30470 standard; DNA; 31 BP
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22-MAY-2000; 2000US-0206129P
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                     Ireland JS,
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                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                        Addison's disease; atrophic gastritis;
Addison's disease; atrophic gastritis;
degenerative nervous system disease; multiple sclerosis;
Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
allergy; type II hypersensitivity; Goodpasture is syndrome;
type IV hypersensitivity; leprosy; infectious disease; viral infection;
HIV; fungal infection; Candida; parasitic infection; schistosome;
filaria; bacterial infection; Mycobacterium; neoplastic disease;
lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease;
                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                           human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                 0.8%; Score 31; DB 1; Length 31;
100.0%; Pred. No. 38;
iive 0; Mismatches 0; Indels
                                   Sequence 31 BP; 3 A; 11 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                       1407 CTGCACGCAGGCGGCCCCTGTACGTGCTG 1437
                                                                                                                                                              Disclosure; SEQ ID NO 711; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                               Human Vbeta gene repeat sequence #307.
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                                                                                       Local Similarity 100.
nes 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast cancer; ds.
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19-SEP-1995;
                                                                                                                                                                                                                                                                                                                               25-MAR-2004
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                                                                            Query Match
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          testing
                                                                                                                                                                                                                                  RESULT 113
                                                                                                            Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
corpus cross-hybridised. Assuming independent distribution of 50
corpus cross-hybridised in the frequency of (T6)n >9 microsatellites
coperatellite sequence were used to generate the 50
compact of the microsatellite sequence were used to generate the 50
corpus cross-hybridised for in vitro amplification of the corresp.
corpus cross-hybridised for in vitro amplification of the corresp.
corpus cross-hybridised for in vitro amplification of the corresp.
corpus cross-hybridised for in vitro amplification of the determinism of 50
compactor in microsatellite septing, and in the genetic 60
connomically important trait loci, or genes involved the determinism of 60
connomically important traits esp.; in cattle, to allow selective
connomically correct PN
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Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a VDeta gene repeat sequence.
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                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                              0.8%; Score 30.8; DB 1; Length 34;
94.1%; Pred. No. 45;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                     Sequence 34 BP; 0 A; 1 C; 17 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                      1 rererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rable 7; Page 215; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00642342.
                                                                                                                                                                                                                                                                                             94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33713 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                      32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 114
                                                                                                                                                                                                                                                                                                                          Matches
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Sequence 35 BP; 1 A; 0 C; 17 G; 17 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonuclocide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
and mboI sites, the frequency of (T6)n >9 microsatellites
con the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteem of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30.4; DB 1; Length 32;
Pred. No. 47;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of a microsatellite from clone TGLA67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2319 GTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grenergrenergrenergrenergrener 32
                                                                                                                                                                                         Microsatellite sequence from clone TGLA111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 196; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping, and selective breeding.
                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.8%;
il Similarity 96.9%;
31; Conservative
                                        AAQ33666 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ34119 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                             WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1992;
                                                                                                                           25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1993
                                                                                                                                                                                                                                                                                                       Bos taurus.
                                                                                  AAQ33666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ34119;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 117
RESULT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ34119
                      AAQ3366
                                                              요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone MdE108 which contains the repeat sequence laring the marker clone MdE108 which contains the repeat sequence having the formula: GTGGTAAAT(AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromsome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                              Gaps
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                    Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 42;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGCACATCCGC 2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGTGIGTGIGTGIGTGIGTGIGTGIGTGIATTIAGCCAC 1
                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence from polymorphic marker clone Mfd108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 BP; 19 A; 17 C; 3 G; 3 T; 0 U; 0 Other;
                                                            7
                    DB 1;
                                                                                                                                               2 rerererererererererererererereres
                    Score 30.8; D
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.8;
Pred. No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-00222177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00754351
                    Query Match

Best Local Similarity 94.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 83.3
Matches 35; Conservative
                                                                                                                                                                                                                                      779/c
AAT65779 standard; DNA;
                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JUN-1997
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                                                                                                                                                                                                                                                                                                  AAT65779;
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AAT65779/ XX AAT6 X

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Gape

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10-DEC-1996

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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

co by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50

co lones cross-Pybridised. Assuming independent distribution of

colones cross-Pybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

colones cub bovine microsatellites is summarised in the

coperation and indexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream and

coperation of the microsatellite sequence waset to generate the

committee PCR primers for in vitro amplification of the corresp.

concept to identify individuals, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

concomically important traits sep. in cattle, to allow selective

concomically important traits sep. in cattle, to allow selective

preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 30.4; DB 1; Length 32; 96.9%; Pred. No. 47; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfdl19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32 BP; 0 A; 1 C; 16 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Table 7; Page 378; 517pp; English.
                                                                                                                                                         92WO-US000340.
                                                                                                                                                                                          91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT65790 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                           Georges M, Massey JM;
                                                                                                                                                                                                                                                                                            WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                             (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5582979-A.
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17-JUN-1997
                                                                                                                                                                                              15-JAN-1991;
                                                                                                                                                             15-JAN-1992;
                                                                                              WO9213102-A1
                                                                                                                               16-AUG-1992
                                                             Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT65790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 118
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Gaps ; 0

BP.

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers APT65789-T6647. Those clone where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdfil9 which contains the repeat sequence is from formula: (AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)nusing novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.4; DB 1; Length 32;
Pred. No. 47;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGI 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT65752 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%;
                       94US-00222177.
                                                   89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 31; Conserv
                                                                                                                                                        WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5582979-A
                                                      21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
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                          04-APR-1994;
                                                                    05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT65752;
                                                                                                                             Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT65752,
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Human alpha-7 neuronal nicotinic acetylcholine receptor and related Claim 9; Page 63; 104pp; English Leonard S, Freedman WPI; 1999-288306/24 polymucleotides. Matches ઠે 셤

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acetylcholine receptor (alpha7-hmAChR). Also described are: (1) a peptide encoded by (1); (2) a vector comprising (1); (3) a host cell transformed with a vector of (2); (4) a polymucleotide comprising at least 15 mucleotides which hybridises under stringent conditions to at least a portion of (1); (5) a method for detection of a polymucleotide encoding alpha 7-hnAChR in a biological sample; and (6) a method for amplification of nucleic acid from a sample suspected of containing nucleic acid encoding alpha 7-hnAChR. The primers and probes from the present invention can be used on brain tissue and blood samples of humans suspected of suffering from schizophrenia, small cell lung carcinoma, breast cancer and nicotine-dependent illness. This is particularly useful for diagnosed are epilepsy (e.g. juvenile myoclonic epilepsy) and prader-Willi and Angelman's syndromes
encoding at least a portion of the human alpha-7 neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
   888888888888888888888888888
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                                                                                                                                                                                                                                                                                                      having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65794-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf55 which contains the repeat sequence is from the marker clone Mdf55 which contains the repeat sequence having the formula: (AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)\,n(dG-dT)\,n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                       sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe;
alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia;
small cell lung carcinoma; breast cancer; nicotine-dependent illness;
epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                       repeat
                                                                                                                                                                                                                                                                                The invention relates to the isolation of polymorphic repea
having the sequence (dC-dA)n.(dG-dT)n which can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Score 30.4; DB 1; Length 32; 96.9%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha-7 nicotinic receptor probe SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                            Disclosure; Col 11-12; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US021762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                       WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FREE/) FREEDMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LEON/) LEONARD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                                                                      sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                 Gaps
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0
 DB 1; Length 32;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                               1;
                                                                2318 IGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                               0; Mismatches
                                                                                               32 rererererererererererererererere
Score 30.4;
Pred. No. 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page 14; 35pp; Japanese.
                                                                                                                                                                                                                                                                         H. discus derived sequence #5.
                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP003551
 0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98JP-00232153
                                                                                                                                                                           AAZ98487 standard; DNA; 32
                                                                                                                                                                                                                                          (first entry)
                                 Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi H, Sekino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-224692/19.
                                                                                                                                                                                                                                                                                                                        Haliotis discus; ss
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                     Haliotis discus.
                                                                                                                                                                                                                                                                                                                                                                                     WO200011156-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L8-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999;
                                                                                                                                                                                                                                            19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000.
                                                                                                                                                                                                                                                                                                       Satellite
                                                                                                                                                                                                            AAZ98487;
                                                                                                                                              RESULT 121
                                                                                                                                                              AAZ98487,
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The present invention describes an isolated nucleotide sequence (I)

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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition particular. The method is useful in the identifying or detecting a concloctide repeat region in a nucleic acid molecule characterised by a nucleotide length. In particular, the method is useful for identification particular in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, associated with a neurodegenerative disease including fragile X syndrome, concerned to indentifying and/or typing microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic concover, the method can be used to provide markers for use in Moreover, the method can be used to provide markers for use in Moreover, the method can be used to provide markers for use in moreorganisms, to ascertain parentage of human or non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individuals, conclicated to identify a particular victim or an alleged perpetrator of a conclicate acid damage. The nucleotide polymorphisms may be used in forme, in gene mapping and population studies. LASA may also be used in crime, in gene mapping and population studies. LASA may also be used in crime, in gene mapping and population studies. LASA may also be used in crepeat regions such as a nucleotide length polymorphism in a eukaryotic genome. The LASA method avoids the time and cost required by prior art methods using gel electrophoresis and southern transfer analysis. In
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay.
                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                     Gaps
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barnard R, Giffard PM;
Length 32;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                    Human microsatellite D1S191 detection PCR primer #4.
  DB 1;
                                                                               2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 2349
                                                                                                                       32 rerererererererererererererere
                   Pred. No. 47;
); Mismatches
    Score 30.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Page 55; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolter L,
                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-2000; 2000US-0202771P.
10-MAY-2000; 2000US-0202559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2001; 2001WO-AU000526.
0.8%;
                                                                                                                                                                                                                                 ABK24296 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                     (first entry)
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                                            31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-121948/16.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200185987-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001.
                                                                                                                                                                                                                                                                                                                     09-APR-2002
                                                                                                                                                                                                                                                                           ABK24296;
        Query Match
Best Local 8
                                                  Matches
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dd-dA)n. (dd-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the page 1 libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly/(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AAT65799-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf107 which contains the repeat sequence is from formula: TGCCCGGCCT(AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                   ö
                       the use of gel electrophoresis, a process that has proved difficult to automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
particular, current diagnosis of Huntington's disease relies heavily upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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6
                                                                                                                                                                                                                                                                                                                Score 30.4; DB 1; Length 32; Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd107.
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                                                                                                                                                                                                                                                          Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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91US-00754351.
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Local Similarity 96.9%;
es 31; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 123
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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XXX AAT66
AAT66
AAT76/
AAT
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

92WO-US000340. 91US-00642342.

WO9213102-A1.

Bos taurus.

36-AUG-1992.

Georges M, Massey JM; WPI; 1992-284684/34.

GENM-) GENMARK.

15-JAN-1991; 15-JAN-1992;

Microsatellite sequence from clone TGLA122.

(first entry) (revised)

25-MAR-2003 02-FEB-1993

AAQ33681;

BP.

AAQ33681 standard; DNA; 41

AAQ33681 ID AAQ3

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AF)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is unmmarised in the sequence information for specification and indexed herein (see below). The sequence supstream and commitream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The sequired PCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.

The sequired pCR primers for in vitro amplification of the corresp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                    ö
                  Length 42;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38 BP; 1 A; 0 C; 19 G; 18 T; 0 U; 0 Other;
                                                    1;
                  DB 1;
                                                                                      2350
                                                                                                                     42 crerererererererererererererer 11
                ; Score 30.4; DE; Pred. No. 65; 0; Mismatches
                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA309.
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                                                                                  2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping, and selective breeding.
                                                                                                                                                                                                           BP.
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                  0.8%;
                                96.98;
                                                                                                                                                                                                         AAQ33894 standard; DNA; 38
                                                                                                                                                                                                                                                                                              (first entry)
Query Match
Best Local Similarity 96...
Best Accade 31; Conservative
                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges M, Massey JM;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                                                                                                                                                                                                                            AAQ33894;
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                                                                                                                                                                         RESULT 124
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- used in genetic identification, gene

rable 7; Page 202; 517pp; English. Polymorphic bovine DNA markers - mapping, and selective breeding.

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 between 250 and 500 clones croses-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the sequence PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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0
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Pred. No. 79;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41 BP; 6 A; 0 C; 15 G; 20 T; 0 U; 0 Other;
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Best Local Similarity 88.9%;
Matches 32; Conservative
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(first entry)
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02-FEB-1993
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Gaps

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0.8%; Score 29.8; DB 1; Length 38; 93.9%; Pred. No. 68; tive 0; Mismatches 2; Indels

2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

31; Conservative

Local Similarity

Best Loca Matches

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Query Match

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AAQ34032
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screening a library of bovine MboI DNA fragments of between 250 and 500
corealing a library of bovine MboI DNA fragments of between 250 and 500
corealing and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
core 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
crequired PCR primers for in vitro amplification of the corresp.
crequired lite (using the program oPTIPRIM). The microsatellites may be
microsatellite (using the program oPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
companies of economic trait loci, or genes involved the determinism of
connectly important traits esp. in cattle, to allow selective
connectly incorrect the construction of the correct PN
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                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 59;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone TGLA27.
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Best Local Similarity 96.8
Matches 30; Conservative
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                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                              (GENM-) GENMARK.
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02-FEB-1993
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                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33867;
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
core forms (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
core cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
committee of the microsatellite sequence were used to generate the
downstream of the microsatellite sequence were used to generate the
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
consomically important trait loci, or parentage testing, and in the genetic
economically important traits esp. in cattle, to allow selective
connomically important traits esp. in cattle, to allow selective
breeding. See also AAQ31501-34437. (Updated on 25-MAR-2003 to correct PN
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96.8%; Pred. No. 59;
ive 0; Mismatches
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91US-00642342.
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(first entry)
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                                                                                                                      Georges M, Massey JM;
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Best Local Similarity
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                                                         (GENM-) GENMARK.
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      15-JAN-1991;
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02-FEB-1993
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Matches
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                                                                                                                                                                                                                                                                                                          Local Similarity 96.8
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                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites on the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information corespecification and indexed herein (see below). The sequences upstream and comnstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important trait loci, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
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                                            Table 7; Page 343; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 258; 517pp; English.
mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping, and selective breeding.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9213102-A1
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 129
AAQ3382.
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AC AAQ338.
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DT 25-WAR
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microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traite sep. in cattle, to allow selective by receding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers – used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 29.4; DB 1; Length 31; 96.8%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 rererererererererererererer 31
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BP
                             AAT65759 standard; DNA; 31
                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                               (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                                                                                                                                          21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                    04-APR-1994;
                                                                                                                                                                                                           Homo sapiens
                                                                                25-MAR-2003
17-JUN-1997
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                                                                                                                                                                                                                                                            10-DEC-1996.
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                                                       AAT65759;
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         RESULT 132
                      AAT65759/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf79 which contains the repeat sequence is from the marker clone Mdf79 which contains the repeat sequence is from formula: (AC)15.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                Gaps
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                       DB 1; Length 31;
                                                1; Indels
                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31 BP; 16 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
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                       Score 29.4; Di
Pred. No. 59;
O; Mismatches
                                                                                                 1 rererererererererererererererer
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91US-00754351.
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                         0.8%;
                                                                                                                                                               AAT65765 standard; DNA; 31
                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 96.8
Matches 30; Conservative
                                     Local Similarity 96.8
hes 30; Conservative
                                                                                                                                                                                                                  (revised)
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05-SEP-1991;
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17-JUN-1997
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                          Query Match
                                                   Matches
                                                                                                                                        RESULT 131
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                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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0.8%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 59;
Matches 30; Conservative 0; Mismatches 1; Indels
Repeat sequence from polymorphic marker clone Mfd64.
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                                                                                                                                                                                                           hybridisation; chromosome; ds.
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ID AAT65753 standard; DNA; 31 BP

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AC AAT65753;

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XX

DT 17-JUN-1997 (first entry)
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91US-00754351.
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(AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                           Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the identification of nucleic acid molecules
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat seguence from polymorphic marker clone Mfd111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31 BP; 7 A; 6 C; 15 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 GCACGTGGAGGTGAATGGCAGCAAGGTGGGC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gcacgreadergaacgecagcaaggregec 31
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96.8%; Pred. No. 59;
                                                                                                                                                                                                               (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                        Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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91US-00754351.
                                                                                                                 07-MAR-2001; 2001WO-US007268
                                                                                                                                                      07-MAR-2000; 2000US-0187510P
22-MAY-2000; 2000US-0206129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 96.8
les 30; Conservative
                                                                                                                                                                                                                                                      Cargill M, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                          WPI; 2001-522952/57.
                                      WO200166800-A2
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05-SEP-1991;
                                                                           13-SEP-2001.
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf57 which contains the repeat sequence is from formula: (CA)15.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; resequence; genotype; disease; forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
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96.8%; Pred. No. 59;
ve 0; Mismatches 1; Indels
                  Repeat sequence from polymorphic marker clone Mfd57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31 BP; 15 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human single nucleotide polymorphism (SNP) FGFR3 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2319 GTGTGTGTGTGTGTGTGTGTGTGTGTG 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers replace (16, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                               89US-00341562.
91US-00754351.
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                                                                                                                                                                                                                                                                        94US-00222177.
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                                                                                                                                                                                                                                                                                                                                                                        (MARS-) MARSHFIELD CLINIC
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es 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-042299/04.
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                        04-APR-1994;
                                                                                                                                                                                                                                                                                                                                   05-SEP-1991;
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                                                                                                                                                                                               US5582979-A.
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Variation
                                                                                                                                                                                                                                                                                                                                                                                                              Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI30471;
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Gaps

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DB 1; Length 31; Indels

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Detection of polymorphic genetic markers of the form (dC-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                           AAT65783 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                 (MARS-) MARSHFIELD CLINIC
                                                                                                                                               Query Match
Best Local Similarity 96.8
Matches 30, Conservative
              WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                      04-APR-1994;
                                                                                                                                                                                                                                                                                                                                 21-APR-1989;
                                                                                                                                                                                                                                                                                                                                       05-SEP-1991;
                                                                                                                                                                                                                                25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                 US5582979-A.
                                                                                                                                                                                                                                                                                                            10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                            Weber JL;
                                                                                                                                                                                                                      AAT65783;
      Weber JL;
                                                                                                                            field.)
                                                                                                                                                                                                 RESULT 136
                                                                                                                                                                                                       AAT65783
8
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
                                                                              repeats, especially for use in e.g paternity or maternity teeting, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdfill which contains the repeat sequence is from the marker clone Mdfill which contains the repeat sequence having the formula: CCACCCCCAG(CA)24.5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "Single nucleotide polymorphism (SNP)"
            The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human N-methyltransferase PEMT gene polymorphic site, #117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Sequence 41 BP; 18 A; 18 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29.4; DB; Pred. No. 83; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 rererererererererererererererer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ43333 standard; DNA; 41 BP.
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%;
96.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 96.8
nes 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-583571/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIKE ) RIKEN KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                               field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              챵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                           The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats. Primers based on these sequences can be used to detect these repeats. Sepecially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65794-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf111 which contains the repeat sequence is from the marker clone Mdf111 which contains the repeat sequence having the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 41 BP; 18 A; 18 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 rerererererererererererererer 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29.4;
Pred. No. 83
                                                                                                                                                                                        Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00341562.
91US-00754351.
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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes

Claim 23; Page 65; 2785pp; English.

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Gaps

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c encoding enzymes associated with drug metabolising. The invention relates
c encoding enzymes associated with drug metabolising caid sample using probes or
c polymorphism in such drug metabolising enzyme-encoding genes. The
c polymorphism may be identified in a nucleic acid sample using probes or
primers specific for a sequence selected from ABZ4317-ABZ50887 using a
variety of detection assays, including hybridisation assays, nucleic acid
arrays and PCR-based methods. The invention also encompasses methods of
c arrays and PCR-based methods. The invention also encompasses methods of
c arrays and prore bused in studying the relationship between
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
cc drugs. SNPs are also useful as polymorphism markers for discovering genes
that cause or exacerbate certain diseases, SNPs are particularly useful
in the above respects as they are stable in populations, occur
that cause or exacerbate certain diseases. SNPs are particularly useful
in the above respects as they are stable in populations, occur
in the above respects as they are stable in populations, occur
in the above respects as they are stable in populations, occur
in the above respects as they are stable in populations, occur
in the above respects as they are stable in population, occur
in the above respects as they are stable in population, or occur
in the above respects are the guessork out of selection the drug with the
greatest therapeutic effect for a particular patient, but would also
c drugs theraples based upon the genetic profile of individual patients.

This would not only take the guessork out of selection for the invention are also useful in the drug discovery and
echods of the invention are also useful in the drug discovery and
c approval processes. For example, individuals could be selected for
c clinical trials only if their genetic profiles individuals could be responded for
c appropriate patient populations. The methods, data and compositions of
the invention may therefore le
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encoding enzymes associated with drug metabolism. The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polymorphic site; drug evaluation; drug screening; genotyphing; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human N-methyltransferase PEMT gene polymorphic site, #5456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41 BP; 4 A; 2 C; 18 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2320 TGTGTGTGTGTGCGTGTGTGTGTGTGTGTGCA 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ48673 standard; DNA; 41 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 138
ABZ48673
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27-DEC-2001; 2001WO-JP011592. 27-DEC-2000; 2000JP-00399443,

04-JUL-2002.

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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism and compositions for identifying individuals who have at least one polymorphisms and compositions for a sequence selected from ABZ4217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of polymorphism data, particularly that relating to single nucleotide polymorphism data. particularly that relating to single nucleotide polymorphism sequence variations and human diseases. SNPs are particularly useful in the above respects as they are stable in populations, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur in the above respects as they are stable in populations of polymorphisms of drug therapueit effect for a particular patient. Dut would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and appropriate patient populations. The methods of adverse and compositions of the invention may therefore lead to an increase in the range of possible drug candidates could be revived if they are action and adverse reactions. The methods of adverse range of the invention may therefore lead they are increase in the
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                                                                                                                                                                                                          Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41 BP; 4 A; 2 C; 18 G; 17 T; 0 U; 0 Other;
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                                                                                                                   Saito S;
                                                                                                                                                                                                                                                                                                                                Claim 23; Page 171; 2785pp; English.
                                                                                                                Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33710 standard; DNA; 37 BP.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                   Nakamura Y, Sekine A,
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                                                                                                                                                                WPI; 2002-583571/62.
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                                                                   (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
Matches
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Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                      Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human glutathione-S-transferase GSTPi gene polymorphic site, #6268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

0.8%; Score 29; DB 1; Length 39;
Best Local Similarity 86.5%; Pred. No. 87;
Matches 32; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2320 TGTGTGTGTGTGCGTGTGTGTGTGTGTGTGCACAT 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39 BP; 19 A; 14 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Claim 1; Col 13-14; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2000; 2000JP-00399443.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ49485 standard; DNA; 41 BP
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                                          89US-00341562
91US-00754351
94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                          (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                                     WPI; 1997-042299/04.
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  04-APR-1994;
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                                               21-APR-1989;
                                                                    05-SEP-1991;
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variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ49485;
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                                                                                                                                                               Weber JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine Mool DNA fragments of between 250 and 500

CC screening a library of bovine Mool DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CM in the bovine genome is estimated at >100, 000. The sequence information

CC in the bovine genome is estimated at >100, 000. The sequence information

CC specification and indexed herein (see below). The sequences upstream and

CM of the microsatellite sequence waset to generate the

CC downstream of the microsatellite sequence waset to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CM introsatellite (using the program OPTIPRIM). The microsatellites may be

CM introsatellity ingoitiduals, for parentage testing, and in the genetic

CM mapping of economic trait loci, or genes involved the determinism of

CM connonically important traits esp. in cattle, to allow selective

CM of the CM of the correct PN

CM of the CM of th
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                                                                                                                                                                                                                                                                                                                                                                                                                 markers - used in genetic identification, gene
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Pred. No. 82;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence from polymorphic marker clone Mfd104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2320 TGTGTGTGTGTGTGTGTGTGTGTGTGTGCACAT 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 BP; 4 A; 0 C; 14 G; 19 T; 0 U; 0 Other;
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           genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Table 7; Page 214; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT65775 standard; DNA; 39 BP
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Best Local Similarity 86.5%;
Matches 32; Conservative
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                                                                                                                                                                                                                                             91US-00642342
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                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                     Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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17-JUN-1997
                                                                                                                                                                                                15-JAN-1992;
                                                                                                        WO9213102-A1
                                                                                                                                                     06-AUG-1992.
                                                                Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT65775;
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Gaps

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SNP; da

RESULT 140 AAT65775/

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CC primers and compositions for identifying intalvatuals who have at least come polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ5881 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphism (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes created to sequence or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur the according drug metabolising enzymes allows the customination of such as repeating sequences. The detection and analysis of polymorphisms cuch as repeating sequences. The detection and analysis of polymorphisms of up an essent dupon the geneswork out of selecting the drug with the drug therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously falled drug candidates could be revived if they were matched with more approvale processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and compositions of the invention may therefore lead to an increase in the range of reactions
                                                                                                                                                                                                 Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                      Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least
                                                                                    Nakamura Y, Sekine A, Iida A, Saito S;
                                                                                                                                                                                                                                                                                                                                                  Claim 23; Page 190; 2785pp; English.
                                                                                                                                           WPI; 2002-583571/62
                           (RIKE ) RIKEN KK.
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Sequence 41 BP; 0 A; 5 C; 21 G; 15 T; 0 U; 0 Other;

ö 0.8%; Score 29; DB 1; Length 41; 86.5%; Pred. No. 92; 5; Indels 2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351 1 Grenerececerecererecererererereres 37 0; Mismatches 32; Conservative Local Similarity Query Match Matches 8

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Gaps

ABZ43946 standard; DNA; 41 BP RESULT 142 ABZ43946 &&&&&&&&&&

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(first entry) 26-JUN-2003

ABZ43946;

Human glutathione-S-transferase GSTPi gene polymorphic site, #730

Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

Location/Qualifiers Homo sapiens.

replace (21, A) variation

/*tag= a /standard_name= "Single nucleotide polymorphism (SNP)"

WO200252044-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-JP011592

27-DEC-2000; 2000JP-00399443. 02-MAY-2001; 2001JP-00135256. 27-AUG-2001; 2001JP-00256862.

(RIKE) RIKEN KK.

Nakamura Y, Sekine A, Iida A, Saito S;

WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid

Claim 23; Page 76; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates conceptions and compositions for identifying individuals who have at least to methods and compositions for identifying individuals who have at least come polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a craitey of detection assays, including hybridisation assays, mucleic acid articles and pre-based methods. The invention also encompasses methods of a variety of detection assays, including hybridisation assays, mucleic acid caraluting and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphism (SMPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful.

CC drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful.

CC drug therapies based upon the genetic profile of individual patients.

CC drug therapies based upon the genetic profile of individual patients.

CC This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

CC This would not only take the guesswork out of selecting the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if that genetic profile and cauge drug candidates could be revived if they were matched with more appropriate patient populations. The embrode, data and compositions of the invention may therefore lead to a an increase in the rumber of adverse reactions, failed drug trials, the time patient

Sequence 41 BP; 0 A; 5 C; 21 G; 15 T; 0 U; 0 Other;

ö DB 1; Length 41; 5; Indels Match 0.8%; Score 29; DB Local Similarity 86.5%; Pred. No. 92; les 32; Conservative 0; Mismatches Louery Match

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AA033965

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grererecerecererecererererecererer 37

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n. (dc-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial analysis unto breading or pedigree analysis. The repeats, when analysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence; 2) imperfect repeats which are defined as 2 consecutive non-repeat bases; 3) compound perfect repeats which are consecutive non-repeat bases; 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats from a run of at least 5 uninterrupted dinucleotide or longer repeats at 10 uninterrupted monouncleotides; and 4) imperfect compound repeats that the compound repeats around that the than a consecutive non-repeat bases to make than a consecutive non-repeat bases around the consecutive non-repeat bases around at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dc-dA)n. (dc-dT)n, or from at least 2 consecutive and a least 3 consecutive non-repeat bases around a least 3 consecutive non-repeat bases around a least 3 consecutive non-repeat bases around a least 5 consecutive non-repeat bases around base and a least 5 consecutive non-repeat bases around base and bases around the least 5 consecutive non-repeat bases around the least 5 consecutive non-repeat bases around the le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               least 10 uninterrupted mononuclectides; and 4) impertect compound repeat which are defined as for the perfect compound repeats except that the runs of CA are interrupted. This sequence is an example of an imperfect repeat sequence of structure: (CA)11CT(CA)4. (Updated on 25-WAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dG-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 28.8; DB 1; Length 32; 33.8%; Pred. No. 72; ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32 BP; 15 A; 16 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         (dC-dA)n.(dG-dT)n polymorphic repeat sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Col 57-58; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                       hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00222177.
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Best Local Similarity 93.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-00341562
91US-00754351
                                               AAT66057 standard; DNA; 32
                                                                                                                                                                                             (first entry)
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                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         correct PF field.)
                                                                                                                                                         25-MAR-2003
18-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber JL;
                                                                                                          AAT66057;
RESULT 143
                          AAT66057
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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

creening a library of bovine Mbol DNA fragments of between 250 and 500

by with an (AC)15 and a (TC)15 oligonoucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

clones cross-hybridised. Assuming independent distribution of

in the bovine genome is estimated at >100, 000. The sequence information

con 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequence upstream and

specification and indexed herein (see below). The sequences upstream

consistent of the microsatellite sequence water used to generate the

crequired PCR primers for in vitro amplification of the corresp.

crequired PCR primers for in vitro amplification of the corresp.

credity individuals, for parentage testing, and in the genetic

used to identify individuals, for parentage testing, and in the genetic

capping of economic trait loci, or genes involved the determinism of

connect PN

predity amportant traits esp. in cattle, to allow selective
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                                                                                                                                                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 74; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat sequence from polymorphic marker clone Mfd118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 reference and the contraction of the contraction 
                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Table 7; Page 316; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - mapping, and selective breeding.
ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
AAQ33965 standard; DNA; 30
                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7
Best Local Similarity 96.7
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
17-JUN-1997
                                                                                                                          25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                 30s taurus.
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                                                                    AAQ33965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT65789/c
ID AAT65
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AC AAT65
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99AU-00004906.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                 PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 74; lve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 15 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 erererererererererererererer 1
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simple sequence repeat, SSR, #59.
                                               hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS13788 standard; DNA; 30 BP
                                                                                                                                                                                                                    89US-00341562.
91US-00754351.
                                                                                                                                                                                    94US-00222177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                      (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042299/04
                                                                                                                                                                                    04-APR-1994;
                                                                                                                                                                                                                                      05-SEP-1991;
                                                                                   Homo sapiens
                                                                                                                                                                                                                      21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002
                                                                                                                 US5582979-A.
                                                                                                                                                   10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NZ509193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                        Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAS13788/c
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence core test (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primar cutable for amplifying an SSR, identifying (MI) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a ssociated with the gene such that the SSR and the gene are contained for DNA profiling grass or cereal species varieties by assessing contained for DNA profiling grass or cereal species varieties by assessing contained for DNA profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the present seed batches, and for DNA profiling to establish the genuity, uniformity and/or stablishty of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                        more tandemly repeated nucleotide
                                                                                                                                                                                                                                                                                   New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 BP; 15 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                   UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                      (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simple sequence repeat, SSR, #58.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99AU-00004906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2001; 2001NZ-00509193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Conservative
                                                                                                                                                                                                                                          WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1999;
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                                                                                                                                                                                                     Forster JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NZ509193-A
                                                                                                                                                                                                                                                                                                                                                         rarieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS13787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                     (UYSC-)
(VICT-)
                                                                SAUS-)
                                                                                                                                    UYAD-)
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vivlemore401-10.rng

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21-JUL-2000; 2000JP-00220339
                                                                                                                                                                                                                                                        21-JUL-2000; 2000JP-00220339
                                                                                                                                              Query Match
Best Local Similarity 96.7
Matches 29, Conservative
                           Forster JW, Jones ES;
                                   WPI; 2001-512563/56.
                                                                                                                                                                                                                            Pyrus pyrifolia
                                                                                                                                                                                                                                   JP2002034597-A.
                                                                                                                                                                                                    28-JUN-2002
                                                                                                                                                                                                                                          05-FEB-2002
                                                                                                                                                                                             AAL42354;
      SAUS-)
              (VICT-)
                 (UYAD-)
                                                                                                                                                                               RESULT 148
                                                                                                                                                                                  AAL42354
ID AAL4
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (Acl)15 and a (TC)15 oilgonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
                                                                                                                  new microsatellite DNA derived from a Pyrus plant and discrimination of
                                                                                                                                                                                                                                                                                         Pyrus plants. The invention also comprises a method for discriminating Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel microsatellite DNA sequence can be used in discriminating Pyrus plants.
                                                                                                                                                                                                                                                                                                                                                                                   The present DNA sequence represents a probe specific for a novel Pyrus pyrifolia (sand pear) microsatellite DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 28.4; DB 1; Length 30; Best Local Similarity 96.7%; Pred. No. 74; Matches 29; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    The invention comprises a novel microsatellite DNA
(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR, selection, primers, OPTIPRIM, breeding, genetic mapping; traits, amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGI 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Grererererererererererererer 30
                                                                                                                                                                                                            Example 1; Page 22; 22pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table 7; Page 307; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33944 standard; DNA; 33 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                    Pyrus plants by using it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
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                                                             WPI; 2002-298819/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L5-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2.6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a clarary of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a sesociated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing.

The second of the selection of genes in grass or cereal seed batches by assessing varieties and testing the purity of grass or cereal seed batches by assessing varieties and testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the grass or cereal seed batches, and for DNA profiling to establish the grass or cereal section within seed batch of a classic profiling transpared by an analyzed by grass or cereal section of grass or cereal section within a cereal breeding, of grass or cereal section of grass or cereal preceding the purity of grass or cereal grass or cereal preceding the purity of grass or cereal grass or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                       New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sand pear; ss; probe; novel microsatellite DNA sequence; Pyrus plant discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
                                                             STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                      UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.4; DB
Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel sand pear microsatellite DNA probe 3.
                                                                                                                                                                             (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 53; 72pp; English.
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   04-MAY-2000; 2000AU-00007310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%;
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sequence derived from

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbo! DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbo! sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                  Length 33;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                              Sequence 33 BP; 1 A; 1 C; 15 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rererererererererererererererer
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                           Score 28.2; 1
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic mapping; traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Table 7; Page 209; 517pp; English.
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                                                                                                                                                                                                                                                                              0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                           Local Similarity 90.5 nes 30; Conservative
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                                                                                                                                                                                                                                                                              Query Match
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AAQ33698

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Score 28.2; DB 1; Length 37; Pred. No. 1e+02;

0.7%;

Best Local Similarity

Query Match

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creening a library of bounder microsactiffe sequence Object. by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellites is summarised in the constream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 1.1e+02;
0; Mismatches 4; Indels
 Indels
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                                GCGTGTGTGTGTGTGT 2350
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0; Mismatches
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                                                                                                                                             AAQ33695 standard; DNA; 35
                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 88.2
Matches 30; Conservative
30; Conservative
                                2318 TGTGTGTGTGTGTGT
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                Bos taurus,
                                                                                                                                                                               AAQ33695;
                                                                                                              RESULT 151
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 Matches
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ID AAQ3
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The sequence is that of a bovine microsatellite sequence obtd. by
conservation a library of bovine MboI DNA fragments of between 250 and 500
conservation and a (TC)15 oligomuclectide probe. One out of 50
conservation across-typridates. Assuming independent distribution of
conservation and MboI sites, the frequency of (T6)n >9 microsatellites
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
conservation and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
constream of the microsatellite sequence ware used to generate the
compacted primers for in vitro amplification of the corresp.
consected in the groad operation of the corresp.
consected in mportant traits sep. in cattle, to allow selective
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                                                                                                                    PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 27.6; DB 1; Length 38; 88.2%; Pred. No. 1.2e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38 BP; 4 A; 0 C; 19 G; 15 T; 0 U; 0 Other;
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                                                                                       Microsatellite sequence from clone TGLA172.
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(first entry)
                                                            (first entry)
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Best Local Similarity 88.2
Matches 30; Conservative
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                                               (revised)
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                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
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02-FEB-1993
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02-FEB-1993
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                                                                                                                                                                             Bos taurus
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                AAQ33767;
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AAQ33687
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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CS specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence ware used to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage teating, and in the genetic

CC used to identify individuals, for parentage teating, and in the genetic

CC mapping of economic trait loci, or genes involved the determinism of

CC conformically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGCGTGTGTGTGT 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 27.4; I larity 96.6%; Pred. No. 93; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rererererererererererererer
                                                                                                                                                                                                                                                                                        Table 7; Page 204; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33846 standard; DNA; 29 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US000340
                                                                                                                             91US-00642342.
                                                                                              92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                      Georges M, Massey JM;
                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 28; Conserv
                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
02-FEB-1993
                                                                                                                             .5-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1992
                                                                                                   LS-JAN-1992;
                                         WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus.
                                                                  06-AUG-1992.
               Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ33846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33846
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91US-00642342

15-JAN-1991;

Table 7; Page 312; 517pp; English.

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Microsatellite sequence from clone TGLA351
                                                                                                                                                                          AAQ33956 standard; DNA; 29 BP
                                                                                                                                                                                               (first entry)
                                                                                                                              Query Match
Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                             Georges M, Massey JM;
                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
   (GENM-) GENMARK.
                                                                                                                                                                                                                                                                     (GENM-) GENMARK.
                                                                                                                                                                                                                                                            15-JAN-1991;
                                                                                                                                                                                                                                                    15-JAN-1992;
                                                                                                                                                                                                                                   WO9213102-A1
                                                                                                                                                                                           25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                            06-AUG-1992
           Georges M,
                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                   AAQ33956;
                                                                                                              field.)
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence upstream and
comparream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites
cused to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites of in the bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

C. used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits epp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 268; 517pp; English.
                                                                                                                                                                                                                                                                            mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%;
                                                                                                    маввеу ЛМ;
                                                                                                                                                                 WPI; 1992-284684/34
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Gaps

; 0

Indels

1;

0; Mismatches

ilarity 96.6%; Conservative

Local Similarity les 28; Conserv

2318 TGTGTGTGTGTGTGCGTGTGTGTGTGT 2346

0.7%; Score 27.4; DB 1; Length 29; 6.6%; Pred. No. 93;

Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 ollgonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the septence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                              Microsatellite sequence from clone TGLA378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 320; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping, and selective breeding.
                  ВР
                                                                                                                                                                                                                                                                                                                92WO-US000340.
                                                                                                                                                                                                                                                                                                                                               91US-00642342
                 AAQ33977 standard; DNA; 29
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
                                                                                                                                                                                                                                                 WO9213102-A1
                                                                                                                                                                                                                                                                                                                  15-JAN-1992;
                                                                                25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                  06-AUG-1992
                                               AAQ33977;
     AAQ3397
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                  Gaps
                                                                                                                                                                                                                                                                                                                              PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                  ö
                                  1; Indels
Score 27.4; DE Pred. No. 93; 0; Mismatches
                                                                  2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                         1 TGTGTGTGTGTGTGTGTGTGTGTGT 29
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92WO-US000340 91US-00642342

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monomer containing
p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ppp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ppp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide clamp q, for producing comb-type brached polymer.
                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                         DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "Modified with -NH-C(=O)CH2Br"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pnp = a linkage or
functionality, and
                                                                                                                                                                                                                                                Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                            Score 27.4; 1
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "A(pnp)C,
bromoacetylamino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "A(pnp)C,
bromoacetylamino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "A(pnp)C,
bromoacetylamino
                                                                                                                                                                                                                                                                                                                                                                  ٥:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-00087386.
                                                                                                                                                                                                                                                                                                            0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linkage"
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ83953 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-060944/08.
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9501365-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gryaznov SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
04-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ83953;
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                          field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
              8 \times 8 
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Example 9; Page 34; 52pp; English

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The sequences given in AAQ83339, AAQ83953 and AAQ839940 are used in the construction of an oligonuclectide clamp. The clamp is a comb-type branched polymer which has 5' termini and was used to bind a target compressing a segment of the HIV pol and nef genes in single stranded or double stranded forms. An oligonuclectide clamp is a compound complex after specifically binding to the target polynuclectide croular complex after specifically binding to the target polynuclectide complex after specific binding to the target molecule and one or more pairs of binding moieties cone or more oligonuclectide control of specific binding to the target molecule and one or more binding moieties covalently linked to the oligonuclectide polynuclectide, the binding moieties of a pair are bought into introperson to that they form a stable covalent or non-covalent linkage or complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonuclectide moieties to the target the specifically annealed oligonuclectide moieties to the target copy polynuclectide. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd65.
                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 14 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2319 GTGTGTGTGTGTGTGTGTGTGTGTGTG 2347
                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 27.4; 1
16.6%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 Grerererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 11-12; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                            96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT65760 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                              28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT65760/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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Gaps

; 0

Score 27.4; DB 1; Length 29; Pred. No. 93; 0; Mismatches 1; Indels

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The invention relates to the isolation of polymorphic repeat sequences markers. Primers based on these sequences can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 by primers AAT65799-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf10 which contains the repeat sequence is from the marker clone Mdf10 which contains the repeat sequence is from
repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(GC-dA). (GG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf6S which contains the repeat sequence is from formula: (CA)14.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA) n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            formula: (AC)14A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd10.
                                                                                                                                                         Sequence 29 BP; 14 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29 BP; 15 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                       Query Match
Best Local Similarity 96.6%;
Matches 28; Conservative
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91US-00754351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.
                           Gaps
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 Length 29;
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16.6%; Pred. No. 93;
                           Indels
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  DB 1;
Score 27.4; DE Fred. No. 93; 0; Mismatches
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                                                                             29 rererererererererererererer
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 0.7%;
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                                                                                                                                               AAF60474 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                           Oligonucleotide clamp #23.
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                           Conservative
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                                                  2318 TGTGTGTGTGT
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  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         US6180777-B1.
                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                            03-JAN-1997;
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02-FEB-1993
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                           28;
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                                                                                                                                                                         AAF60474;
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                                                                                                                     RESULT 160
                                                                                                                                    AAF60474/c
                          Matches
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15-JAN-1991;

15-JAN-1992; 06-AUG-1992.

WO9213102-A1.

Bos taurus

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbo! DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of
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                                                                                                                                                                                                                                   New tyrosine kinase receptor protein related to FGF receptor proteins - and corresponding DNA sequences, used in treatment and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - used in genetic identification, mapping, and selective breeding.
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                                                                                                                                               Strebhardt K, Ruebsamen-Waigmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 26.4; DB 1; Length 28; Best Local Similarity 96.4%; Pred. No. 1.2e+02; Matches 1; Indels Matches 1; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 BP; 6 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                  (GEOR-) GEORG-SPEYER-HAUS CHEMOTHERAPEUTISCHES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1632 TGCCCGCAATGTGCTGGTGACCGAGGAC 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 idcccccanigidciddidacrdaddac
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                                                                                                                                                                                                                                                                                                                                        Example 2; Page 11; 12pp; German.
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                 91DE-04104240.
                                                             91DE-04104240
                                                                                                                                                         Holtrich U, Braeuninger A,
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02-FEB-1993
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                 12-FEB-1991;
                                                                12-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

consisted that and a (TC)15 oligonuclectide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

confirmation in the bovine genome is estimated at >100, 000. The sequence information

confirmation and indexed herein (see below). The sequences upstream and

confirmation and indexed herein (see below). The sequences upstream and

confirmation of the microsatellite sequence were used to generate the

confirmation of the program of the corresp.

confirmation of the program of the corresp.

confirmation of economic trait loci, or genes involved the determinism of

confirmation of economic trait loci, or genes involved the determinism of

confirmation of economic trait loci, or genes involved the determinism of

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confirmation of economic trait (Updated on 25-MAR-2003 to correct PN

correct PN
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                                                                       PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 26.6; DB 1; Length 33; ilarity 87.9%; Pred. No. 1.4e+02; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR Primer TKF1 corresponds to TKF receptor nts. 675-648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 3 A; 0 C; 13 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TATATATGTGTGTGTGTGTGTGTGTGTGT 33
                                Microsatellite sequence from clone TGLA149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 222; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
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Matches 29; Conserv
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Synthetic.

AAQ27543;

RESULT 162

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Query Match

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Gaps

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The sequence is that of a bovine microsatallite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

In sequence to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
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microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                           Score 26.4; DB 1; Length 28;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              2318 TGTGTGTGTGTGTGCGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ34074 standard; DNA; 28 BP.
                                                                                                                                                                                                                                                                                                 0.7%;
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                                                                                                                                                                                                                                                                                                                 Local Similarity 96.4 es 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ34074;
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                      field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 164
                                                                                                                                                                                                                                                                                                                                       Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (ushing the program opTIPRIM). The microsatellites may be
incommically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct
field.)
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                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 1.2e+02;
                                                                                     Score 26.4; DB 1; Length 28;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                    Indels
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                                                      Sequence 28 BP; 1 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                  0; Mismatches
                                                                                                                                                  2322 TGTGTGTGTGCGTGTGTGTGTGTGTG 2349
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                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone MTGT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Table 7; Page 187; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping, and selective breeding.
                                                                                                                                                                                                                                                             BP.
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                                                                                   Query Match 0.7%;
Best Local Similarity 96.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                             AAQ33645 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENM-) GENMARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1992;
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02-FEB-1993
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GIGTGTGTGTGTGTGTGTGTGT 28

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
conservation of an (TC)15 and a (TC)15 oligomucleotide probe. One out of 50
conservations are severable probe. One out of 50
microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
conservation and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
conservation and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellity individuals, for parentage testing, and in the genetic
concomically important trait loci, or genes involved the determinism of
concomically important traits esp. in cattle, to allow selective
prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 26.4; DB 1; Length 28; 96.4%; Pred. No. 1.2e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                  Sequence of a microsatellite from clone TGLA82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2319 GIGIGIGIGIGIGIGIGIGIGIGIGI 2346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rable 7; Page 395; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ34035 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                 92WO-US000340.
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Conservative
                                                                                                                                                                                                                                                                                                                                                    91US-00642342
AAQ34161 standard; DNA; 28
                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
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Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
                                                                                                                                                                                                                                                 WO9213102-A1
                                                                                                                                                                                                                                                                                                                   15-JAN-1992;
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                                                                                                                                                                                                                                                                                  06-AUG-1992.
                                                                     25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                               Bos taurus.
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                                    AAQ34161;
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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC in the bovine genome is estimated at >100,000. The sequence information

CC for ca. 230 such bovine microsatellite sequence were used to generate the

CC downstream of the microsatellite sequence were used to generate the

CC downstream of the microsatellite sequence was used to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

Final D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence found in the human chromosomal clone SW10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2319 GIGIGIGIGIGIGIGIGIGIGIGI 2346
                                                 Microsatellite sequence from clone TGLA431.
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                                                                                                                                                                                                                                                   92WO-US000340.
                                                                                                                                                                                                                                                                                       91US-00642342.
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Matches 27; Conservative
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                             Georges M, Massey JM,
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                                                                                                                                                                                                                                                                                                                             (GENM-) GENMARK.
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18-JUN-1997
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25-MAR-2003
02-FEB-1993
                                                                                                                                                                                 W09213102-A1
                                                                                                                                                                                                                   06-AUG-1992.
                                                                                                                                               Bos taurus.
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Claim 6; Page 51; 72pp; English.
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2002US-0374379P.
2002US-0384543P.
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15-AUG-2002; 2002US-0403748P.
04-NOV-2002; 2002US-00287226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK51120 standard; DNA; 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 27; Conservative
                                                           WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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22-APR-2002;
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                     Forster JW,
                                                                                                                                                                  rarieties.
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  THE HEART SERVICE STATES AND ASSOCIATED ASSOCIATED AND ASSOCIATED ASSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone SW10. The sequence is amplified by primers AAT66103-4. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simple sequence repeat; plant, ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 26.4; DB 1; Length 28; 96.4%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 14 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
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INT MAIZE & WHEAT IMPROVEMENT CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Col 61-62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple sequence repeat, SSR, #8.
                                                                                                                       94US-00222177
                                                                                                                                                             89US-00341562
91US-00754351
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04-MAY-2000; 2000AU-00007310
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Matches 27; Conservative
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                                                                                                                                                                                                                           (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                                                                                                                                          WPI; 1997-042299/04.
    Homo sapiens.
                                                                                                                         04-APR-1994;
                                                                                                                                                                21-APR-1989;
                                                                                                                                                                                   05-SEP-1991;
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                                        US5582979-A
                                                                                 10-DEC-1996
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                                                                                                                                                                                                                                                                    Weber JL;
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(VICT-) (
(UYAD-) (
(ITWA-)
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AAS13711/c
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acid (1) firm rygerass or feacue appeared micloting a simple sequence repeat (SSR), having 2 or more tandemly repeated miclocide core elements 2-6 mucleotides in length. Also included are a micloid acid primer suitable for amplifying an SSR, identifying (MJ) an SSR by preparing a library of rygrass or fescue genomic DNA enriched for SSRs and core fleatifying clones in the library containing SSRs, a library of rygrass or fescue genomic DNA enriched for SSRs prepared by the MJ, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a sesociated with the gene such that the SSR and the gene are core associated with the gene such that the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the present seed batches, and for DNA profilling to establish the sequence is a ryegrass or fescue SSR
                  more tandemly repeated nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer;
New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a substantially purified or isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOVX protein-related oligonucleotide probe SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28 BP; 14 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.4%; Pred. 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; human; probe; ss.
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Matches
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                                                                                                                                                             This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furtak K;
Spytek KA;
                                                                                                                 ö
                                        Casman SJ, Furtak K;
MP, Li L, Spytek KA;
Patturajan M;
                                                                                                              New NOVX polypeptide, useful for preparing a composition for treating
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W, Bento P, Boldog FL, Burgess CE, Casman SJ,
Gould-Rothberg BE, Gunther E, Heyes MP, Li L,
                                                                                                                                                                                                                                                                                         0.7%; Score 26; DB 1; Length 26;
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOVX protein-related oligonucleotide probe SeqID.
                                         W, Bento P, Boldog FL, Burgess CE,
Gould-Rothberg BE, Gunther E, Heyes
Zhong M, Malyankar UW, Edinger SR,
ME, Smithson G;
                                                                                                                                                                                                                                                                        Sequence 26 BP; 9 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                          preventing e.g. cancer or for chromosome mapping
                                                                                                                                               Example C; SEQ ID NO 141; 433pp; English.
                                                                                                                                                                                                                                                                                                                                     714 CGCTAACACCACCGACAAGGAGCTAG 739
                                                                                                                                                                                                                                                                                                                                                   chromosome mapping; human; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-0370969P.
30-MAY-2002; 2002US-0374739P.
30-MAY-2002; 2002US-0374739P.
03-UNJ-2002; 2002US-00166619.
15-AUG-2002; 2002US-0403748P.
04-NOV-2003; 2002US-00287226.
31-MAR-2003; 2003US-00403161.
                                                                                                                                                                                                                                                                                                                                                                                                           ADK51126 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-00115479
  31-MAR-2003; 2003US-00403161
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                             WPI; 2003-812539/76.
                                                             Stone DJ, Zhong M,
Rothenberg ME, Smi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003083046-A2.
                                                                                                                                                                                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004
                                           Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-OCT-2003
                                                       Gorman L,
Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK51126;
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 171
ADK51126
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptide, useful for preparing a composition for treating or
                                                                                                                                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Furtak K;
Spytek KA;
                                                                                                                                   New NOVX polypeptide, useful for preparing a composition for treating preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Edinger SR, Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casman SJ,
MP, Li L,
Patturajan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOVX protein-related oligonucleotide probe SegID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 BP; 10 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 26; DB 1; Li
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                          Example C; SEQ ID NO 147; 433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1306 AAAGACGATGCCACTGACAAGGACCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAGACGATGCCACTGACAAGGACCT 26
Stone DJ, Zhong M, Malyankar UM,
Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-2002; 2002US-00115479.
05-APR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-0372019P.
22-APR-2002; 2002US-037379P.
30-WAX-2002; 2002US-038439P.
03-UNN-2002; 2002US-0160619.
15-AUG-2002; 2002US-0403748P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-2003; 2003WO-US010142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK51123 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                    WPI; 2003-812539/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003083046-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-2003
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The present

for the inspection of flat epithelial cells.

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The present invention describes a method for the inspection of flat
c epithelial cells in which it is judged that flat epithelial cells
separated from an organism can proceed to flat epithelial cancer when the
c 128th base in fibroblast growth factor receptor (FGFR) gene of the cells
is mutated from guanine to thymine. Also described is a method for
screening treating or preventive agents for flat epithelial cancers in
which a candidate substance of treating agent for flat epithelial cancer
is applied to flat epithelial cancer cells producing FGFR protein in
which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from
guanine to thymine or the 697th amino acid is mutated from glycine to
c ysterine and said candidate substance is selected by using the facts that
the 2128th base in the flat epithelial cell FGFR3 gene after the
application returned to guanine and that the 697th amino acid of FGFR3
protein produced returned to glycine as the indices. The method is used
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                          This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                  Query Match 0.7%; Score 26; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human fibroblast growth factor 3 PCR primer SEQ ID NO:1.
                                                                                                                                                                                                                                                                                               Sequence 26 BP; 9 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
preventing e.g. cancer or for chromosome mapping
                                       SEQ ID NO 144; 433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       714 CGCTAACACCACCGACAAGGAGCTAG 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGCTAACACCACCGACAAGGAGCTAG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZERI ) ZERIA SHINYAKU KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2001; 2001JP-00083352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC79666 standard; DNA; 29 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001; 2001JP-00083352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
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                                         Example C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
 represents a PCR primer for human FGFR3, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hyperensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; desease; typersensitivity disease; typersensitivity disease; typersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; diffectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Voeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant Vejection and diagnosing and treating T-cell associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a kit for diagnosing and treating T-cell
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                                                                                                        0.7%; Score 25.8; DB 1; Length 29; 93.1%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indel8
                                                                        Seguence 29 BP; 8 A; 9 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                    1049 TGGAGTCCAACGCGTCCATGAGCTCCAAC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 665; 164pp; English.
                                                                                                                                                                                                              1 TGGAATTCAACGCGTCCATGAGCTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Vbeta gene repeat sequence #261.
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95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00263959
                                                                                                                                                                                                                                                                                                                  ADH70471 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                             Best Local Similarity 93.1
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002150891-A1.
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                                                                                                                                                                                                                                                                                                                                                         ADH70471;
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                                                                                                             Query Match
                                                                                                                                                                                                                                                                              RESULT 174
ADH70471
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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markets in improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
             allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HVV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Wheta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                                    Gaps
hypersensitivities such as contact with allergens that lead to
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                                                                                                                                                                                                                                           / Match 0.7%; Score 25.8; DB 1; Length 29; Local Similarity 93.1%; Pred. No. 1.4e+02; Indels 27; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                          Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                          2319 Grererererererecerererere 2347
                                                                                                                                                                                                                                                                                                                                                             Grererererriererererererere 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. discus derived sequence #20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ98502 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haliotis discus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1998;
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
cscreening a library of bovine Mbol DNA fragments of between 250 and 500
cc bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
in the bovine genome is estimated at .310, 000. The sequence information
cf or ca. 230 such bovine microsatellites is summarised in the
sequence the microsatellite sequence were used to generate the
downstream of the microsatellite sequence were used to generate the
crequired PCR primers for in vitro amplification of the corresp.
crequired PCR primers for in vitro amplification of the corresp.
cued to identify individuals, for percentage testing, and in the genetic
cued to identify individuals, or genes involved the determinism of
connecally important trait loci, or genes involved the determinism of
connecally important trait loci, or genes involved the correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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Pred. No. 1.58+02;
0; Mismatches 1; Indels
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0.7%; Score 25.4; I
Best Local Similarity 96.3%; Pred. No. 1.5e
Matches 26; Conservative 0; Mismatches
TGTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGTGTGTGT 2344
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                     Table 7; Page 348; 517pp; English
                                                                                                                        AAQ34044 standard; DNA; 27 BP.
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                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
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                                                                                                                                                                                                                                                                                                                                         Bos taurus.
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AAQ33678
                                                                                           RESULT 176
                                                                                                             AAQ34044
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Gaps

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Score 25.8; DB 1; Length 30; Pred. No. 1.5e+02; 0; Mismatches 2; Indels

0; Mismatches

Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACl)s and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herain (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primars for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                               - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 0.7%; Score 25.4; DB 1; Length 27; Local Similarity 96.3%; Pred. No. 1.5e+02; nes 26; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGTGTGTGTGTGTGTGT 2344
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                                                                                                                                                                                                                                                                                                                                                                                               Table 7; Page 251; 517pp; English
                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                                                         92WO-US000340.
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(first entry)
                                                                                                                                                                                                                                        Georges M, Massey JM;
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                                                                                                                                                                                             GENM-) GENMARK.
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                      WO9213102-A1
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at .3100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellites is summarised to generate the specification and indexed herein (see below). The sequences upstream and commissionent for in vitro amplification of the corresp.

In second the microsatellite sequence were used to generate the required por primers for in vitro amplification of the corresp.

In second the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                    Microsatellite sequence from clone TGLA12.
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                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Маввеу JM;
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                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1991;
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02-FEB-1993
                    25-MAR-2003
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                                                                                                                                                                                                  Bos taurus
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AAQ33804
XX
AC AAQ3380
DT 25-WAR.
DT 02-FEB
XX
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KW PCR; 86
KW Genetic
KW Genetic
KW Genetic
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                          Table 7; Page 403; 517pp; English.
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(first entry)
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nes 26; Conservative
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      Маввеу ЈМ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
                     WPI; 1992-284684/34.
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02-FEB-1993
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      Georges M,
                                                                                                                                                                                                                                                                                                                             AAQ34012;
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                                                                                                                                                                                                                                                                                               RESULT 180
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screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of for microsatellites and mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine genome microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and comparized of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

To equired PCR primers for in vitro amplification of the corresp.

To used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective field.
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Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ34143
                                                    8$888888888888888%&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an Library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligomordleotide probe. One out of 50 clones cross-bybridised. Assuming independent distribution of microsatellites and Mbol stees, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine (ace below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primars for in vitro samplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait for, or genes involved the determinism of economically important traits ego. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 250 parentage to principle of conomically important traits and on the parentage set loss presset involved the determinism of economically important traits on the parentage also pages in the page of pages in
                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                  Gaps
                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                  ö
0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                   Sequence of a microsatellite from clone TGLA76.
                                                                   2318 renergrenergrenergrener 2344
                                                                                              1 rererererererererererer 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 388; 517pp; English.
                                                                                                                                                                           AAQ34143 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00642342.
                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seorges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             L5-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
                                                                                                                                                                                                                                        25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                    Bos taurus.
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                                                     Μ
used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthesis of branched polymers and novel branched polymeric structures used as molecular probes esp. for detecting poly-nucleotide(s).
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide clamp 1, containing loop-and-branch forming region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
                                                                                                                                                                             ö
                                                                                                                                     Score 25.4; DB 1; Length 27;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                        Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "Modified with -OP(O-)(=O)S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "Modified with SP(O-)(=O)-"
                                                                                                                                                                                                             2318 TGTGTGTGTGTGTGTGTGTGTGT 2344
                                                                                                                                                                                                                                 1 TGTGTGTGTGTGTGTGTGTGTGT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 33; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US007557.
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                                                                                                                                         0.7%;
                                                                                                                                                                                                                                                                                                                                     AAQ83951 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-060944/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gryaznov SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                        AAQ83951;
                                                                         field.)
                                                                                                                                                                                                                                                                                                    RESULT 182
AAQ83951/c
                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AprGS79-T66047. Those clones where the repeat sequence has been determined are shown in APTGS704-797. This repeat sequence is from the marker clone Mdf31 which contains the repeat sequence is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; dis.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   formula: (AC)13A. (Updated on 25-MAR-2003 to correct PF field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 25.4; DB 1; Length 27; 6.3%; Pred. No. 1.5e+02; ve 0; Mismatches 1; Indels ...
                                                               Score 25.4; DB 1; Length 27; Pred. No. 1.5e+02;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd31.
                               Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 14 A; 13 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                   Pred. No. 1.5e
0; Mismatches
                                                                                                                                   2319 GTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2318 TGTGTGTGTGTGTGTGTGTGTGTGT 2344
                                                                                                                                                                   27 drererererererererererere
on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                        ВP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00341562.
91US-00754351.
                                                                 0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%;
Best Local Similarity 96.3%;
                                                                                                                                                                                                                                                      AAT65733 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARS-) MARSHFIELD CLINIC.
                                                              Ouery Match 0.79
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1991;
                                                                                                                                                                                                                                                                                                                        25-MAR-2003
17-JUN-1997
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                                                                                                                                                                                                                                                                                          AAT65733;
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27 TGTGTGTGTGTGTGTGTGTGTGT 1

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The invention relates to compositions for the treatment of cancers, comprising purified hyaluronic acid (HA) and a second antineoplastic comprising purified hyaluronic acid (HA) and a second antineoplastic agent such as Mycobacterium phlei DNA, a Mycobacterium phlei DNA/cell accomplex, a cytotoxic chemotherapeutic drug or a synthetic contineoplastic oligonuclecide. On its own, HA stimulates the production attineoplastic oligonuclecide. On its own, HA stimulates the production of the cytokines interleukin-6 (IL-6) and IL-12 by immune system cells. Or combination, HA and the second antineoplastic agent of the composition act synergistically to potentiate each other's ability to inhibit or proliferation and induce apoptosis in cancer cells. Due to the synergy consistent the HA and the second antineoplastic agent, a reduced standard dose of the second antineoplastic agent can be used without compromising the therapeutic effectiveness of the cancer treatment. The reduction in cases the pate for reduce adverse side-effects and the development of drug complexity of interpretation, thereby improving the quality of life for the patient. In addition, as HA is inexpensive and as most communicative and a most communicative and a most communicative and a most communicative and a consistence of the consistence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    decrease in cost address provide important benefits for mammals, including humans. The present sequence represents a synthetic antineoplastic oligonucleotide which was used in a composition with HA in an exemplification of the invention
                                                                                                                                                                                                                                               Antineoplastic oligonucleotide; hyaluronic acid; HA; cytokine production; interleukin; IL-6; IL-12; synergistic action; standard dose reduction; side-effect reduction; drug resistance reduction; immunosensitisation reduction; cancer; tumour; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemotherapeutic drug can significantly reduce the cost of cancer treatment. The increase in dose effectiveness, decrease in toxicity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synergistic compositions comprising hyaluronic acid and Mycobacterium phlei DNA and cell walls, useful for treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 25.4; DB 1; Length 27; 6.3%; Pred. No. 1.5e+02;
                                                                                                                                                                                        Synthetic antineoplastic oligonucleotide, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 96.3%; pred. No. 1.5e Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 23; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BION-) BIONICHE LIFE SCI INC.
                           AAH24300 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000; 2000WO-CA001562.
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-408766/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200147561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phillips NC,
                                                                                                                                          21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                     AAH24300;
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 invention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple compared in the invention of second in the invention of specific compositions of for inducing call cativity. The oligonucleotide compositions care useful for inducing call cycle arrest, inhibition of proliferation, care useful for inducing call cycle arrest, inhibition of proliferation, care useful for induction of apoptosis or production of activation of caspases and induction of apoptosis or production of activation of archive in interleukin (II)-1-beta, IL-10, IL-12 and tumour cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4), drug independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4), drug independence caspase 3, transforming growth factor (IGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising synthetic oligonuclectides which comprise multiple repeats of dinuclectides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                       Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BION-) BIONICHE LIFE SCI INC
           AAH46017 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                         12-DEC-2000; 2000WO-CA001467.
                                                                                                                         Synthetic oligonucleotide 17.
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                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phillips NC, Filion MC;
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                                                                                                                                                                                                                                                                                                   WO200144465-A2.
                                                                                       12-SEP-2001
                                                                                                                                                                                                                             lymphoma; ss
                                                                                                                                                                                                                                                                                                                                       21-JUN-2001.
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                                                                                                                                                                                                                                                               Synthetic.
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                                                   AAH46017;
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AAH46017
               SXXX
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleakin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNP)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Ras, p53/p21, p21/waf-1/CIP, p15(ink48), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                   Synthetic oligonucleotide, dinucleotide repeat, cytostatic, apoptosis, cell cycle arrest, cell proliferation, caspase, cytokine, interleukin, tumour necrosis factor; TNF; cancer, carcinoma, sarcoma, leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic oligonucleotide, dinucleotide repeat, cytostatic, apoptosis, cell cycle arrest; cell proliferation, caspase, cytokine; interleukin, tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.4; DB 1; Length 27; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grenererererererererere 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 16; 77pp; English.
                  Synthetic oligonucleotide 1.
                                                                                                                                                                                                                                                                                                                                                 (BION-) BIONICHE LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ
                                                                                                                                                                                                                                                        12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                                                                                                                                                          99US-0170325P.
                                                                                                                                                                                                                                                                                                           29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic oligonucleotide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH46005 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and hormone dependence
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-398150/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                  WO200144465-A2.
                                                                                                                                                                                                                                                                                                                                                                                 Phillips NC,
                                                                                                                                                                                                                                                                                          13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphoma; ss.
                                                                                                           lymphoma; ss
                                                                                                                                                                                                                    21-JUN-2001.
                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific corrivation of the inducing call cativity. The oligonucleotide compositions are useful for inducing call cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-12 and tumour of cycokines such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Ras, ps3/p21; p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                             Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGT 2344
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                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 16; 77pp; English.
                                                                                                                                                                                   BION-) BIONICHE LIFE SCI INC
                                                                                                         12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                     29-AUG-2000; 2000US-0228925P.
                                                                                                                                      99US-0170325P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF60473 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide clamp #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide clamp; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26, Conservative
                                                                                                                                                                                                                  Phillips NC, Filion MC;
                                                                                                                                                                                                                                                 WPI; 2001-398150/42.
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                                             WO200144465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6180777-B1
                                                                                                                                      13-DEC-1999;
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                                                                            21-JUN-2001
                Synthetic.
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1; Indels

97US-00787321.

03-JAN-1997;

96US-0009918P

12-JAN-1996;

WPI; 2004-059052/06

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human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; arcophic gastritus; Addison's disease; hypersensitivity disease; type I hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; exhistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                                                                                                    Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                     2319 GTGTGTGTGTGTGCGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                  Human Vbeta gene repeat sequence #366.
                                                                                                                Disclosure; Col 29-30; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                            ch 0.7%;
1 Similarity 96.3%;
26; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                  WPI; 2001-201911/20
                                                                                                                                                                                                                                                                                         Best Local Similarity
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E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast cancer; ds
      (FARB ) BAYER CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002150891-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADH70576;
                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                               Query Match
                             Horn T;
                                                                                                                                                                                                                                                                                                      Matches
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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers especifically priming and allowing amplification of each Vbeta gene, vbetaRNA or CDNA. The kit is useful for diagnosing organ transplant crejection and diagnosing and treating T-cell associated diseases.

Crejection and diagnosing and treating T-cell associated diseases including autoimmune disease, degenerative nervous system diseases, and neoplastic diseases, hypersensitivity diseases, infectious disease, and neoplastic diseases, hypersensitivity diseases, include Multiple screppic gastritis. Degenerative nervous system diseases include multiple screppic gastritis and hypersensitivities such as contact with allergens that lead to in hypersensitivities such as contact with allergens that lead to configurate such as sontact with allergens that lead to configurate in leprosy. Infectious diseases include viral infections caused by the yeast genus Candida, parasitic infections such as those caused by chistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by configurative involved infections such as those caused by chistosomes, filaria and bacterial infections such as those caused by configurative diseases include lymphoproliferative diseases and canner of the berain. Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence. Disclosure; SEQ ID NO 770; 164pp; English. Vbeta gene ö The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonucleotide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprise signal generation moieties capable of generating a detectable signal in the presence of the target molecule. In addition the OCs are connected to one present sequence is an OC used in the present invention Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothicate groups. Gaps ö Score 25.4; DB 1; Length 27; Pred. No. 1.5e+02; 1; Indels

Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other; Similarity Query Match Best Local S Matches

0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels (dC-dA)n. (dG-dT)n polymorphic repeat sequence #7. 2318 rejerererererererererer 2344 AAT66066/c ID AAT66066 standard; DNA; 30 BP. 96.3%; (first entry) 26; Conservative (revised) 25-MAR-2003 18-JUN-1997 AAT66066; RESULT 190 ద ò

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Gaps ö

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds. 89US-00341562. 91US-00754351. 94US-00222177 (MARS-) MARSHFIELD CLINIC. 04-APR-1994; Homo sapiens 21-APR-1989; 05-SEP-1991; US5582979-A 10-DEC-1996

Weber JL;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The repeats, when canalysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence; 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are consecutive non-repeat bases; 3) compound perfect repeats which are consecutive non-repeat bases; 5 uninterrupted dinucleotide or repeat bases from a run of at least 5 uninterrupted dinucleotide or least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of CA are interrupted. This sequence is an example of an imperfect repeat sequence of structure: (CA)5G(ACA)G(AC)7A. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzhaimer's disease; hypersensitivity disease; type I hypersensitivity; doodpasture's syndrome; type II hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; solistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                         Detection of polymorphic genetic markers of the form (dG-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which are defined as for the perfect compound repeats except that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25.2; DB 1; Length 30; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 15 A; 13 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                       Example 8; Col 57-58; 186pp; English
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95US-00531241.
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Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat sequence of st
to correct PF field.)
WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast cancer; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2002150891-A1
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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers of specifically priming and allowing amplification of each Vbeta gene, becatand or construction and allowing amplification of each Vbeta gene, vbetaRNA or CDNA. The kit is useful for diagnosing organ transplant crejection and diagnosing and treating T-cell associated diseases.

Crejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases.

Crejection and diagnosing and treating T-cell associated diseases.

Crejection and diagnosing and treating treating the diseases include Malsamer's disease. Hypersensitivity diseases include multiple atrophic gastritis. Degenerative nervous system diseases include multiple in lypersensitivities such as those present in allergies. Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Wycobacterium. Neoplastic diseases include viral infections such as those caused by Mycobacterium. Neoplastic diseases include as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                             Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25.2; DB 1; Length 30; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30 BP; 1 A; 1 C; 13 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chopin D, Radvanyi F, Ricol D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGTGTGTCTGTATGTGTGTGTGTGTGTG 30
                                                                                                                                                                                                             Disclosure; SEQ ID NO 600; 164pp; English.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.0 Matches 27; Conservative
                                                                         WPI; 2004-059052/06
(ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200068424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAS4587;
                                    Hood LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 192
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The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful for diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression
                                                                                                                                                          The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful for diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA54430, AAA54587) were used in PCR reactions on urine samples to detect the Y375C mutation in FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                              Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer used for detecting mutant fibroblast growth factor receptor 3. \dot{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 25; DB 1; Length 25;
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 5 A; 4 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 CAAGATCTCCCGCTTCCCGCTCAAG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radvanyi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 CAAGATCTCCCGCTTCCCGCTCAAG 1
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                                                                                                                                Example 4; Page 14; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURI-) INST CURIE.
(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA54586 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-016103/02.
                WPI; 2001-016103/02
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2001
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AAA54586/
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The present invention describes a method for determining if an individual has a tumour cell or site of angiogenesis, or if a treatment is effective in changing angiogenesis or changing a status of a set of target cells, comprising determining is asmple of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an indicator of angiogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to ABQ82006 represent nucleotide sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA54429, AAA54586) were used in PCR reactions on urine samples to detect the G372C mutation in FGFR3
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 25; DB 1; Length 25;
100.0%; Pred. No. 1.5e+02;
:ive 0; Mismatches 0; Indels
                                                                                                          Length 25;
                                                                                                                                           0; Indels
                                                                      Sequence 25 BP; 5 A; 4 C; 11 G; 5 T; 0 U; 0 Other;
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                                                                                                      0.7%; Score 25; DB 1; Lu
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Kaposi's Sarcoma TAG PCR primer SEQ ID NO:105.
                                                                                                                                                                               1011 CAAGAICTCCCGCTTCCCGCTCAAG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMST-) AMSTERDAM SUPPORT DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 23; 38pp; English.
                                                                                                                                                                                                              25 CAAGATCTCCCGCTTCCCGCTCAAG
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                                                                                                                                                                                                                                                                                                         ABQ81955 standard; DNA; 25 BP
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28-SEP-2001; 2001US-0325722P
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Best Local Similarity 100.0
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                              Local Similarity 100.
Les 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Der Kuyl AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1225233-A2
                                                                                                                                                                                                                                                                                                                                                                                19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                             ABQ81955;
                                                                                                             Query Match
                                                                                                                                                                                                                                                                          RESULT 194
                                                                                                                                                 Matches
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1648 GTGACCGAGGACAACGTGATGAAGA 1672

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Thiery J;

Ricol D,

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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell in (PBMC) expressed Keratin 14, TIE I, Salioadhesin, or Siglec I sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for cetecting the presence of a tumour cell in an individual. The expression product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This
                                                                                                                                                                                                                                                                   marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 9 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Kaposi's sarcoma tag PCR primer, SEQ ID No 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 107; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1648 GIGACCGAGGACAACGIGAIGAAGA 1672
GTGACCGAGGACAACGTGATGAAGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Der Kuyl AC, Cornelissen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2001; 2001EP-00203703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2001; 2001EP-00203703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRIM-) PRIMAGEN HOLDING BV
                                                                                                    ADC13440 standard; DNA; 25
                                                                                                                                                                                    18-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                           ADC13440;
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program oPTIPRIM). The microsatellites may be
microsatellite (using the program oPTIPRIM). The microsatellites may be
microsatellite (using the program oPTIPRIM). The microsatellites may be
conomically important trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                               , <del>,</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                        OPTIPRIM; breeding; cattle; parentage; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.8; DB 1; Length 28; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 BP; 0 A; 1 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 0.7%; Score 24.8; D Similarity 92.9%; Pred. No. 1.8e 26; Conservative 0; Mismatches
                                                                                                        Microsatellite sequence from clone TGLA255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGTGTGTGT 2346
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                                                                                                                                                                                                                                                                                                    92WO-US000340.
                                                                                                                                                                                                                                                                                                                                       91US-00642342.
                                                                    (first entry)
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                                                                                                                                        PCR; selection; primers; genetic mapping; traits;
                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
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Best Local Similarity
Matches 26; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                       15-JAN-1991;
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                                                  25-MAR-2003
02-FEB-1993
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02-FEB-1993
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                                                                                                                                                                                              Bos taurus.
                AAQ33843;
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ID AAQ3

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XX AQ3

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XX Mic XX

XW PCR

KW PCR
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Gaps ;

GTGACCGAGGACAACGTGATGAAGA 25

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AAQ33843 standard; DNA; 28 BP.

RESULT 196 AAQ33843 ID AAQ3

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
compared by with an (AF)15 and an (TF)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
compared bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The determinism of
cusping of economic trait loci, or genes involved the determinism of
connectally important traits esp. in cattle, to allow selective
preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 1.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2319 GTGTGTGTGTGTGTGTGTGTGTGT 2344
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                                                                                                                                                               Table 7; Page 203; 517pp; English
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                                             Georges M, Massey JM;
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                                                                               WPI; 1992-284684/34.
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               (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33704;
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                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
c by with an (ACI)5 and a (TC)15 oligonucleotide probe. One out of 50
c lones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
c pecification and indexed herein (see below). The sequence information
c specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
c mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                 - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.4; DB 1; Length 26;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                                                                92WO-US000340
                                                                                                                                                 91US-00642342
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Best Local Similarity 96.29
***rhes 25; Conservative
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                                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                                                WPI; 1992-284684/34.
                                                                                                                                                                                (GENM-) GENMARK.
                                                                                                                                                 15-JAN-1991;
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02-FEB-1993
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                                                WO9213102-A1
                                                                                                                .5-JAN-1992;
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                 Bos taurus.
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Gaps

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Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                      The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One ou of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine ganome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and
                                                                                                            specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic expansion of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                     0.6%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 1.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                             Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                          GIGIGIGIGIGIGIGIGIGIGIGI 2344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                  Local Similarity
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02-FEB-1993
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                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                    field.)
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Matches
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 and and a (TC)15 a
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downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.4; DB 1; Length 26; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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(first entry)
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Best Local Similarity 96.2
Matches 25; Conservative
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02-FEB-1993
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WPI; 2004-215730/21.
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02-FEB-1993
           29-JUL-2004
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                                                                                                                                              Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                       Gaps
                                                                                                                                                                                                                                                              Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
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            Length 26;
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                                       Indels
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           Score 24.4; DB 1;
Pred. No. 1.8e+02;
    0.6%; Scor.
96.2%; Pred. No. 1.0c..
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                                                                 2318 TGTGTGTGTGTGTGTGTGTGTG 2343
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                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1999; 99AU-00004907
28-MAR-2000; 2000AU-00006520
                                                                                                                                                            AAI64469 standard; DNA; 26
                                                                                                                                                                                                                (first entry)
                         Local Similarity 96.2
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-431058/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                           SSR motif #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koelliker R,
                                                                                                                                                                                                                23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                   NZ509194-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO81053;
                                                                                                                                                                                     AAI64469;
               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 203
ADO81053/c
ID ADO8109
XX
AC ADO8109
                                                                                                                               RESULT 202
AAI64469/c
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                                       Matches
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a core PML, and prediagnosis of such diseases, especially prion diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and commones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cow prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                      gene typing; polymorphic microsatellite loci; PML; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; cow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24.4; DB 1; Length 26;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 BP; 13 A; 13 C; 0 G; 0 T; 0 U; 0 Other;
                                                                         Cow prion protein microsatellite locus primer #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 rerererererererererererei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 27; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Han Y;
                                                                                                                                                                                                                                                                                                                    microsatellite; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2002; 2002DE-01036711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
  (first entry)
(first entry)
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Best Local Similarity 96.2
Matches 25; Conservative
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RESULT 206
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                                                                                                                                                                                                                                                  The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by this and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of a pecification and indexed herein (see below). The sequence information consistence of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTTRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 0.6%; Score 24.4; DB 1; Length 34; Local Similarity 96.2%; Pred. No. 2.56+02; res 25; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence from clone GBPRLGR.
           genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGTGTGTGTG 2343
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                                                                                                                                                                                                                                  Table 7; Page 223; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33630 standard; DNA; 29 BP.
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                                                                                          92WO-US000340
                                                                                                                91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                          Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                              WPI; 1992-284684/34.
                                                                                                                                    (GENM-) GENMARK
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                                                  WO9213102-A1
                                                                                          15-JAN-1992;
                                                                                                                15-JAN-1991;
                                                                       06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1992
                              Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 205
AAQ33630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program opplied). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer used in generation of FGFR3 G380R achondroplasia mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibroblast growth factor receptor; FGFR3; achondroplasia; antagonist; malignant cell transformation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening assay for antagonists of fibroblast growth factor receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 24.2; DB 1; Length 29; Best Local Similarity 89.7%; Pred. No. 2.2e+02; Matches 26; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29 BP; 1 A; 0 C; 13 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2315 GTCTGTGTGTGTGTGTGCGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drrrichdrererererarerererere 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 181; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                     mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (PROC-) PROCHON BIOTECH LTD.
91US-00642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2000 (first entry)
                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
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                                                                                (GENM-) GENMARK.
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15-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA72753;
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vivlemore401-10.rng

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This invention relates to an in vitro screening assay for an antagonist of fibroblast growth factor receptor (FGFR)-mediated malignant cell transformation. The assay comprises: (a) providing a stable cell line corresponding relations the cell line is modulated by the FGFR, or 3, where the malignant potential of he cell line is modulated by the FGFR; (b) cubjecting the cell line to treatment with corresponding FGF ligand and a candidate antagonist; and (c) measuring an FGFR downstream signalling event. The present sequence represents a PCR primer downstream signalling event. The FGFR3 achondroplasia G380R mutant. The cresulting DNA encoding mutant FGFR3 a schondroplasia G380R mutant. The cresulting DNA encoding mutant FGFR3 as used in the construction of a cell line for use in the assay of the invention. The method is useful for in vivo and in vitro screening of antagonist of FGFR-mediated malignant cell transformation and tumor formation and progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention concerns an anti-Tie (Tyrosine kinase-Immunoglobulin like domain-EGF (epidermal growth factor) homology domain) monoclonal antibody (MAb) which specifically recognises the Tie extracellular domain, and a hybridoma producing it. The MAb can be used in the diagnosis of leukaemia and also in separation and concentration of haematopoietic stem cells. The MAb can also be used to detect and determine levels of (soluble) Tie. AAT33121-22 are primers used to amplify a 160 bp probe based on a
mediated malignant cell transformation and tumor formation, by using stable cell lines expressing recombinant or wild type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Tie monoclonal antibody and hybridoma producing it - useful in diagnosis of leukaemia and detection of haematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-Tie monoclonal antibody; extracellular domain; hybridoma; Tyrosine kinase-Immunoglobulin like domain-EGF homology domain; epidermal growth factor; leukaemia; diagnosis; separation; haematopoietic stem cells; detection; primer; probe; PCR; amplify; polymerase chain reaction; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29 BP; 6 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.2; DB 1;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5' primer to amplify 160 bp probe for Tie gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 CAGGCATCCTCAGCTACGGGGTGGGCTTC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 caggaarrcrcagcracaggargggcrrc 29
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                                                                 Disclosure; Page 22; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%;
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Les 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                            Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
tyrosine kinase domain, to detect the human Tie gene from a UT-7 cDNA library. A 3933 bp cDNA clone, ptk-1, was identified, encoding a 1138 amino acid residue protein
                                                                                                                                                                                                                                                                                                                                                                                           Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 0.6%; Score 24; DB 1; Length 24; Local Similarity 100.0%; Pred. No. 1.9e+02; nes 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiery J;
                                                                                                  0.6%; Score 24; DB 1; Length 24; 100.0%; Pred. No. 1.90+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 4 A; 7 C; 6 G; 7 T; 0 U; 0 Other;
                                                                     Sequence 24 BP; 3 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                            1622 GGGACCTGGCTGCCGCAATGTGC 1645
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(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                              AAAS4427 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 100.0
Matches 24, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-016103/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200068424-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                      AAA54427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for determining if an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                        Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 24; DB 1; Length 24;
100.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaposi's sarcoma tag PCR primer, SEQ ID No 108.
                                                                                                                                    Kaposi's Sarcoma TAG PCR primer SEQ ID NO:106.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1933 ACACACGACCTGTACATGATCATG 1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Der Kuyl AC, Cornelissen M;
                                ABQ81956 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                             23-JAN-2001; 2001EP-00200228.
28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
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                                                                                                   (first entry)
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                                                                                                                                                                                                                                           EP1225233-A2.
                                                                                                   19-NOV-2002
                                                                                                                                                                                                          Homo sapiens
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                                                                  ABQ81956;
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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell (PBMC) expressed keratin 14, TIE 1, Salioadhesin, or Siglec 1 sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for detecting the presence of a tumour cell in an individual. The expression product of a gene compound is useful for preparing a medicament. This polymuclective sequence represents a PCR primer of a Kaposi's Sarcoma tag
                                                                                                                                                                                                                                                                                                                                             Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis;
drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 24; DB 1; Length 24;
100.0%; Pred. No 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone TGLA47.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 108; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1933 ACACACGACCTGTACATGATCATG 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ACACACGACCTGTACATGATCATG
                                                                                                                                                                                                                                                                        Cornelissen M;
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                                                                                                                                                                                                 28-SEP-2001; 2001EP-00203703.
                                                                                                                                                              28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                                                    (PRIM-) PRIMAGEN HOLDING BV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of the invention.
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                            WPI; 2003-589342/56.
                                                                                                                                                                                                                                                                        Van Der Kuyl AC,
                                                    Unidentified
                                                                                       EP1298221-A1
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02-FEB-1993
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Extracellular form of human fibroblast growth factor receptor treat tumours, abnormal angiogenesis e.g. diabetic retinopathy, rheumatoid arthritis and arteriosclerosis and as contraceptives.
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                                                                                                                                                                                                                                                                                                                                    29-JUL-2004
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Matches
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XFFFXXXXCCCXX
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                                                                                                                                                                                           The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC1)5 and a (TC1)5 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
c specification and indexed herein (see below). The sequences upstream and
constructed PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traite sep. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                      - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23.8; DB 1; Length 27;
Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27 BP; 1 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Basic fibroblast growth factor; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2319 GTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     crcrcrcrcrcrcrcrcrcrcrcrcrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe OAB984 for bFGF receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARM ) FARMITALIA ERBA SRL CARLO
                                                                                                                                                                           rable 7; Page 362; 517pp; English.
                                                                                                                                        Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%;
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                        92WO-US000340
                                               91US-00642342
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                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Conservative
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                                                                                             Georges M, Massey JM;
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                                                                                                                    WPI; 1992-284684/34.
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Best Local Similarity
                                                                      GENM-) GENMARK.
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                          15-JAN-1992;
                                                15-JAN-1991;
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28-OCT-1991
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   06-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant expression cassette comprising a promoter that is functional in plants, operably linked with a coding sequence and a nonplant 3' termination sequence, useful for gene expression in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heterologous gene; expression cassette; gene expression; PCR; primer; ss.
                                        The probe was used to screen a human placental lambda gt11 cDNA library for the gene encoding basic FGF receptor. It was designed from the partial cDNA clone published by Ruta et al, 1988. See also AAQ13308-Q13311. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                   Gaps
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Local Similarity 86.7%; Pred. No. 3e+02;
les 26; Conservative 0; Mismatcher 4. т.д.л.
                                                                                                                                                                                                              Sequence 33 BP; 4 A; 1 C; 11 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                    Sequence 30 BP; 5 A; 8 C; 11 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          1963 TGCTGGCATGCCGCGCCCTCCCAGAGGCCC 1992
                                                                                                                                                                                                                                                                                                                                                                                       30 TGCTGGCATGCAGTGCCTCACAGAGACCC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bertain S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the invention.
Example 1; Page 11; 29pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO39641 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcbride K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WILK/) WILKINSON J Q. (MCBR/) MCBRIDE K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-374960/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MCBR/) MCBRIDE K. (BERT/) BERTAIN S.
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RESULT 214 AAQ33918

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC115 and a (TC1)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
consistenam of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program opripRLM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 23.4; DB 1; Length 25; Best Local Similarity 96.0%; Pred. No. 2.3e+02; Matches 1; Indels Matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA354.
                                                                Microsatellite sequence from clone MTGT13B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                     (first entry)
  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                GENM- | GENMARK.
                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1991;
                                                                                                                                                                                                                            WO9213102-A1
                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by thin an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of apporting penome is estimated at >100, 000. The sequence information in the bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait losi, or genes involved the determinism of economic trait to see also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                          PCK; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                     TCTATGTATGTGTGTTTTGTGTGTGTGTG 33
                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2318 TGTGTGTGTGTGTGTGTGTGTGTGT 2342
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                                                                                                                                   AAQ33918 standard; DNA; 25 BP
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                                                                                                                                                                                                                            (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9213102-A1.
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02-FEB-1993
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Gaps

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AAQ33642

AAQ33642 ID AAQ3 XX AC AAQ3 XX

RESULT 215

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                              specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conomically important traits esp. in cattle, to allow selective reeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                            Table 7; Page 274; 517pp; English
                                                                                                                 mapping, and selective breeding.
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91US-00754351.
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ID AAT65734 standard; DNA; 25
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(first entry)
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Georges M, Massey JM;
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05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 c. bp with an (AC1)5 and a (T0)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of consistent on and indexed herein (see below). The sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the crequired PCR primers for in vitro amplification of the corresp.

The consistent of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait losi, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.4; DB 1; Length 25; Pred. No. 2.3e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA264.
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                                                                                            92WO-US000340
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1 Similarity 96.0%;
24; Conservative
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                                                                                                                                                                                                                                   маввеу ЛМ;
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                                                                                                                                                                                      (GENM-) GENMARK
                                                                                                                                         15-JAN-1991;
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    WO9213102-A1
                                                                                              15-JAN-1992;
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02-FEB-1993
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                                                 06-AUG-1992
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                                                                                                                                                                                                                                   Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33861;
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Best Local S
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Matches

RESULT 217

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AAQ33861 11D AAQ3 AAC AAQ3 XXX XXX XXX DDT 25-h DDT 25-h DDT 02-i XXX XXX PD Micro XXX PD WO95 PD 06-2 XXX XXX PD WO95 PD 06-2 XXX XXX PD WO95 PD 06-2 XXX XXX XXX XXX PD DT 06-1 XXX XXX PD DT 06-1 PD DT 06-1 XXX XXX XXX PD DT 06-1 PD

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Gaps . 0

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performing a single-nucleotide primer extension reaction.

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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesia imperfecta; autoimmune disease; acute intermittent porphyria; rheumanoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
                             The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from formula: (AC)12A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                               0.6%; Score 23.4; DB 1; Length 25; 96.0%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                Sequence 25 BP; 13 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTGT 2342
Disclosure; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP specific SNPE primer SEQ ID 1099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Picoult-Newburg L, Pohl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH38303 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                              Local Similarity 96.0
nes 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH38303
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic

WPI; 2001-290930/30.

Claim 1; Page 55; 83pp; English.

acid sample.

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Gaps

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perioring a single-mid-lor determining the presence, absence or digonucleotides are useful for determining the presence, absence or digonucleotides are useful for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. or agammaglobulinamenia, diabetes insiphdus, besch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic craits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and patemntry analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAQ47176-77 represent triplex forming oligonucleotides which bind to the mRNA sequence of the MHC class II locus DR A structural gene at positions 851-876. The sequences given in AAQ47178-80 represent control oligomers which contain base compositions similar to that around this DR A region but not containing the correct sequences. DR A is a transplantation antigen. Binding of this sequence to the DR A gene inhibits antigen production. This method may be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC; major histocompatability complex; class II; control oligomers; DR A; transplantation; antigen; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Depletion of transplantation antigens in donor cells - using anti-sense or triplex-forming oligonucleotide(s), used for treating auto-immune disease and in transplants.
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                                                                                                                                                                                                                                                                                                                                                                                         Score 23.4; DB 1; Length 25; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weiss TL, Garovoy MR, Hunt A, Huey B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2319 GTGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC DR A intron binding oligomer GTcon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTGTGTGTGTGTGTGTGTGTG 25
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                                                                                                                                                                                                                                                                                                                                                                                         0.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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AAQ47179
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                 Matches
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expression of a transplantation antigen. It may also be used to produce cells which are more essily transplanted into a recipient. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                      0.6%; Score 23.4; DB 1; Length 26; 96.0%; Pred. No. 2.46+02; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd97.
                                                                                                                                           Sequence 26 BP; 0 A; 0 C; 14 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           2319 GIGIGIGIGIGIGIGIGIGIG 2343
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91US-00754351.
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(first entry)
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                                                                                                                                                                                                     Query Match
Best Local Similarity 96.0
Matches 24; Conservative
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17-JUN-1997
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AAT65770/C

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XXX
AAT65770/C

DDT 25-M
DDT 17-U
DDT 17-U
DDT 17-U
DDT 17-U
DDT 17-U
DDT 18-M
DDT
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0.6%;

Query Match Best Local Similarity

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The sequence is that of a bovine microsatellite sequence obtd. by

constrainty a library of bovine MboI DNA fragments of between 250 and 500

constrainty a library of bovine MboI DNA fragments of between 250 and 500

constrainty by idiased. Assuming independent distribution of

colones cross-tybridised. Assuming independent distribution of

colones cross-tybridised. Assuming independent distribution of

constraints and MboI sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100,000. The sequence information

constrainty and indexed herein (see below). The sequence information

constraint and indexed herein (see below). The sequences upstream and

constraint of the microsatellite sequence where used to generate the

constraint of corresp.

constrainty individuals, for parentage testing, and in the genetic

constant in important traits esp. in cattle, to allow selective

constant in incorrect PN

constraints and incorrect PN

constant traits esp. in cattle, to allow selective

constant in the pagenent of the correct PN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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Conservative 0; Mismatches 3; Indels
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2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG
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Best Local Similarity
Matches 25; Conserval
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02-FEB-1993
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ID AAO9
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genetic mapping; traits; amplification; ss.
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                                                                                                                                                                       WPI; 1992-284684/34.
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les 25; Conserv
                                                                                                                             (GENM-) GENMARK.
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                                                                                   15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA54428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Locy
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA54428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of a poly(GT) sequence found in the promoter of the gene encoding the natural resistance-associated macrophage protein (NRAMP) from mice (RAQ2940) or humans. The NRAMP protein controls the response of macrophages to pathogenic microorganisms. The DNA sequence encoding the NRAMP was isolated and cloned into plasmid pBabe lambda 8.1 which can be used for gene transfer to haematopoietic cells, especially in vitro to bone marrow or progenitor cells, in cases of NRAMP deficiency such as cancer. The full-length murine DNA can be used to isolate the human analogue from a yeast artificial chromosome library (see AAQ92942)
                                                                                                                                                                                                                                                                                                                                                         New natural resistance associated macrophage protein - with N-terminal region contg. SH3 binding domain, also related nucleic acid, vectors, primers, antibodies etc., useful for diagnosis and treatment e.g. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       26. .27
/*tag= a
//note= "this pair of nucleotides can be repeated any
number of times"
                                                                        Natural resistance-associated macrophage protein; phage lambda 8.1; gene therapy; plasmid pBabe lambda 8.1; retro virus; therapy, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.2; DB 1; Length 28;
Pred. No. 2.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 2 A; 2 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of a microsatellite from clone TGLA78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2322 TGTGTGTGTGTGTGTGTGTGTGTGTG 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blackwell JM;
                                                   NRAMP promoter poly(GT) sequence #2
                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 57; 72pp; English
                                                                                                                                                                                                                                       95WO-GB000095.
                                                                                                                                                                                                                                                            94GB-00000929.
                                                                                                                                                                                                                                                                     94GB-00022021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cn 0.6%;
1 Similarity 89.3%;
25; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ34149 standard; DNA; 32
                               01-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                White JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           (LYNX-) LYNXVALE LTD
                                                                                                                                                                                                                                                                                                                                     WPI; 1995-269457/35.
                                                                                                                                                                                                                                                                       31-OCT-1994;
                                                                                                                                       misc feature
                                                                                                                                                                                            WO9520044-A1
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02-FEB-1993
                                                                                                                                                                                                                27-JUL-1995
                                                                                                                                                                                                                                                                                                                 Barton CH,
                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34149;
           AAQ92939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ34149
ID AAQ3
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AC AAQ3
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DT 25-N
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by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of an aircrosatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of peconomically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 23.2; DB 1; Length 32; larity 89.3%; Pred. No. 3.3e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEGEGGGGGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rerecrerererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Table 7; Page 390; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - mapping, and selective breeding.
92WO-US000340
                                                                                         91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA54428 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2311 TTTGGTCTGTGTGTG
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Gaps

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population cells to differentiate into osteoblast growth factor receptor 3 (FGFR3) (CC with an agent which increase in FGFR3 protein expression or extivity, where increase in FGFR3 protein expression or activity, where increase in FGFR3 protein expression or activity, where increase in FGFR3 protein expression or cativity results in differentiation of the stem cells into osteoblast cells. The method is useful for stimulation of the population of stem cells increases bone density. The method is useful for screening the agent increases bone density, or ameliorates the effects of osteoblast cells, contracted is useful for diagnosing a condition characterised by abnormal condition the cell of stempolaries formation and treating a patient with a condition characterised by an abnormal rate of osteoblast formation, bone density or osteoporosis. The present cof osteoblast formation, bone density or osteoporosis. The present cof osteoblast formation, and the density or osteoporosis. The present cof osteoblast formation, bone density or osteoporosis. The present cof osteoblast formation and tissues condition the density or of the density or step operation in human tissues
                                                                             Example 3; Page 58; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ70239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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\mathbb{Z} \times 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful cor diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA5428, AAA5458) were used in PCR reactions on urine samples to detect the K652B mutation in FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; stem cell; fibroblast growth factor receptor 3; FGFR3;
osteoblast cell; bone density; osteoporosis; osteopathic; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cook JS, Axelrod DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 0.6%; Score 23; DB 1; Length 23; Local Similarity 100.0%; Pred. No. 2.3e+02; Indels tes 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Thiery J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe used for FGFR3 expression in human tissues.
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                                                                                                                                                                                                                                                           Ricol D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1646 TGGTGACCGAGGACAACGTGATG 1668
                                                                                                                                                                                                                                                                Radvanyi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mertz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 13; 41pp; English.
                                                                                                                      (CURI-) INST CURIE.
(CNRS ) CNRS CENT NAT RECH SCI
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24-APR-2001; 2001US-0285691P.
23-JUL-2001; 2001US-0306879P.
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(PROC ) PROCTER & GAMBLE CO.
                              99US-0132705P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                           Chopin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-519881/55
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-016103/02
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                                                                                                                                                                                                                                                                           Cappellen D,
                              05-MAY-1999;
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The present invention relates to murine tricarboxylic acid carrier 13.53 (see ABPS9163). The protein is useful for treating various diseases, such as malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine; tricarboxylic acid carrier 13.53; tumour; cytostatic; haemopathy; HIV infection; anti-HIV; immunological disease; inflammation; PCR;
                                                                                                         Gaps
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                                                0.6%; Score 23; DB 1; Length 23;
100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide murine tricarboxylic acid carrier 13.53 polynucleotides encoding this polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine tricarboxylic acid carrier 13.53 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 10 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
Sequence 23 BP; 5 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                  3727 AAACCGGCAGGTGCGATTTTGTT 3749
                                                                                                                                                                                                                        23
                                                                                                                                                                                                       1 AAACCGGCAGGTGCGATTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000CN-00136313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000CN-00136313
                                                                                                                                                                                                                                                                                                                                             1239/c
ABZ70239 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                     Local Similarity 100.
nes 23; Conservative
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
consomically important trait loci, or genes involved the determinism of
connomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ouely match 0.6%; Score 22.4; DB 1; Length 24; Best Local Similarity 95.8%; Pred. No. 2.9α+02; Matches 23; Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of a microsatellite from clone TGLA80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGT 2342
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                                                                                                                                                                                                                                                                                                                                                                            Table 7; Page 324; 517pp; English.
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                                                                                                                              92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                              Georges M, Massey JM;
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                                                                                                                                                                                                         GENM-) GENMARK
                                                     WO9213102-A1.
                                                                                                                                                                 15-JAN-1991;
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02-FEB-1993
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                                                                                          06-AUG-1992
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                   Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human p70 ribosomal S6 kinase 13.97 (see ABB81103). The kinase and its coding sequence can be used for treating diseases such as cancer and HIV infection. The present sequence is a PCR primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide-human P70 ribosome S6 kinase 13.97 and polynucleotide for
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                          Human; p70 ribosomal S6 kinase 13.97; enzyme; cancer; HIV infection;
cytostatic; anti-HIV; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 3.8e+02;
   DB 1; Le...
3. 2.40+02; Indels
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                                                                                                                                                                                                                                                                                                                                       Human p70 ribosome S6 kinase 13.97 PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 18 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2326 TGTGTGTGTGTGTGTGTGTGTGTGCAC 2354
               Query Match 0.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 2.4 Matches 23; Conservative 0; Mismatches
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                                                                                          2319 GTGTGTGTGTGTGCGTGTG 2341
                                                                                                              23 GTGTGTGTGTGTGCGTGTG 1
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Local Similarity 86.2%;
les 25; Conservative (
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ABL58122 standard; DNA; 32
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(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                              ABL58122;
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ABLS8122/ NX ABLS8122/ NX ABLS NX ABLS NX ABLS NX ABLS NX ABLS NX CN13 NX CN

RESULT 229

AAQ33986

EXXXXXXXXXX

Matches

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Gaps

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                                                                                                                                                                                                     by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of forestablishes and Mbol sites, the frequency of (T6)n >9 microsatellites and mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the septence information for ca. 230 such bovine microsatellites is summarised in the reperition and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresponded to identify individuals, for parentage testing, and in the genetic mapphing of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                      - used in genetic identification, gene
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                                                                                                                                                                                           sequence is that of a bovine microsatellite sequence obtd. by sening a library of bovine Mbol DNA fragments of between 250 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGTGTGTG 2341
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                                                                                                                                                              Table 7; Page 394; 517pp; English.
                                                                                                             Polymorphic bovine DNA markers - mapping, and selective breeding.
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(first entry)
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                                             Georges M, Massey JM;
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                                                                             WPI; 1992-284684/34.
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Best Local Similarity
Matches 23; Conserv
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               (GENM-) GENMARK.
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by

conservating a library of bovine MboI DNA fragments of between 250 and 500

conservation and (TC)15 oligonuclocided probe. One out of 50

conservation and (TC)15 oligonuclocided probe. One out of 50

conservation and MboI sites, the frequency of (T6)n >9 microsatellites

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100,000. The sequence information

conservation and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence waset to generate the

downstream of the microsatellite sequence waset to generate the

confidentity individuals, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

concomically important trait loci, or genes involved the determinism of

concomically important traits esp. in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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0
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95.8%; Pred. No. 2.9e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGTGTGTGTGTGTGTGTGTGT
Table 7; Page 293; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                           95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local S:
Matches 23
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Gaps

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Indels

Score 22.4; DB 1; Pred. No. 2.9e+02; 0; Mismatches 1;

0.68;

Query Match 0.6% Best Local Similarity 95.8% Matches 23; Conservative

2318 TGTGTGTGTGTGTGTGTGTGTG 2341

24

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AAQ33707 standard; DNA; 24

RESULT 234

Length 24;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACL)1s and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loid, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used in genetic identification, gene
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                           Length 24;
                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                       Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                         Score 22.4; DB 1;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA423.
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                                                                                                                                                                                                                                                                                                                     1 ererererererererererer 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                           0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ34024 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                         Query Match 0.6
Best Local Similarity 95.8
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ34024;
                                                                                                                                  field.)
                                                                                                                                                                                                                                                                                                                                                                              RESULT 233
                                                                                                                                                                                                                                                                                                                                                                                                  AAQ3402,
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

WO9213102-A1

Bos taurus.

06-AUG-1992.

Microsatellite sequence from clone TGLA131.

(first entry)

(revised)

25-MAR-2003 02-FEB-1993

AAQ33707;

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
constant an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n 39 microsatellites
control bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
control of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program oPTIPRIM). The microsatellites may be
microsatellite (using the program oPTIPRIM). The microsatellites may be
controlled to invituals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
connomically important traits esp. in cattle, to allow selective
breeding. See also AAQ31501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22.4; DB 1; Length 24; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGTGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 rererererererererere 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 213; 517pp; English.
                                                                                                                                                                                                                                                                                                     92WO-US000340
                                                                                                                                                                                                                                                                                                                                      91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O.6%;
Local Similarity 95.8%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                         (GENM-) GENMARK,
                                                                                                                                                                                                                                                                                                                                      15-JAN-1991;
                                                                                                                                                                                                                                                                                                     15-JAN-1992;
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Matches
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Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

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WPI; 2001-398150/42.
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Best Local Similarity
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                                         WO200144465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2001
lymphoma; ss
                                                              21-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH46016;
                     Synthetic.
                                                                                                                                                                                                                                     caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone JW42. The sequence is amplified by primers AAT66097-8. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                      Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 22.4; DB 1; Length 24;
95.8%; Pred. No. 2.9e+02;
ive 0; Mismatches 1; Indels
                                                                                               Repeat sequence found in the human chromosomal clone JW42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2318 TGTGTGTGTGTGTGCGTGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Col 61-62; 186pp; English.
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                         AAT66096 standard; DNA; 24 BP
                                                                                                                                                                                                                                        94US-00222177
                                                                                                                                                                                                                                                             89US-00341562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                             (first entry)
                                                                                                                                                                                                                                                                                             (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Conservative
                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                         04-APR-1994;
                                                                                                                                                                                                                                                              21-APR-1989;
05-SEP-1991;
                                                                   25-MAR-2003
18-JUN-1997
                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                JS5582979-A.
                                                                                                                                                                                                                     10-DEC-1996.
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                                                                                                                                                                                                                                                                                                                   Weber JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                               AAT66096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 236
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      RESULT 23
AAT66096/
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The present sequence is that of a synthetic oligonuclectide useful to the cinvention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligonuclectide which comprises multiple crepats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, cretivation of cappases and induction of apoptosis or production of cytokines such as interlaukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour cytokines such as interlaukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(iMk4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising synthetic oligonuclectides which comprise multiple repeats of dinuclectides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 17; 77pp; English.
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                                                                                                                                                                                                        (BION-) BIONICHE LIFE SCI INC.
2-DEC-2000; 2000WO-CA001467.
                                                                              13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                 Phillips NC, Filion MC;
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response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acid. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a limmune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                               Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                    invention relates to a method for stimulating an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22.4; DB 1; Length 24; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGCGTGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGTGTGTGTGTGTGTGTGTGTG 24
                                                                                                                                                                                                                                        Claim 101; Page 59; 338pp; English.
                                                                         Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2001; 2001NZ-00509194
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(IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA164467 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 23; Conservative
                                                                         Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koelliker R, Forster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-431058/46.
                                                                                                                WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSR motif #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2001
                                                                                                                                                                                                                                                                                         present
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                                                                         Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI64467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-0H, 5'-0H synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having and secondary sarcoma such as primary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, olorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Eas, p53/p21, p21/waf-1/CIP, p15/inA48), p16(inA4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                  Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection, bacterial infection, fungal infection; parasitic infection; cancer, asthma; infectious disease; allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2319 GTGTGTGTGTGTGTGTGTGT 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTGTGTGTGTGTGTGTGTGT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid #978.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 17; 77pp; English.
                                                                                                                                              (BION-) BIONICHE LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                             12-DEC-2000; 2000WO-CA001467.
                                                                         99US-0170325P
                                                                                               29-AUG-2000; 2000US-0228925P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF99862 standard; DNA; 24
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Best Local Similarity 95.8
Matches 23; Conservative
                                                                                                                                                                                            Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and hormone dependence
                                                                                                                                                                                                                                        WPI; 2001-398150/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200122972-A2
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                                                                         13-DEC-1999;
                                                                                                                                                                                          Phillips NC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF99862;
                                                                                                                                                                                                                                                                                                                                                              caspases.
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neovascularisation, telangiectasia, haemophiliac joints, angiofibroma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to inhibiting angiogenesis in a subject, comprising
                                                       The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rubeosis; Osle-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting angiogenesis in a subject, involves administering at least antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                               Score 22.4; DB 1; Length 24;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 11 A; 11 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #1068.
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                     Example 1; Page 19; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-2000; 2000US-025534P.
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                                                                                                                                                                                                                                                                                                                                                                            0.68;
                                                                                                                                                                                                                                                                                                                                                                                                 95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS78584 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABS78584;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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ABS78884
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                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; zinc finger protein 9.46; recombinant production; gene therapy; malignant tumour; cancer; blood disease; human immunodeficiency virus; HIV infection; immune disorder; inflammatory condition; cytostatic; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
wound granulation, intestinal adhesions, atheroscierosis, scleroderma hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                   0.6%; Score 22.4; DB 1; Length 24; 95.8%; Pred. No. 2.98+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human zinc finger protein 9.46 RT-PCR primer, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 0 A; 0 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 16 (Disclosure); 31pp; Chinese.
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                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTG 2341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ57678 standard; DNA; 24
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                                                                                                                                                                                                                                       Conservative
                                                                    acid of the invention
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                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer; ss.
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                                                                                                                                                                                  Query Match
Best Local S
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Matches
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RESULT 242

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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                      Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease predisposition, microsatellite marker, prion disease, cystic fibrosis, malignant hyperthermia syndrome, metabolic disease, milk protein, hormone, transcription factor, p77-blue-vector, sheep,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%; Score 22.4; DB 1; Length 24; Best Local Similarity 95.8%; Pred. No. 2.9e+02; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheep prion protein microsatellite locus primer #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphic microsatellite loci; PML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 TGTGTGTGTGTGTGCGTGTG 2341
                                                                                                                                                                                                                                                                                                       Fouron Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      milk protein; hormone; transcri;
microsatellite; PCR; primer; ss
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                                                                                                                                        02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                                                                                                                       Bratzler RL, Petersen DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYHO-) UNIV HOHENHEIM
                                                                                                                                                                                                                    (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                            WPI; 2003-657977/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-215730/21.
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                   Synthetic.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                             Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22.4; DB 1;
Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTGTGTG 2341
                                                                                                                                                                                                                      Immunostimulatory nucleic acid #1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGTGTGTGTGTGTGTGTGTG 24
GTGTGTGGGTGTGTGTGTGTGT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 36; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2002; 2002US-00112653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB37364 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Conservative
                                                                                                 ACH03377 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                           US2003050268-A1
                                                                                                                                                                              25-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                        ACH03377;
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Query Match

Matches

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Gaps

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Ovis aries.
                                            ADO81099;
                                    24
                             Query Match
  identify
                                       RESULT 245
                               Matches
                                        ADO81099/
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR camplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and cetermining the length of the resulting amplicon(8). Also described are: determining the length of the resulting amplicon(8). Also described are: concerpML; and prediagnosis (M3) of diseases associated With gene that includes one or prediagosition to a disease, associated With a prediagosition to concerpML. The method is used to identify microsatellite markers, in a include PML. The method is used to identify microsatellite markers, in a consease related gene, that are associated With a predisposition to disease and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, confirmed by less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion contein (PrP) comprising a polymorphic microsatellite locus. genes that contain polymorphic microsatellite loci, useful for tying predisposition to disease, by amplification and determining Example 3; Page 30; 64pp; German length of amplicons.

0.6%; Score 22.4; DB 1; Length 24; ilarity 95.8%; Pred. No. 2.9e+02; Conservative 0; Mismatches Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGTGTG 2341 Local Similarity les 23; Conserv

ADO81099 standard; DNA; 24 BP (first entry) 29-JUL-2004

gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep; microsatellite; PCR; primer; ss. Sheep prion protein microsatellite locus primer #70.

09-AUG-2002; 2002DE-01036711. DE10236711-A1 26-FEB-2004

09-AUG-2002; 2002DE-01036711. (UYHO-) UNIV HOHENHEIM: Han Y; Geldermann H, Preuss S,

Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons. WPI; 2004-215730/21.

Example 3; Page 30; 64pp; German.

The invention describes a method of typing (MI) a gene (I) that has one compared or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and cetermining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML; and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a cinclude PML. The method is used to identify microsatellite markers, in a disease and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, anilgnant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, comparising factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep.prion cyntein (PrP) comprising a polymorphic microsatellite locus.

0.6%; Score 22.4; DB 1; Length 24; 95.8%; Pred. No. 2.9e+02; ive 0; Mismatches 1; Indels Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other; Similarity Query Match Best Local Si Matches 23,

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Gaps

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23; Conservative

Cow prion protein microsatellite locus primer #63. ВР ADO81051 standard; DNA; 24 (first entry) 29-JUL-2004 ADO81051; ADO81051/

RESULT

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Gaps

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gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; cow; microsatellite; PCR; primer; ss.

09-AUG-2002; 2002DE-01036711. 09-AUG-2002; 2002DE-01036711. DE10236711-A1. 26-FEB-2004, Bos taurus.

Han Y; Preuss S, (UYHO-) UNIV HOHENHEIM. WPI; 2004-215730/21. Geldermann H,

Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.

Example 3; Page 27; 64pp; German.

The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are:

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predisposition to a disease, associated with a gene that includes one or more PML; and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a diseases-related gene, that are associated with a predisposition to diseases related gene, that are associated with a predisposition to diseases and for prediagnosis of such diseases, especially prion diseases mustabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the cow prion protein (PrP) comprising a polymorphic microsatellite locus.
determining (M2) microsatellite markers (MM)
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88888888888888888888888888
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Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Length 24; 1; Indels Score 22.4; DB 1; Pred. No. 2.9e+02; 0; Mismatches 2318 TGTGTGTGTGTGTGTGTGTGTG 2341 0.6%; 23; Conservative Local Similarity Query Match Matches ઠે

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Gaps ö

> 24 rerererererererererere ద

RESULT 247 AAH40163/c

AAH40163 standard; DNA; 25

(first entry) 14-AUG-2001 AAH40163

SNP specific SNPE primer SEQ ID 2959.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000WO-US028436

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Piccoult-Newburg L, Pohl M;

WPI; 2001-290930/30

primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention factorides kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide Claim 1; Page 65; 83pp; English. acid sample.

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assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNBs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA
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Pred. No. 3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 12 A; 12 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%;
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nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                       sequence
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Matches
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2319 GTGTGTGTGTGTGTGTGTGT 2342 24 drefererererererererer ઠે 임

RESULT 248 AAI64452/

AAI64452 Btandard; DNA; 32

AAI64452;

(first entry) 23-NOV-2001

SSR motif #12.

Simple Sequence Repeat; SSR; clover; microsatellite; genome mappir trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.

Unidentified.

NZ509194-A.

25-MAY-2001

03-JAN-2001; 2001NZ-00509194.

99AU-00004907 24-DEC-1999;

28-MAR-2000; 2000AU-00006520

(AGRI-) AGRIC VICTORIA SERVICES PTY LTD

Koelliker R, Forster JW;

WPI; 2001-431058/46.

Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.

Claim 6; Page 35; 52pp; English.

clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers of genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention The present invention relates to Simple Sequence Repeats (SSRs) from

Sequence 32 BP; 16 A; 10 C; 6 G; 0 T; 0 U; 0 Other;

Query Match

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Matches

ò 셤 AAD34805;

Mus sp.

32

RESULT 249 AAD34805

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Compounds that modulate the activity of a multiple lineage kinase protein treating a cell that contains MLK with a test compound and determining if the decreases or increases the activity of MLK and promotes cell survival or death. Compounds identified as having MLK modulating activity have applications as anti-neurodegenerative agents, antiinflammatory agents and anticancer agents and are potentially useful for treatment of neurodegenerative diseases (e.g. Alzheimer's, Huntington's and Parkinson's diseases, amyotrophic lateral sclerosis, ischaemia etc.) and amalignant cell growth. DLK was cloned for its use in pFLAG-DLK by using degenerate primers derived from the highly conserved VID and IX subdomains of PTK polypeptides. Two primers (AAZ93406, AAZ93407) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds that modulate multiple lineage.kinase proteins, useful e.g. for treating neurodegeneration or cancer, from their effect on survival or death of kinase-expressing cells.
                                                                                                                                                                                                   Multiple linkage kinase; MLK; PYK; modulation; antiinflammatory; anticancer; Alzheimer's disease; Huntington's disease; primer; Parkinson's disease; amyotrophic lateral sclerosis; ischaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 22.2; DB 1; Length 31; 70.4%; Pred. No. 4.1e+02; ative 7; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31 BP; 7 A; 6 C; 6 G; 5 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neff N,
                                                                                                                                                                Degenerate conserved sequence of PTK domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1740 GCTCCCCGTGAAGTGGATGGCGCCTGA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 19; Page 50; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in the amplification reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dionne CA,
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                                     AAZ93407 standard; DNA; 31 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US018864.
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Matches 19; Conservative
                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CEPH-) CEPHALON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-282953/24.
                                                                                                                                                                                                                                                                                                                                                 WO200013015-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1998;
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                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                   AAZ93407;
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RESULT 250
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                  4AZ93407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) encluding a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-associated chondrodysplasia, particularly FGFR3 achondroplasia, e-g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect mouse FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; chondrodysplasia; achondroplasia; transgenic mouse; therapy; fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;
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81.2%; Pred. No. 4e+02;
tive 0; Mismatches 6; Indels
/ Match 0.6%; Score 22.4; DB 1; Length 32; Local Similarity 81.2%; Pred. No. 40+02; les 26; Conservative 0; Mismatches 6; Indels
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                                                                                             2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2347
                                                                                                                                                                                                                                                                                                                                                                                    Mouse FGFR3 allele detecting sense PCR primer.
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(PROC-) PROCHON BIOTECH LTD.
                                                                                                                                                                                                                                                      AAD34805 standard; DNA; 32
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Best Local Similarity 81.2
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                            (first entry)
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Glicksman MA;

Knight E,

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                                                                                                                        A method for increasing the differentiation of undifferentiated central nervous system (CNS) cells in culture. This novel method involves culturing the cells in low ambient oxygen conditions. Differentiated CNS cells can be used to treat neurodegenerative diseases such as Parkinson's
                                                                                                                                                                                             disease. In order to determine the differentiated phenotype messenger RNA levels can be measured using reverse transcription PCR. This involves using PCR primers specific to certain genes. The present sequence is the reverse PCR primer used to monitor the message level of FGFR.
                                   Low oxygen culturing of central nervous system progenitor cells useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a PCR primer for the fibroblast growth factor receptor gene (PGPR3). It was used in reverse transcription PCR to determine expression patterns of the FGFR3 gene in cultured cells. These cells had been grown in low oxygen conditions, and had differentiated to form various types of neuronal cell. The different expression patterns can be used to determine which set of conditions promotes the differentiation of each type of neurone. The different cell types can be differentiation of each type of neurone. The different cell types can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Culturing of neural crest stem cells useful for treatment of neurodegenerative disorders comprises culturing in low ambient oxygen conditions.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; cell differentiation; neurodegenerative disorder; stroke; brain injury; spinal cord injury; Alzheimer's disease; epilepsy; Huntington's disease; Parkinson's disease; neurological disorder; cell transplantation; FGFR3; fibroblast growth factor receptor 3; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                         DB 1; Length 22; 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                         Sequence 22 BP; 4 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             0.6%; Sco.
100.0%; Pred. No. ...
0; Mismatches
                                                      treatment of neurodegenerative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GAGAACAAGTTTGGCAGCATCC 1
                                                                                          Example 1; Page 36; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  466 GAGAACAAGTTTGGCAGCATCC
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WPI; 2000-387772/33
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for increasing the differentiation of undifferentiated central nervous system (CNS) cells in culture. This novel method involves culturing the cells in low ambient oxygen conditions. Differentiated CNS cells can be used to treat neurodegenerative diseases such as Parkinson's disease. In order to determine the differentiated phenotype messenger RNA levels can be measured using revorse transcription PCR. This involves using PCR primers specific to certain genes. The present sequence is the forward PCR primer used to monitor the message level of FGFR3.
                                                                                                                                                                                                                                                                                                                                                              Low oxygen culturing of central nervous system progenitor cells useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Parkinson's disease; neurodegenerative disorder; PCR primer; FGFR3;
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Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                         Studer L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.6%; Score 22; DB 1 Similarity 100.0%; Pred. No. 2.9 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               treatment of neurodegenerative disorders.
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                                                                                                                                                                                                                                                     (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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fibroblast growth factor R3; ss
                    fibroblast growth factor R3; ss
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99US-00425462
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99US-00425462
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22-OCT-1999;
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                                                      Rattus sp.
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GAGAACAAGTTTGGCAGCATCC

466

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The present sequence is a PCR primer for the fibroblast growth factor receptor gene (FGFR3). It was used in reverse transcription PCR to determine expression patterns of the FGFR3 gene in cultured cells. These cells had been grown in low oxygen conditions, and had differentiated to form various types of neuronal cell. The different expression patterns can be used to determine which set of conditions promotes the used for tissue transplantation, to treat disorders such as stroke, brain and spinal cord injury, Alzheimer's disease, Huntington's disease, other neurodegenerative disorders, epilepsy, Parkinson's disease, neurological
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used for tissue transplantation, to treat disorders such as stroke, brain and spinal cord injury, Alzheimer's disease, Huntington's disease, other neurodegenerative disorders, epilepsy, Parkinson's disease, neurological disorders and psychiatric disorders
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; cell differentiation; neurodegenerative disorder; stroke; brain injury; spinal cord injury; Alzheimer's disease; epilepsy; Huntington's disease; Parkinson's disease; neurological disorder; cell transplantation; FGFR3; fibroblast growth factor receptor 3;
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Pred. No. 2.9e+02;
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                                                                                                                                                                    Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                       162 ATCCTCGGGAGATGACGAAGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                     22
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99US-00425462.
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                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGFR3 mRNA PCR primer #2.
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AAA30354/C
ID AAA30354/C
XXX AAA30
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The present invention relates to a method for identifying a genetic marker for spider lamb syndrome (SLS). The method comprising, obtaining a sheep DNA sample, and analysing the sample DNA with a probe to determine the presence or absence of a polymorphism in fibroblast growth factor receptor 3 (FGFR). The invention is used for diagnosing if sheep carry the gene for SLS, used to eliminate carriers of the syndrome from a flock. SLS or hereditary chondrodysplasia is a semi-lethal congenital disorder in sheep causing severe skeletal abnormalities. The present sequence is a PCR primer used to amplify sheep FGFR3 gene. The FGFR3 gene is located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to diagnose
                                                                                                                                                                                                           Sheep, spider lamb syndrome; SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; chromosome 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a genetic marker for spider lamb syndrome, used to diagno
if sheep carry a gene for the syndrome, involves analyzing sheep DNA
samples for mutations in fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                       /*tag= a //note="Represented in the specification as M in the sequence shown in column 24 of the specification"
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                 Sheep FGFR3 gene amplifying PCR primer #2.
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22 GAGAACAAGTTTGGCAGCATCC
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                                                                                          AAD21621 standard; DNA;
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nes 22; Conserv
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Matches
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                                                             RESULT 255
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ID AAI6
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AAI67714 standard; DNA; 22

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Gaps

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0.6%; Score 22; DB 1; Length 22; 00.0%; Pred. No. 2.9e+02;

Query Match 0.6%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 22; Conservative 0; Mismatches

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The invention provides a method of culturing cells. The method involves expanding a culture of undifferentiated embryonic stem (BS) cells, generating embryoid bodies (BB), culturing the bodies to select for central nervous system (CMS) precursor cells (PC), culturing PC in an expansion medium comprising a neurologic factor, and differentiating and culturing the expanded PC to form a culture of differentiated neuronal cells. The method is useful for reluting undifferentiated neuronal cells, The method is useful for culturing disease in a patient. A gene product such as tyrosine hydroxylase, nerve growth factor (NGP), brain derived neurorophic factor (BDNF), bFGF, glial derived growth factor (GNF) main derived neurotrophic factor (BDNF), bFGF, glial derived growth centrophic factor (BNF), bFGF, glial derived growth centrophic such as tyrosine hydroxylase, nerve growth factor (NGF), combject. The method is useful for culturing dopaminergic, cholinergic of for treating neurological disorders such as Hutington's disease, in the interval of the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dopamine or serotonin. Cell cultures comprising 50%-85% neurons which comprise 20-40% dopaminergic neurons and 1-3% astrocytes are useful for studying the mechanism of neurotransmitter synthesis and release, particularly for serotonin and dopamine, neuronal cell survival, and the electrophysicochemical properties of differentiated neuronal cells. Sequences ABIG762-721 represent gene specific PCR primers for CNS and dopaminergic specific regulatory genes, used for examining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Culturing cells such as neuronal cells for use in treating neurological disorders, comprises generating embryoid bodies from undifferentiated embryonic stem cells, selecting precursor cells, expanding and differentiating them.
                                                                                                                                                                                                                                                                                                                                                                                                                         dopaminergic; cholinergic; serotonergic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; tranquilizer; vulnerary; neuroleptic; cerebroprotective; cell therapy; gene therapy; CNS; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                            Cell culturing; embryonic stem; ES; central nervous system; FGFR3;
                                                                                                                                                                                                                                            Receptor FGFR3 cDNA amplifying forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Studer L, Mckay RDG;
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                                                                                                                         27-FEB-2002 (first entry)
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(MCKA/) MCKAY R D G.
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STUDER L.
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AAI67714;
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(STUD/)
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(LEES/)
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0.6%; Score 22; DB 1; Length 22;

Query Match

Seguence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

ö Gaps ö Indels ö Pred. No. 2.9e+02; 0; Mismatches 183 1 ATCCTCGGGAGATGACGAAGAC 22 162 ATCCTCGGGAGATGACGAAGAC 100.0%; 22; Conservative Best Local Similarity Matches 셤 ð

Cell culturing; embryonic stem; ES; central nervous system; FGFR3; dopaminergic; cholinergic; nercotonergic; and notropic; neuroprotective; anticonvulsant; tranquilizer; vulnerary; neuroleptic; cerebroprotective; cell therapy; gene therapy; CNS; PCR primer; se. Receptor FGFR3 cDNA amplifying reverse primer. AAI67715 standard; DNA; 22 BP. 27-FEB-2002 (first entry) AAI67715; RESULT 257 AAI67715/c

01-MAY-2001; 2001WO-US014051. 01-MAY-2000; 2000US-0201005P. WO200183715-A2. Homo sapiens. 38-NOV-2001. usgo >

US GOVERNMENT. LEE S. STUDER L. MCKAY R D G. LUMELSKY N. (LUME/) MCKA/)

Lumelsky N, Studer L, Mckay RDG; Lee S,

WPI; 2002-049345/06.

Culturing cells such as neuronal cells for use in treating neurological disorders, comprises generating embryoid bodies from undifferentiated embryonic stem cells, selecting precursor cells, expanding and differentiating them.

Example 10; Page 41; 66pp; English.

The invention provides a method of culturing cells. The method involves expanding a culture of undifferentiated embryonic stem (ES) cells, generating embryoid bodies (EB), culturing the bodies to select for central nervous system (CNS) precureor cells (PC), culturing PC in an expanded PC to form a culture of differentiated neuronal cells. The method is useful for culturing undifferentiated neuronal cells. The method is useful for culturing undifferentiated ES cells to corn differentiated neuronal cells which are useful for treating a neurological disorder. especially Parkinson's disease in a patient. A gene product such as tyrosine hydroxylase, nerve growth factor (MGF), brain derived neurotrophic factor (BDNF), bFGF, glial derived growth factor. The method is useful for culturing dopaminergic, cholinergic and subject. The method is useful for culturing dopaminergic, cholinergic and subject. The method is useful for culturing dopaminergic, cholinergic for treating neuronal cells. The differentiated neuronal cells are useful for culturing dopaminergic, cholinergic and serotonergic neuronal disorders successive severe seizure disorders including epilepsy, familial dysautonomia as well as injury or trauma to the nervous system such as neurotoxic injury or disorders of mod and behavior such as addiction and schizophrenia, cerebrovascular disorders such as stroke and CNS disorders resulting from aging. Assays are useful for developing drugs capable of regulating the survival, proliferation or genesis of neuronal cells and to screen for antagonist or agonist of dopamine or serotonin. Cell cultures comprising 50%-85% neurons which

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research
comprise 20-40% dopaminergic neurons and 1-3% astrocytes are useful for studying the mechanism of neurotransmitter synthesis and release, particularly for serotonin and dopamine, neuronal cell survival, and the electrophysiochemical properties of differentiated neuronal cells. Sequences AAI67692-721 represent gene-specific PCR primers for CNS and dopaminergic specific regulatory genes, used for examining the developmental progression of ES cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; PCR; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                  ;
                                                                                                                                                                  Score 22; DB 1; Length 22;
Pred. No. 2.9e+02;
                                                                                                                                                                                                  0; Indels
                                                                                                                                    Sequence 22 BP; 4 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                     Local Similarity 100.0%; Pred. No. 2.5 tes 22; Conservative 0; Mismatches
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/note= "TAMRA labelled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human FGFR-3 DNA specific PCR probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                      487
                                                                                                                                                                                                                                                                 22 gagaacaagtriggcagcarcc 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER
                                                                                                                                                                                                                                      466 GAGAACAAGTTTGGCAGCATCC
                                                                                                                                                                                                                                                                                                                                                  AAD55414 standard; DNA; 22 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2002; 2002WO-US028549
                                                                                                                                                                          0.68;
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/mod_base=
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                                                                                                                                                                                                                                                                                                                                                                                      AAD55414;
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                       RESULT 258
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The present invention relates to a method of inducing differentiation of mammalian embryonic stem cells into functioning cells, which comprises culturing embryonic stem cells in a medium comprising leukaemia inhibitor culturing embryonic stem cells in a medium comprising leukaemia inhibitor factor and basic fibroblast growth factor. In particular, the invention carelates to the differentiation of murine embryonic stem cells. The method is useful for inducing differentiation of mammalian embryonic stem cells is useful for inducing discretes in pancreatic function, and in nerve function. Comparing the present comparing discretes in pancreatic function, and in nerve function. Comparing the present comparing the present comparing induced from embryonic stem cells using the present comparing may be used for treating disorders in pancreatic islet function (e.g. diabetes), neuronal degeneration (e.g. Alzheimer's disease and creuzfeldt-Jakob disease) or spinal cord disorders. The functioning cells are useful not only for cell transplant therapy, but for in vitro cells are useful ont only for cell transplant therapy, but for in vitro cells are useful or safety evaluation of new drugs. The present sequence is function, and for safety evaluation of the invention
                                                                                                                                                                                                                        ö
reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is human FGFR-3 DNA specific PCR probe. This probe is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing differentiation of mammalian embryonic stem (ES) cells into functioning cells, for treating e.g. diabetes, comprises culturing ES cells in a medium containing leukemia inhibitor factor and basic
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryonic stem cell; ES cell; mouse; differentiation; nerve cell; pancreatic islet cell; cell transplant therapy; antidiabetic; neuroprotective; nootropic; PCR; primer; ss.
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0
                                                                                                                                                                                0.6%; Score 22; DB 1; Length 22;
ilarity 100.0%; Pred. No. 2.9e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                             Sequence 22 BP; 4 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine embryonic cell line FGFR3R PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OKUM-) OKUMA CONTACTLENS KENKYUSHO YG. (INOU/) INOUE K.
                                                                                                                                                                                                                                                                  1271 CCGCCAAGCCTGTCACCGTAGC 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 70; 70pp; English.
                                                                                                                                                                                                                                                                                            CCCCCAAGCCTGTCACCGTAGC 22
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                                                                                                                                                                                                                                                                                                                                                                                                             ACF04260 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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nes 22; Conserva
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fibroblast growth
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                                                                                                                   of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACF04260;
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                              RESULT 259
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Gaps

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cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOYX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                  ;
0
                             Query Match 0.6%; Score 22; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 22; Conservative 0; Mismatches 0; Indels
 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DW, Bento P, Boldog FL, Burgess CB, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 6 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     Human NOVX protein-related PCR primer SegID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example C; SEQ ID NO 148; 433pp; English
                                                                                                 162 ATCCTCGGGAGATGACGAAGAC 183
                                                                                                                              1 Arccreegagardaccaagac 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-2002; 2002US-00115479.

05-APR-2002; 2002US-0370349P.

12-APR-2002; 2002US-0370369P.

12-APR-2002; 2002US-0372019P.

22-APR-2002; 2002US-0374379P.

30-MAY-2002; 2002US-0314543P.

03-JUN-2002; 2002US-040160619.

15-AUG-2002; 2002US-0403748P.

04-NOV-2002; 2002US-0403748P.

31-MAR-2003; 2003US-002087226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                    ADK51127 standard; DNA; 22
                                                                                                                                                                                                                                                                                    17-JUN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Sequence 22
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                                                                                                                                                                                                                                                     ADK51127;
                                                                                                                                                                                   RESULT 260
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The invention relates to a method for inducing differentiation of mammalian embryonic stem (ES) cells into functioning cells. The method is useful for inducing differentiation of mammalian ES cells into functioning cells. The pancreatic islet-like cell clusters induced from allogenic ES cells are useful for treating a mammalian patient having disorders in pancreatic islet function, such as when the patient is a type I diabetic patient. The nerve-like cells induced from allogenic ES cells can be used for treating a mammalian patient having disorders in nerve function. The method is a lso useful in cell therapy. The present sequence is a reverse transcription (RT)-PCR primer used to amplify mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing mammalian embryonic stem (ES) cell differentiation into functioning cells, for treating e.g. diabetes, by culturing mammalian ES cells in a medium having leukemia inhibitory factor and basic FGF to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibroblast growth factor receptor (FGF 3R) cDNA. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                        Embryonic stem cell; ES cell; pancreatic islet-like cell; type I diabetis; nerve-like cell; nerve function; cell therapy; reverse transcription; RT; PCR; primer; mouse; ss; cell differentiation; fibroblast growth factor receptor; FGF 3R.
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                         Mouse FGF 3R cDNA amplifying RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; SEQ ID NO 47; 30pp; English.
1343 TGTCTGAGATGGAGATGAA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 ATCCTCGGGAGATGACGAAGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCCTCGGGAGATGACGAAGAC 22
                   22 TGTCTGAGATGGAGATGATGAA 1
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                                                                                                                      ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2002; 2002US-00054789.
                                                                                                                    ADN03543 standard; DNA; 22
                                                                                                                                                                                       01-JUL-2004 (first entry)
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Best Local Similarity 100.
Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-328577/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonic bodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim D,
                                                                                                                                                                                                                                                                                                                                                                                US2004072344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INOU/) INOUE K. (KIMD/) KIM D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GUYY/) GU Y.
(ISHI/) ISHII M.
                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-2004.
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                                                                                                                                                     ADN03543;
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RESULT 262 AAV44045/c

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Gaps

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0.6%; Score 22; DB 1; Length 22; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels

Query Match 0.6 Best Local Similarity 100. Matches 22; Conservative

Jackson D, Ramanathan C, Siemers N;

AAV44045;

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New polynucleotide encoding a potassium channel alpha subunit polypeptide or its variants, useful for diagnosing, preventing or treating a pathological condition e.g. diabetes.
                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                   02-NOV-2000; 2000US-0245383P.
21-DEC-2000; 2000US-0257780P.
20-FEB-2001; 2001US-0269854P.
                                                     01-NOV-2001; 2001WO-US045385.
                                                                                                                                                                                Chen J,
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                             WPI; 2002-636623/68.
                                                                                                                                                                                Lee LM,
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WO200264732-A2
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                             22-AUG-2002
                                                                                                                                                                                Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS64526;
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                                                                                                                                                                                                 Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS64526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANY44043-V44045 are PCR primers used to amplify a murine basic fibroblast growth factor (bFGF) which is a member of the heparin-binding growth factor receptor family. This protein is used in a method which assays the ability of a substance to bind to a high-affinity heparin-binding growth factor (HBGF) receptor. The assay screens for potential antitumour agents that inhibit binding of HBGF to high-affinity receptors, or for potential wound healing agents that promote such binding. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assays for high-affinity heparin-binding growth factor receptor ligands -using receptor-overexpressing cells or cell-free system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potassium channel alpha subunit; K+alphaMI; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism; SNP; K+alphaMI.v2; ds.
                                                                                                                                          Basic fibroblast growth factor receptor; bFGF; heparin binding; murine; antitumour agent; inhibitor; wound healing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          Klagsbrun M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 BP; 6 A; 11 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Ornitz DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human K+alphaM1.v2 SNP polynucleotide #4.
                                                                                                                  Mouse bFGF receptor DNA PCR primer #3.
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                                                                                                                                                                                                                                                                                                                                                                                                            Leder P, Yayon A, Flanagan JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Col 7; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE. (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                    90US-00631717.
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           AAV44045 standard; DNA; 28
                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                       14-DEC-1993;
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                                                                       25-MAR-2003
                                                                                                                                                                                                                                            US5789182-A
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                                                                                      01-OCT-1998
                                                                                                                                                                                              Synthetic.
Mus sp.
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                                         The present invention relates to a new polymucleotide encoding potassium channel alpha subunit (KralphaM1) polypeptide. The KralphaM1 polymucleotides, polypeptides and antibodies are useful for diagnosing, preventing, treating or ameliorating a pathological condition or a susceptibility to a pathological condition such as neuronal disorders e.g. Addison's disease, male reproductive disorders e.g. infertility, metabolic disorders e.g. candidic disorders e.g. infertility, failure, or wounds. The present nucleic acid sequence represents a single nucleotide polymorphism (SNP) oligonuclocitde, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potassium channel alpha subunit; K+alphaM1; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 0.6%; Score 22; DB 1; Length 31; 1 Similarity 83.3%; Pred. No. 4.3e+02; 25; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GATGACGAAGACGGGAGGACGAGGCTGAG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human K+alphaM1 SNP polynucleotide #3.
Disclosure; Page 73; 465pp; English.
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21-DEC-2000; 2000US-0257780P.
20-FEB-2001; 2001US-0269854P.
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Query Match

Matches

RESULT 263

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ABS6455

Homo

vivlemore401-10.rng

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Homo sapiens
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                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH40159;
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                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                        The present invention relates to a new polynucleotide encoding potassium channel alpha subunit (K+alphaM1) polypeptide. The K+alphaM1 polypeptide. The K+alphaM1 polynucleotides, polypeptides and antibodies are useful for diagnosing, preventing, treating or ameliorating a pathological condition or a susceptibility to a pathological condition such as neuronal disorders e.g. Addison's disease, male reproductive disorders e.g. infertility, metabolic disorders e.g. diabetes, cardiac diseases e.g. congestive heart failure, or wounds. The present nucleic acid sequence represents a single nucleotide polymorphism (SNP) oligonucloeitde, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a potassium channel alpha subunit polypeptide or its variants, useful for diagnosing, preventing or treating a pathological condition e.g. diabetes.
                                                                                                    New polynucleotide encoding a potassium channel alpha subunit polypeptide or its variants, useful for diagnosing, preventing or treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potassium channel alpha subunit; K+alphaMI; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                              Siemers
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                                                                                                                                                                                                                                                                                                                                                                                     ch 0.6%; Score 22; DB 1; Length 31; 1 Similarity 83.3%; Pred. No. 4.3e+02; 25; Conservative 0; Mismatches 5; Indels
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                             Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                           Sequence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 GATGACGAAGACGGGGAGGACGAGGCTGAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGACGAGGGGAGGAGGACCAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human K+alphaM1.v1 SNP polynucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jackson D,
                              Jackson D,
                                                                                                                     or its variants, useful for diagnosin
pathological condition e.g. diabetes.
                                                                                                                                                              Disclosure, Page 34; 465pp; English.
(BRIM ) BRISTOL-MYERS SQUIBB CO
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21-DEC-2000; 2000US-0257780P.
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                              Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS64541 standard; DNA; 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       congestive heart fail
SNP; K+alphaMl.v1; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-636623/68
                                                                        WPI; 2002-636623/68
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                              Lee LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200264732-A2.
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                             Feder JN,
Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feder JN,
                                                                                                                                                                                                                                                                                                                                  invention
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                                           Chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 265
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channel alpha subunit (K+alphaMI) polypeptide. The K+alphaMI polymucleotides, polypeptides and antibodies are useful for diagnosing, preventing, treating or ameliorating a pathological condition or a susceptibility to a pathological condition such as neuronal disorders e.g. Addison's disease, male reproductive disorders e.g. infertility, matabolic disorders e.g. diabetes, cardiac diseases e.g. congestive heart failure, or wounds. The present nucleic acid sequence represents a single nucleotide polymorphism (SNP) oligonucloeitde, as described in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; se.
                                              The present invention relates to a new polynucleotide encoding potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                tch 0.6%; Score 22; DB 1; Length 31; al Similarity 83.3%; Pred. No. 4.3e+02; 25; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                     Seguence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 GATGACGAAGACGGGGAGGACGAGGCTGAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GAAGACGAAGACGGGGAGGAGGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP specific SNPE primer SEQ ID 2955.
Disclosure; Page 54; 465pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 65; 83pp; English
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Best Local Similarity
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identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, lesch-Nyhan syndrome, muscular detrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptomes of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune configuration, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide configuration (SNPE) primer specific for a human SNP containing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the apportification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                       Sequence 25 BP; 11 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
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Local Similarity 92.0%;
hes 23; Conservative
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(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ34000;
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                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                 sednence
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ID AAQ3
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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

co by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

co clones cross Hybridised. Assuming independent distribution of

co microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

microsatellites and mbol sites, the frequency of (T6)n >9 microsatellites

co rac. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

co specification and indexed herein (see below). The sequences upstream and

committee PCR primers for in vitro amplification of the corresp.

comparing the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

comparing of economic trait looi, or genes involved the determinism of

compaping of economic trait looi, or genes involved the determinism of

content of the microsatellite sep. in cattle, to allow selective
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used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used in genetic identification, gene
                                                                                                                                                                             Gaps
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                                                                                                                                          Length 28;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                          Sequence 28 BP; 2 A; 5 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                            Score 21.6; DB 1;
Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA110.
                                                                                                                                                                                                               2328 TGTGTGTGTGTGTGTGTGTGTGCACA 2355
                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Table 7; Page 195; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                        AAQ33663 standard; DNA; 23 BP.
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                                                                                                                                                0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                    24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
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Best Local Similarity
                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                            AAQ33663;
                                                                                    field.)
                                                                                                                                                                                                                                                                                                           RESULT 268
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(GENM-) GENMARK.
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                                                                                                                                           WO9213102-A1
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18-JUN-1997
                              25-MAR-2003
02-FEB-1993
                                                                                                                                                                06-AUG-1992.
                                                                                                                     Bos taurus.
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           AAQ33885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 3.6e+02;
0; Mismatches 1; Indels
 Indels
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 1;
                                                                                                                                                                           Microsatellite sequence from clone TGLA176.
 Mismatches
                     2318 TGTGTGTGTGTGTGTGTGT 2340
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Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                              AAQ33773 standard; DNA; 23
                                                                                                                                           (revised)
(first entry)
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                  Georges M, Маввеу JM;
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                             (GENM-) GENMARK.
                                                                                                                                                                                                                                                    WO9213102-A1
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02-FEB-1993
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                                                                                                                                                                                                                                 Bos taurus
                                                                                                                     AAQ33773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 270
AAQ33885
ID AAQ3388
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AAQ33773
 Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
con the sequence of (TC)15 and and (TC)15 olds one probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
con the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
constream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
consomically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence found in the human chromosomal clone SW13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                          Microsatellite sequence from clone TGLA304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGCGTGTGT 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Table 7; Page 283; 517pp; English.
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ID AAT66105 standard; DNA; 23
                                       (first entry)
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(revised)
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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

adrenergic receptor beta1; ADBR1; aryl hydrocarbon; ARNY; cathepain S; CTSS;

cytochrome as 2; COX2; diazepam binding inhibitor; DB1; haematological;

cytochrome as 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cytochrome hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cytochrome cytochrome as 2; EPHX2; bistamine-N-methyl transferase;

cytochrome cytochrome cytochrome activating protein; STM;

cytochrome cytochromesyl transferase 28; UPC-glucuronosyl transferase;

cytochrome cytochrome associated protein; orphan nuclear receptor;

cytochrome metabolism; cardiovascular function; colorectal tumour;

cytochrome cytochrome cytochrome cytochrome colorectal tumour;

cytochrome cytochrome cytochrome cytochrome cytochrome colorectal tumour;

cytochrome c
                                                                                                                                                                                                The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonuclectide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprises signal generation moieties capable of generating a detectable signal in the presence of the target molecule. In addition the OCs are connected to one another by thioalkylamino, or thiophosphorylakylamino bridges. The present sequence is an OC used in the present invention
                                        Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 21.4; DB 1; Length 23; 95.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 11 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2319 GTGTGTGTGTGTGTGTGTG 2341
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                                                                                                                                                             Example 7; Col 19; 20pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2000; 2000US-00724389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2001; 2001WO-US044838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS97836 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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WPI; 2001-201911/20.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone SW13. The sequence is amplified by primers AAT66106-7. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
        linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 12 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0009918P
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                                                                                                                                                                                                                                                                  94US-00222177.
                                                                                                                                                                                                                                                                                                                        89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide clamp #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide clamp; ds
                                                                                                                                                                                                                                                                                                                                                                                                        (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6
Best Local Similarity 95.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6180777-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-2001
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                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                       14-APR-1994;
                                                                                                                                                                                                                                                                                                                           21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                        05-SEP-1991;
                                                                                                                                                             US5582979-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber JL;
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à g ö

Gaps

Blackwell JM;

Barton CH, White JK, (LYNX-) LYNXVALE LTD

31-OCT-1994;

95WO-GB000095. 94GB-00000929.

19-JAN-1995;

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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 O2B1 (CYP4501A1), cytochrome P450 O2B1 (CYP4501A1), cytochrome P450 O2B1 (CYP4501A1), ddrenergic receptor beta1 (ADBR1), cytochrome P450 O2B1 (CYP4501A1), adrenergic receptor beta1 (ADBR1), cytochrome P450 O2B1 (CYP5), cytochrome
                      Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 11 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphic DNA sequence of the invention
                                                                                                                                                           Example 16; Page 131; 714pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system function.
                                                                                                        disorder-related traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peripheral
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Gaps
                                       ö
0.6%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 3.7e+02;
                                      1; Indels
                                       0; Mismatches
                                                                            2322 TGTGTGTGTGCGTGTGTGT 2344
                                                                                                              23 rérarérérérécérérérérer 1
                    Best Local Similarity 95.7
Matches 22; Conservative
     Query Match
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NRAMP promoter poly (GT) sequence.
AAQ92938 standard; DNA; 26 BP.
                                                                                              01-APR-1996 (first entry)
                                               AAQ92938;
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Natural resistance-associated macrophage protein; phage lambda 8.1; gene therapy; plasmid pBabe lambda 8.1; retro virus; therapy, ss.

WO9520044-A1 Synthetic RESULT 27 AAQ92938 ò g

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The sequence of a poly(GT) sequence found in the promoter of the gene encoding the natural resistance-associated macrophage protein (NRAMP) from mice (AAQ92940) or humans. The NRAMP protein controls the response of macrophages to pathogenic microorganisms. The DNA sequence encoding the NRAMP was isolated and cloned into plasmid pBabe lambda 8.1 which can be used for gene transfer to haematopoietic cells, especially in vitro to bone marrow or progenitor cells, in cases of NRAMP deficiency such as cancer. The full-length murine DNA can be used to isolate the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                            New natural resistance associated macrophage protein - with N-terminal region contg. SH3 binding domain, also related nucleic acid, vectors, primers, antibodies etc., useful for diagnosis and treatment e.g. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             analogue from a yeast artificial chromosome library (see AAQ92942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.4; DB 1; Length 26; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP; 2 A; 2 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGRI-) AGRIC VICTORIA SERVICES PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2322 TGTGTGTGTGTGCGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 rerererereracerererer 23
                                                                                                                                                                                                                                                                                         Claim 24; Page 57; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%;
Best Local Similarity 95.7%;
Matches 22; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA164470 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-2001 (first entry)
                                                                                                                                                                                                                             region contg. SH3 binding primers, antibodies etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coelliker R, Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-431058/46.
                                                                                                                                                                                 WPI; 1995-269457/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSR motif #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA164470;
                                                                                                                                                                                                                                                             cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 275
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MooI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MooI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be
                                                                                                   The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNa. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                             ch 0.6%; Score 21.2; DB 1; Length 26; 1 Similarity 88.5%; Pred. No. 4.3e+02; 23; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                              Sequence 26 BP; 11 A; 12 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                         2319 GTGTGTGTGTGTGTGTGTGTGT 2344
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                                                                            Example 1; Page 19; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33740 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ33740;
                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 276
                                                                                                                                                                                                                                                                                                                                                            Matches
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Moo! DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of mapping of the contract of the corresp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                       .;
0
                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 1; Length 21;
Pred. No. 3.6e+02;
                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                    Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                    Score 21.2; DB 1;
Pred. No. 4.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA2.
                                                                                                                                                                                                        2318 TGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                              Table 7; Page 245; S17pp; English.
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100.0%;
                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                         0.6%;
                                                                                                                                                                                                                                                                                                                             AAQ33789 standard; DNA; 21
                                                                                                                                                                          23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
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Best Local Similarity
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9213102-A1.
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                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                AAQ33789;
                                                                           field.)
                                                                                                                                                                              Matches
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Matches

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGFR-3. ACH, JT44 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is human exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem cell; dental follicle; tooth; membrane structure;
periodontal ligament; pluripotent mesenchymal stem cell; osteopathic;
antiniflammatory; stem cell therapy; tissue replacement; tissue repair;
transplantation; periodontal tissue; periodontitis; dental cementum;
gene therapy; PCR primer; ss.
                                                            Human, antisense, fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast growth factor receptor 3-IIIC forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 21; DB 1; Length 21;
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                       Human FGFR-3 DNA specific reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; Page 76; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1297 AAGATGCTGAAAGACGATGCC 1317
                                                                                                                                                                                                                                                                                                                                     10-SEP-2001; 2001US-00953047.
                                                                                                                                                                                                                                                                                         06-SEP-2002; 2002WO-US028549.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                           Monia BP, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-313244/30.
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2003
                                                                                                                                                                                                                                               20-MAR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC64705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for identifying a genetic marker for spider lamb syndrome (SLS). The method comprishing, obtaining a sheep DNA sample, and analysing the sample DNA with a probe to determine the presence or absence of a polymorphism in fibroblast growth factor receptor 3 (FGFR). The invention is used for diagnosing is sheep carry the gene for SLS used to eliminate carriers of the syndrome from a flock. SLS or hereditary chondrodysplasia is a semi-lethal congenital disorder in sheep causing severe skeletal abnormalities. The present sequence is a PCR primer used to amplify sheep FGFR3 gene. The FGFR3 gene is located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a genetic marker for spider lamb syndrome, used to diagnose if sheep carry a gene for the syndrome, involves analyzing sheep DNA samples for mutations in fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                               Sheep; spider lamb syndrome; SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; chromosome 6;
  Gaps
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  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 3 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 21; DB 1; Le
100.0%; Pred. No. 3.6e+02;
ive 0; Mismatches 0;
  Mismatches
                                                                                                                                                                                                                                                                                                                                       Sheep FGFR3 gene amplifying PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1425 CCTGTACGTGCTGGTGGAGTA 1445
                                            2324 TGTGTGTGTGCGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGTACGTGCTGGTGGAGTA 21
                                                                                      rerererecerererer 21
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                                                                                                                                                                                                   BP
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                                                                                                                                                                                                 AAD21620 standard; DNA; 21
                                                                                                                                                                                                                                                                                           19-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTAH ) UNIV UTAH STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cockett NE, Beever JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-662278/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6306591-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1998;
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                                                                                      Н
                                                                                                                                                                                                                                               AAD21620;
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Ovis sp.

RESULT 278
AAD21620
ID AAD2165
XX
AC AAD2165
XX
DT 19-MAR
XX
DE Sheep
XX
Sheep;
XW Sheep;
XX Cocket
XX (UTAH
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Gaps

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Query Match

Best Loca Matches

ð g RESULT 279
AAD55413/C
ID AAD554
XX
AC AAD554
XX
DT 07-AUG

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06-FEB-2002; 2002US-0354152P.
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                                                                                                                                                                                                                                                                                                                         The present invention describes a stem cell (A) that is obtained from non-embryonic tissue isolated from the dental follicle of a (wisdom) tooth which can differentiate in vitro into a membrane structure that resembles concluding the concluding and an invention of a stem cell (A1), derived from periodontal ligament. Also described: (I) a stem cell (A1), derived from con-embryonic or post-natal animal cells or tissue, that is capable of self-renewal and differentiation to cells of endo-, ecto- or meso-dermal concluding self-renewal and differentiation to cells of endo-, ecto- or meso-dermal concluding self-renewal and antiinflammatory activities, and can be used (A). (A) has osteopathic and antiinflammatory activities, and can be used differentiated from them, can be used to prevent or treat cellular differentiated from them, can be used to prevent or treat cellular. Confector, dysfunction and/or disease, e.g. tissue repair or transplantation. They can especially be used to rebuild periodontal crasses of periodonticis) or dental cementum, and to improve tissue (in cases of periodonticis) or dental cementum, and to improve tissue (in cases of periodonticis) or dental cementum, and to improve tissue (in cases) or seaffold, for growing teeth (or associated bone) or association with a scaffold, for growing teeth (or associated bone) or present sequence represents a PCR primer which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stem cell; dental follicle; tooth; membrane structure; periodontal ligament; pluripotent mesenchymal stem cell; osteopathic; antiinflammatory; stem cell therapy; tissue replacement; tissue repair; transplantation; periodontal tissue; periodontitis; dental cementum; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                    Morsczeck C;
                                                                                                                                                                                                                               Pluripotent embryonic-like stem cells derived from dental follicle, useful e.g. for engineering teeth or dental tissue, and for transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor receptor 3-IIIB forward PCR primer.
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.00.0%; Pred. No. 3.6e+02;
.ve 0; Mismatches 0; Indels
                                                                                                                                                                    Zeilhofer F, Hoffmann KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
0.6%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 AACGGCAGGGAGTTCCGCGGC 366
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                                                                                                                                                                                                                                                                                                    Example; Page 23; 68pp; English.
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                                                                      05-FEB-2003; 2003WO-EP001131.
                                                                                                         06-FEB-2002; 2002US-0354152P
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                                                                                                                                                                         Schierholz J, Brenner N,
                                                                                                                                          (CAES-) STIFTUNG CAESAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                        WPI; 2003-663591/62.
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            WO2003066840-A2.
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The present invention describes a stem cell (A) that is obtained from non-
cembryonic tissue isolated from the dental follicle of a (wisdom) tooth
which can differentiate in vitro into a membrane structure that resembles
cc which can differentiate in vitro into a membrane structure that resembles
cc periodontal ligament. Also described: (I) a stem cell (A1), derived from
cc non-embryonic or post-natal animal cells or tissue, that is capable of
cc non-embryonic or post-natal animal cells of endo-, ecto- or meso-dermal
cc self-renewal and differentiation to cells of endo-, ecto- or meso-dermal
cc lineages; and (2) pluripotent mesonchymal stem cells (A2) obtained from
lineages; and (2) pluripotent mesonchymal stem cells (A), and calls
cc in stem cell therapy, and in tissue replacement. (A), and cells
cc differentiated from them, can be used to prevent or treat cellular
cc differentiated from them, can be used to prevent or treat cellular
cc transplantation. They can especially be used to rebuild periodontal
cc transplantation. They can especially be used to rebuild periodontal
cc tissue (in cases of periodontitis) or dental cementum, and to improve
tissue (in cases of periodontitis) or dental cementum, and to improve
cc healing of tooth extraction or skin lesions. They can also be used in
association with a scaffold, for growing teeth (or associated bone) or
caterial/venous vessels in the mouth or as gene therapy carriers. The
component in the mouth or as gene therapy carriers. The
contraction of the contraction of the primer which is used in an example from
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                                                                             Morsczeck C;
                                                                                                                                                                                                                                                                                Pluripotent embryonic-like stem cells derived from dental follicle, useful e.g. for engineering teeth or dental tissue, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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100.0%; Pred. No. 3.66+02;
tive 0; Mismatches 0; Indels
                                                                             Zeilhofer F, Hoffmann KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
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ADK51121/C
ID ADK51121 standard; DNA; 21 BP.
XX
AC ADK51121;
XX
DT 17-JUN-2004 (first entry)
XX
KW Cytostatic; NOVX-agonist; NOVX-as
KW Chromosome mapping; human; PCR; I
XX
Chomosome mapping; human; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 23; 68pp; English.
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                                                                                                    Brenner N,
(CAES-) STIFTUNG CAESAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                              WPI; 2003-663591/62.
                                                                                                                                                                                                                                                                                                                                                                          useful e.g. for transplantation.
                                                                                                               Schierholz J,
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This primer and its 5' partner (AAG52727) correspond to regions highly conserved among mouse BEK, human FLG and chicken fibroblast growth factor
                                                                                                                                                                                     New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                            This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
  Casman SJ, Furtak K;
MP, Li L, Spytek KA;
Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cells having high-affinity heparin-binding growth factor binding sites are used for screening substances for e.g. anti-tumour agents or wound healing promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
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     Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smittbson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse fibroblast growth factor 3' DNA primer.
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                                                                                                                                                                                                                                                                   Example C; SEQ ID NO 145; 433pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast growth factor; DNA primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742 GITCICCTIGCACAACGIC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yayon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 7; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ52728 standard; DNA; 27 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-404932/50.
                                                                                                                                    WPI; 2003-812539/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nvention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                  or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel isolated polypeptides and the DNA decences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                               Furtak K;
Spytek KA;
                                                                                                                                                                                                                                                                                                                                            New NOVX polypeptide, useful for preparing a composition for treating preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                       Gorman L, Gould-Rothberg BE, Gunther E, Heyes MP, Li L, S Stone DJ, Zhong M, Malyankar UM, Edinger SR, Patturajan M; Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 3.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOVX protein-related PCR primer SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                           Example C; SEQ ID NO 142; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCTCTCCTTGCACAACGTC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCTCTCCTTGCACACGTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-2002; 2002US-00115479.
05-APR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-0372019P.
22-APR-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0314543P.
33-MAY-2002; 2002US-00160619.
15-AUG-2002; 2002US-0403748P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
15-AUG-2002; 2002US-0403748P.
04-NOV-2002; 2002US-00287226.
31-MAR-2003; 2003US-00403161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                           WPI; 2003-812539/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742
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Matches
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1572 CCAGGTGGCCCGGGGCATGGAGTACTTGG 1600

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acids (NAs) comprising contacting a sum-popuration in records acids (NAs) comprising contacting a sum-popuration physiological conditions to enzymatically generate sub-population of NAs, where each conditions to enzymatically generate sub-population of NAs, where each cach labeled NA is generated using a single gene specific primer. The each labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of labeled NAs which is useful for analysing the differences in the method comprises producing different physiological sources, where the method comprises producing subpopulation of labeled NAs for the different physiological sources, comprising the population, where the comparison is preferably differences in the population, where the comparison is preferably differences in the population, where the comparison is preferably confidence by hybridising the labeled NAs for each of the distinct surface of a substract to produce a hybridisation pattern for each of the sources, where differential gene expression assays are utilised in differential expression analysis of diseased a normal tissue e.g. neoplastic a normal expression analysis of diseased a normal tissue e.g. neoplastic a normal expression analysis of the printed of the invention. Note: The sequence data for this patent did not form part of the printed peculic comparing in electronic format of free printed procession, but was obtained in electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to producing a sub-population of labeled nucleic
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               Primer; ss; DNA microarray; differential expression analysis; human.
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82.8%; Pred. No. 5.4e+02;
tive 0; Mismatches 5; Indels
Length 27;
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 8 A; 11 C; 5 G; 6 T; 0 U; 0 Other;
                       4.8e+02;
0.6%; Score 21; DB 1;
100.0%; Pred. No. 4.8e+0
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3xample 3; SEQ ID NO 172; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                Human gene specific PCR primer #172.
                                                                                  1349 AGATGGAGATGATGAAGATGA 1369
                                                                                                           99US-00225928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00859998
                                                                                                                                                                                                                           ABK66084 standard; DNA; 30
                                                                                                                                                                                                                                                                                                            02-JUL-2002 (first entry)
                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chenchik A, Jokhadze G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-314699/35.
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6352829-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-2002
                                                                                                                                                                                                                                                                      ABK66084;
                                              Matches
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sequences AAH40205 - AAH40944 represent PCR primers, single nucleotide primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the coligonucleotides are useful for genocyping a genotyping primer. SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genocyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The coligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to identity of a SNP and for genotyping nucleic acid samples, for e.g. to individuals, having pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. caused by one or more SNPs. Phenotypic traits include diseases e.g. osteogenesis imperfects and acute intermittent pophyria. Phenotypic craits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, conflammation, cancer, inervous system diseases and infection by machine confidence extension (SNPE) primer sequence represents a single nucleotide paternity analysis. The present sequence represents a single nucleotide sequence conflamence.
                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 11 A; 11 C; 2 G; 1 T; 0 U; 0 Other;
29 ccaagregeraaggecargagrererieg 1
                                                                                                                                                                                                                                      SNP specific SNPE primer SEQ ID 2951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 65; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORCH-) ORCHID BIOSCIENCES INC
                                                                                                             AAH40155 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0160096P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Picoult-Newburg L, Pohl M;
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-290930/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200129262-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                              14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2001.
                                                                                                                                                        AAH40155;
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                                                                       RESULT
                                                                                           AAH401
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0.5%; Score 20.8; DB 1; Length 25;

Query Match

Gaps

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24; Conservative

Query Match Best Local Similarity Matches 24; Conserv

bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predipposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; single nucleotide polymorphism; SNP; ss.

Location/Qualifiers replace(12. .17,TA) /*tag= a

variation

Homo sapiens

98US-00009913. 97US-0035663P. 97US-0051432P.

21-JAN-1998;

US6087485-A. 11-JUL-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ95132 and M13U are a pair of primers for the PCR amplification of AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1) mucleic acid. The nucleic acid and its protein product (AAR71111) can be used to develop products, for the presymptomatic detection of a SCA 1 disorder. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - us to develop prods. for detection or presymptomatic diagnosis of a SCA1 disorder.
               Gaps
                                                                                                                                                                                                                                         Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
BamCA PCR primer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 20.6; DB 1; Length 27;
85.2%; Pred. No. 5.3e+02;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 10 A; 14 C; 2 G; 1 T; 0 U; 0 Other;
 Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                 Spinocerebellar ataxia type 1 BamCA PCR primer.
                                      2317 CTGTGTGTGTGTGTGTGTGT 2340
                                                        24 CCGTGTGTGTGTGTGTGTGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example I, Page 37; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                           94WO-US007336
                                                                                                                                                                                                                                                                                                                                                                                  93US-00084365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zoghbi HY
91.78;
                                                                                                                          AAQ95132 standard; DNA; 27
                                                                                                                                                                                           (first entry)
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (MINU ) UNIV MINNESOTA.
                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-061001/08
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chung M,
                                                                                                                                                                                                                                                                                                         WO9501437-A2
                                                                                                                                                                                                                                                                                                                                                          29-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1994;
                                                                                                                                                                            25-MAR-2003
28-SEP-1995
                                                                                                                                                                                                                                                                                                                                  12-JAN-1995
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                    AAQ95132;
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              Matches
                                                                                                               AAQ95132,
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New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein, for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.

Buckler A;

Cardon L,

Galvin M, Miller A, North M, Brooks-Wilson AR, Carey AH;

WPI; 2000-505109/45.

(AXYS-) AXYS PHARM INC.

01-JUL-1997; 21-JAN-1997;

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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH11 and ASTH1J genes, which are associated with a genetic predisposition to asthma and bronchial hyperreactivity. The ASTH11 and ASTH1J genes are oriented in opposite directions with the ASTH11 and ASTH1J genes are oriented in opposite and rections with the ASTH1 locus, and have similar patterns of expression and common sequence motifs. They are both expressed in traches, lung and several other tissues. ASTH1I and ASTH1J are novel members of the ets activation of a variety of genes including the TCRs gene and cytokine cativation of a variety of genes including the TCRs gene and cytokine genes hnown to be important in the aeticlogy of asthma. Both ASTH1I and ASTH1J mRNAs are alternatively spliced. Alternative splicing of transcripts has no effect on the open reading frame of ASTH1J and ASTH1I manacripts has no effect on the open reading frame of ASTH1I and transcripts has no effect on the open reading frame of ASTH1I and excons involved are all 5' to the start codon in exon b. In contrast, alternative splicing of ASTH1I transcripts results in 3 different ASTH1I is softentifying expression of ASTH1I proteins are useful as diagnosetics to identifying appression of the gene in a biological specimen, and for genetating genetically modified non-human animals or site specific gene modifications that mimic or modulate activity or expression of ASTH1I cand/or ASTH1I genes or fragments thereof, enoroged proteins, and are allowed as therapeutic. The ASTH1 genes or fragments thereof, enoroged proteins, and therapeutic purposes in dividuals predisposed to development of asthma, and for modulation of gene activity in vivo for prophylactic and therapeutic purposes in the intent of asthma, and for modulation of gene activity in an absent of proteins or activity in the identification of individuals predisposed to bronchial hyperreactivity. Sequences ASTH1I or ASTH1I or ASTH1I or ASTH1I or ASTH1I or ASTH1I or ASTH2I o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent polymorphic sites within the ASTH1J or ASTH1I genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.6; DB 1; Length 27;
Pred. No. 5.3e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 27 BP; 1 A; 2 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Col 41-42; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%;
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Gaps

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0; Mismatches

Local Similarity 85.2 nes 23; Conservative

2335 GTGTGTGTGTGTGCACATCCGCG 2361

<u> crerererererereresexreces</u>

27

ઠ 셤 AAA80358 standard; DNA; 27

RESULT 288

(first entry)

22-NOV-2000

AAABO358 ID AAA XX AAC AAA XX ZX Z2-XX DE Hum XX AST

AAA80358;

2319 GTGTGTGTGTGTGCGTGTGTGTGT 2345

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ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma; Human ASTHII 5' region polymorphic site, SEQ ID NO:103 (b)

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WPI; 2003-345602/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-2002.
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                                                                                                                                ACC79667;
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The sequence is that of a bovine microsatellite sequence obtd. by

conservation a library of bovine Mbol DNA fragments of between 250 and 500

conservation and (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

conservation and (AC)15 oligonucleotide probe. One out of 50

conservation and Mbol sites, the frequency of (T6)n >9 microsatellites

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

conservation and indexed herein (see below). The sequence information

conservation and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence where used to generate the

constream of the microsatellite sequence was used to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellity individuals, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

conomically important traits esp. in cattle, to allow selective

conomically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                       PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 0.5%; Score 20.4; DB 1; Length 22; Local Similarity 95.5%; Pred. No. 4.4e+02; Indels 1; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA117.
                                                               Microsatellite sequence from clone TGLA214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2319 GTGTGTGTGTGTGTGTGT 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 253; 517pp; English.
                                                                                                                                                                                                                                                                                                                                      92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                      91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33675 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
                                                                                                                                                                                                                                                                                                                                         5-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                30s taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for the inspection of flat

c epithelial cells in which it is judged that flat epithelial cells

separated from an organism can proceed to flat epithelial cells

c 128th base in fibroblast growth factor receptor (FGFR) gene of the cells

c 128th base in fibroblast growth factor receptor (FGFR) gene of the cells

c is mutated from quanine to thymine. Also described is a method for

c screening treating or preventive agents for flat epithelial cancers in

c spapied to flat epithelial cancer cells producing FGFR protein in

which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from

c quanine to thymine or the 697th amino acid is mutated from glycine to

c quanine to thymine or the 697th amino acid is mutated from glycine to

c quanine to thymine or the 697th amino acid is whether for the

c quanine to thymine or the 697th amino acid is mutated from glycine to

c quanine to thymine or the 697th amino acid is mutated from glycine to

c quanine to thymine or the 697th amino acid is protein produced returned to glycine as the indices. The method is used

c the inspection of flat epithelial cells. The present sequence

for the inspection of flat epithelial cells. The present sequence

c represents a FGFR primer for human FGFR3, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                         Human; fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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ilarity 85.2%; Pred. No. 5.3e+02;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                Human fibroblast growth factor 3 PCR primer SEQ ID NO:2.
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     27 gegecreecedacereaagaarrere 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZERI ) ZERIA SHINYAKU KOGYO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001; 2001JP-00083352
                                                                                                                                                          ACC79667 standard; DNA; 27
                                                                                                                                                                                                                                                          27-AUG-2003 (first entry)
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Gaps

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Bos taurus

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vivlemore401-10.rng

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
con the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
concomically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 20.4; DB 1; Length 22;
llarity 95.5%; Pred. No. 4.4e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
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                                                                                                                                            Table 7; Page 346; 517pp; English.
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(first entry)
Маввеу ЛМ;
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                                      WPI; 1992-284684/34.
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les 21; Conserv
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02-FEB-1993
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Georges M,
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 293
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                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 between 260 and 500 with an (AC15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at .910, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information for caulted PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTTRAIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2318 TGTGTGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 199; 517pp; English.
                                                                                                                                                                                                                                                                                                             mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34038 standard; DNA; 22 BP
                                                                               92WO-US000340
                                                                                                                        91US-00642342
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                                                                                                                                                                                                          Маввеу ЛМ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1991;
                                                                                                                      15-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1992;
  WO9213102-A1
                                                                                 15-JAN-1992;
                                        06-AUG-1992.
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02-FEB-1993
                                                                                                                                                                                                          Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
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Query Match Matches

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screening a library of bovine MboI DNA fragments of between 250 and 500 cC bp with an (AC115 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information crossitellites are summarised in the specification and indexed herein (see below). The sequences upstream and commerce more used to generate the downstream of the microsatellite sequence were used to generate the crequised PCR primers for in vitro amplification of the corresp.

CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIRRIM). The microsatellites may be microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connectant traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.) Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02; 0; Mismatches 1; Indels Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other; Query Match

2318 TGTGTGTGTGTGTGTGTGTG 2339 rerererererererere ch 0.5%; 1 Similarity 95.5%; 21; Conservative (Local Similarity Matches ö g

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Gaps

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22 AAQ33991 standard; DNA; AAQ33991; RESULT 294

BP.

PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss. Microsatellite sequence from clone TGLA39. (first entry) (revised) WO9213102-A1 25-MAR-2003 02-FEB-1993 06-AUG-1992 Bos taurus AAQ33991

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cattle; parentage;

92WO-US000340 91US-00642342 15-JAN-1991; 15-JAN-1992;

(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

markers - used in genetic identification, gene Table 7; Page 327; 517pp; English. Polymorphic bovine DNA markers - mapping, and selective breeding.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the appecification and indexed herein (see below). The sequences upstram and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the construction of an oligonuclectide clamp. The clamp is a comb-type

ö ಗ used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN Synthesis of branched polymers and novel branched polymeric structures used as molecular probes esp. for detecting poly-nucleotide $(\mbox{s})\,.$ ppp = a linkage or monomer containing functionality, and p = phosphodiester pnp = a linkage or monomer containing functionality, and p = phosphodiester pnp = a linkage or monomer containing functionality, and p = phosphodiester Gaps HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss. Oligonucleotide clamp n, for producing comb-type brached polymer. ö Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02; Indels /*tag= a
/note= "Modified with BrCH2(=0)CNH-" Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other; 0; Mismatches 2318 TGTGTGTGTGTGTGCGTGTG 2339 Location/Qualifiers bromoacetylamino fulinkage" Example 8; Page 33; 52pp; English. 1 TGTGTGTGTGTGTGTGTGTG 22 /*tag= c
/note= "C(pnp)A,
promoacetylamino /*tag= d /note= "C(pnp)A, bromoacetylamino (LYNX-) LYNX THERAPEUTICS INC 94WO-US007557. AAQ83952 standard; DNA; 22 BP. 93US-00087386. 0.5%; 8. .9 /*tag= b /note= "C((first entry) Query Match Best Local Similarity 95.5' Matches 21; Conservative inkage, linkage (revised) WPI; 1995-060944/08. modified base modified base modified_base modified base 05-JUL-1994; 02-JUL-1993; WO9501365-A1 Gryaznov SM; 12-JAN-1995. 25-MAR-2003 04-OCT-1995 Synthetic AAQ83952; field.) RESULT 295 AAQ83952 ð g 8X3838XX

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branched polymer which has 3' termini and was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded or double stranded forms. An oligonucleotide clamp is a compound capable of forming a covalently closed macromolecule or a stable circular complex after specifically binding to the target polynucleotide.

Oligonucleotide clamps generally comprise one or more oligonucleotide moieties capable of specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the oligonucleotide moieties. Upon annealing of the oligonucleotides moieties to the target polynucleotide, the binding moieties of a pair are bought into juxtaposition so that they form a stable covalent or non-covalent linkage to complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonucleotide moieties to the target polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences having the sequence (dG-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dG-dA), (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymorsase chain reaction; paternity; maternity; human; padigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 4.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfd25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
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91US-00754351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.5
Matches 21; Conservative
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone MG25 which contains the repeat sequence having the formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
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                                                                                                                    0.5%; Score 20.4; DB 1; Length 22; ilarity 95.5%; Pred. No. 4.4e+02; Conservative 0; Mismatches 1; Indels
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                                                                                    Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                         2319 GTGTGTGTGTGTGTGTGT 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was used in the present invention
                                                                                                                                                                                                                                                                                                               ВР
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*Best Local Similarity 95.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                               AA164468 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                      Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    SSR motif #18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001
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                                                                                                                       Query Match
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Matches
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and markers assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which
                                                                                                                                                                                                                                                                                                       Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human uridine diphosphate glucuronosyltransferase gene polymorphism #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 20.4; DB 1; Length 22; ilarity 95.5%; Pred. No. 4.4e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 10 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                   (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iyer L, Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 35; 52pp; English.
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                                                                                                                                               24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                           03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2003 (first entry)
                                                                                                                                                                                                                                             Koelliker R, Forster JW;
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Matches 21; Conserva
                                                                                                                                                                                                                                                                               WPI; 2001-431058/46.
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Unidentified.
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                                                                         25-MAY-2001
                                       NZ509194-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNs. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                           Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
0.5%; Score 20.4; D
Best Local Similarity 95.5%; Pred. No. 4.4e
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGTG 2339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI64456 standard; DNA; 22 BP.
                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2001; 2001NZ-00509194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1999; 99AU-00004907
28-MAR-2000; 2000AU-00006520
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                                                                   AAI64448 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-431058/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koelliker R,
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                                                                                                                                                                                       SSR motif #8.
                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                               23-NOV-2001
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RESULT 299 AAI64456,

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Gaps

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.

Claim 8; Page 9; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism

Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;

Gaps ; 0 0.5%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 4.4e+02; 1; Indels 0; Mismatches Matches 21; Conservative Best Local Similarity Query Match

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2823 TATATACATATATATATA 2844 쉽 ઠ

AAL50669 standard; DNA; 22

ВЪ

16-JAN-2003 (first entry) AAL50669;

Human uridine diphosphate glucuronosyltransferase gene polymorphism #3.

Human, polymorphism, TA repeat, ds, UGT, thymidine-adenine repeat, uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1, drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens.

US2002115097-A1.

22-AUG-2002

01-FEB-2002; 2002US-00061693

99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Ratain MJ; Rienzo AD, Iyer L,

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.

Claim 8; Page 9; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug denages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that

are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism ន្តដ្ឋប្រ

Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;

Gaps ö Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02; 0; Mismatches 1; Indels 0.5%; Query Match 0.5 Best Local Similarity 95.5 Matches 21, Conservative

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> g ò

RESULT 302 ABS97834/c

ABS97834 standard; DNA; 22

BP

ABS97834;

23-DEC-2002 (first entry)

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #42.

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

adrenergic receptor beta1; ADBR1; aryl bydrocarbon; AHR; MRP3; NRIL2;

A aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

Cyclooxgenase 2; COXZ; dazepam binding inhibitor; DBI; haematological;

My aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

Cyclooxgenase 2; COXZ; dazepam binding inhibitor; DBI; haematological;

My glutathione-Stransferase 12; GST12; histamine-N-methyl transferase;

My HADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;

WDP-glucuronosyl transferase 284; UDP-glucuronosyl transferase 2B7;

Wultidrug resistance 1; lactotransferin; orphan nuclear receptor;

W acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR4; CHMR5;

Altered drug metabolism; cardiovascular function; colorectal tumour;

Central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism

Homo sapiens.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB

Hall J;

Guida M,

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A2 (CYP4501A2), cytochrome P450 A2 (CYP4501A2), attachrome P450 O2E1 (CYP45002E1), adrenergic receptor betal (ADBR1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator arkley and acatepaths S (CTSS), cyclooxyenaes 2 (CCX2), diazespam binding inhibitor (DB1), epoxide hydrocylane 2 (EPHX2), 5-lipoxygenae activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl

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transferase (HNWT), (kallikrein 2) KLKZ, nicotinamide -N-methyl

transferase (NNWT), NADPH quinone oxidoreductase 2 (NQO2),

sulfotransferase theranciabile (STM), UDP-glucuronosyl transferase 284

(UGT2B4), UDP-glucuronosyl transferase 237 (UGT2B4), UDP-glucuronosyl

transferase (UGT2B4), unckinase receptor (UPA), multidrug resistance 1

transferase (UGT2B4), unckinase receptor (UPA), multidrug resistance associated protein 3

(MRD1), lactotransferrin (LTF), multidrug resistance associated protein 3

(MRD1), lactotransferrin (LTF), multidrug resistance associated protein 3

(MRD1), orphan nuclear receptor (NHZ12), or acetylcholine muscarinic creeptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2), CHMR3, CHMR4 or CHMR5) sequence. Creeptor 1. 1 in Kage markers for locating and characterising the genes that genes responsible for a variety of disorder-related correction are responsible for specific traits within the genome and eventually care responsible for their e.g., overexpression, constitutive correction or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the golymorphic sequences contained in CYP4501A1, CYPP4501A2, CARNY, EPHX2, GST12, NNMT, NOO2, NRI12, STM, UGT2B4, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for acted to screen for altered cardiovascular function, in COX2 for altered central cused to screen for altered cardiovascular function, in COX2 for altered cuscoptibility to colorectal tumours, in DBI or CHMR1 for altered serine concerned tumours, in DBI or CHMR1 for altered serine immunological tunction, in CHMR3, CHMR4 or CHMR3 for altered central and concerned tumours, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR3 for altered series and concerned to altered series and concerned tumours, in LTF for altered series and concerned tumours and concerned tumours of the invention many concerned to the invention of the invention many concerned to the invention of the invention or concerned 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene typing; polymorphic microsafellite 1061; FML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
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55.5%; Pred. No. 4.4e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 10 A; 10 C; 1 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphic DNA sequence of the invention
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Best Local Similarity
Matches 21; Conserv
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR captemplate a DNA semple one DNA region of (I) that includes PML, using a template a DNA semple containing at least one segment of (I); and cast template a DNA semple containing at least one segment of (I); and cast template a DNA semple containing at least one segment of (I); and cast template a DNA semple containing (M2) microsatellite markers (MM) for a method of determining (M2) microsatellite markers (MM) for a method of datase, associated with a gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to disease and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and methods at a such diseases, and because that encode milk proteins, malignant hyperthermia syndrome; quicker and barmones or transcription factors. The method is simpler, quicker and contains a prion protein polymorphic microsatellite marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyping genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining
Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep; microsatellite; PCR; primer; ss.
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                                                                                   German.
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                                                                                     Claim 9; Page 50; 64pp;
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                                                                                                                                                                                                                                                                                                                                                                                                             consensus sequence.
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Best Local 9
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the leagth of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion protein (PrP) comprising a polymorphic microsatellite locus. The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter. Human uridine diphosphate glucuronosyltransferase gene polymorphism #4. Gaps Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity. ö 0.5%; Score 20.4; DB 1; Length 22; 1; Indels Seguence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other; Pred. No. 4.4e+02; 0; Mismatches 2318 TGTGTGTGTGTGTGCGTGTG 2339 22 TGTGTGTGTGTGTGTGTGTGT 1 Claim 8; Page 9; 13pp; English Ratain MJ AAL50670 standard; DNA; 24 BP. 01-FEB-2002; 2002US-00061693 95.5%; (first entry) 21; Conservative (ARCH-) ARCH DEV CORP. Rienzo AD, Iyer L, WPI; 2002-740095/80. Local Similarity US2002115097-A1 Homo sapiens 16-JAN-2003 22-AUG-2002 AAL50670; Query Match 305 Matches \$ ઠ g

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are glucuronidated by UGT. The present DNA sequence represents a UGT gene
TA repeat polymorphism
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                                                              0.5%; Score 20.4; DB 1; Length 24; al Similarity 95.5%; Pred. No. 4.9e+02; 21; Conservative 0: Minmarch
                                                           Sequence 24 BP; 12 A; 0 C; 0 G; 12 T; 0 U; 0 Other;
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Matches 21; Conserv
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AAL50670/c
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RESULT 307

US2002115097-A1

AAL50671;

AAL50671

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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
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/note= "thiophosphate backbone"
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(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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*tag=
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
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uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
drug dosage optimisation; xenobiotic sensitivity.
                                                                                                                                                                              Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                           AAL50671 standard; DNA; 26
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Best Local Similarity 95.5
Matches 21; Conservative
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RESULT 308

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Gaps

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WPI; 2002-740095/80.
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                                                                                                                          (DDN) molecule, ODN 21, including decoyuridine monophosphates. The invention is based on the discovery that ODNs containing decoyuridine residues (U-ODNs) have an immunostimulatory effect comparable to, or innumbers (U-ODNs) have an immunostimulatory effect comparable to, or innumbers of specific T cells to a given antigen. The U-ODNs do not induce the systemic production of pro-inflammatory cytokines and, in contrast to CQG ODNs, are not dependent on a specific motif or a palindromic sequence. Use of a U-ODN for the preparation of a vaccine is claimed. Combining the U-ODN with an antigen strongly increases the potential of the antigen to raise the protection/immune response of a vaccinated individual. An example of the invention demonstrated the generation of a specific immune response against a melanoma-derived peptide (see
                                                                                                                  The present sequence is that of a thiosubstituted oligodeoxynucleic acid
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                                                    New oligodeoxynucleic acid molecules useful for the preparation of
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(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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 Schmidt W;
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                                                                                        Example 7; Page 31; 57pp; English
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Schellack C,
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                        WPI; 2003-183880/18
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The present sequence is that of a thiosubstituted oligodeoxynucleic acid (ODN) molecule, ODN 21, including deoxyuridine monophosphates. The invention is based on the discovery that ODNs containing deoxyuridine residues (U-ODNs) have an immunostimulatory effect comparable to, or in many instances greater than, ODNs containing CpG motifs, producing higher the systemic production of pro-inflammatory cytokines and, in contrast to CpG ODNs, are not dependent on a specific motif or a palindromic CpG ODNs, are not dependent on a specific motif or a palindromic Combining the U-ODN for the preparation of a vaccine is claimed. Combining the U-ODN with an antigen strongly increases the potential of the antigen to raise the protection/immune response of a vaccinated individual. An example of the invention demonstrated the generation of a specific immune response against a melanoma-derived peptide (see
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uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1,
drug dosage optimisation; xenobiotic sensitivity.
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Pred. No. 5.4e+02;
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Example 7; Page 31; 57pp; English.
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Local Similarity 95.5%;
Gs 21; Conservative
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The present invention relates to identifying a rice variety as amplification genetic marker and identifying whether test rice variety is any one of the 32 rice varieties e.g., Kasalath, breath which came or Alayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22, Nihonbare. The method is useful for identifying rice variety and identifies excellent rice variety. The present sequence represents a base containing SSR sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying rice variety using base sequence containing SSR sequence and amplifying genetic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 0.5%; Score 20.4; DB 1; Length 28; Local Similarity 95.5%; Pred. No. 5.8e+02; les 21; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                              rice variety; amplification genetic marker; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
(HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 50; SEQ ID NO 13; 30pp; Japanese.
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                              ADK61709 standard; DNA; 28
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                                                                         ADX61709;
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ADK61709/c
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RESULT 313
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individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
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ilarity 95.5%; Pred. No. 5.88+02;
Conservative 0; Mismatches 1; Indels
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0.5%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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                                                                               Sequence 28 BP; 14 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
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Best Loca Matches

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AAL50672;

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Homo

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Gaps

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Identifying rice variety using base sequence containing SSR sequence and amplifying genetic marker.
        HOKKAIDO GREEN BIO KENKYUSHO KK
                                                                      Claim 50; SEQ ID NO 13; 30pp; Japanese.
(HOKU-) HOKUREN NOGYO KYODO KUMIAI
                         WPI; 2004-003560/01
        (HOKK-)
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ö The present invention relates to identifying a rice variety as amplification genetic marker and identifying whether test rice variety is any one of the 32 rice varieties e.g., Kasalath, breath which came or Hayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22, Nihombare. The method is useful for identifying rice variety and identifies excellent rice variety. The present sequence represents a base containing SSR sequence of the invention. Gaps ; 0 Length 28; 1; Indels Sequence 28 BP; 14 A; 0 C; 0 G; 14 T; 0 U; 0 Other; Score 20.4; DB 1; Pred. No. 5.8e+02; 0; Mismatches 0.5%; 21; Conservative Sest Local Similarity Query Match Matches

2823 TATATATACATATATATATA 2844 28 TATATATATATATATATATA 7 ઠે 원

ACIS8589 standard; DNA; 25 13-OCT-2003 (first entry) ACI58589; RESULT 315
AC158518/C
AC158518
XX
XX
AC AC15851
XX
DT 13-OCT
XX
DE Human 1
XX
Cross-1
XX

BP.

Human microarray DNA oligonucleotide SEQ ID NO 58580.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1

05-JUN-2003.

15-MAR-2002; 2002US-00098263

16-MAR-2001; 2001US-0276759P

(AFFY-) AFFYMETRIX INC

Mittmann MP;

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene. WPI; 2003-567953/53.

Claim 1; SEQ ID NO 58580; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mesmatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises

nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html hybridising at least one or more nucleic acids to at least two or more

Sequence 25 BP; 5 A; 3 C; 7 G; 10 T; 0 U; 0 Other;

Gaps ö Length 25; 3; Indels Score 20.2; DB 1; Pred. No. 5.4e+02; 0; Mismatches 0.5%; Query Match 0.5 Best Local Similarity 88.0 Matches 22; Conservative

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ACIS8588 standard; DNA; 25 RESULT 316 ACI58588/

BP

ACI58588;

(first entry) 13-OCT-2003 Human microarray DNA oligonucleotide SEQ ID NO 58579.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1

05-JUN-2003.

15-MAR-2002; 2002US-00098263

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58579; 9pp; English

acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acids to at least two or more nucleic acids to at least two or more nucleic acids to a nucleic acid The invention discloses a microarray comprising a plurality of nucleic

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probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific blot hybridisation to identify or detect the sequence or specific by primer extensions or in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
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Query Match 0.5%; Score 20.2; DB 1; Length 25; Best Local Similarity 88.0%; Pred. No. 5.4e+02; Matches 22; Conservative 0; Mismatches 3; Indels Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other; 3763 ACTITICGAAAATAAAGACACCIG 3787

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Gaps

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25 ACTTACCGAAAAGTTAAGACACCTG 1 à

ADB38952 standard; DNA; 25 RESULT 317 ADB38952

H.

ADB38952;

(first entry) 04-DEC-2003 Human interleukin 1RNic single nucleotide polymorphism (SNP) region 21.

interleukin 1 gene cluster; IL-1 gene cluster; IL-1 like gene; IL-1 locus; single nucleotide polymorphisms; SNP; IL-1 haplotype; inflammatory disease; IL-1 associated inflammatory phenotype; primary inflammatory cytokine; IL-1 alpha; IL-1 beta; ILIA; ILIB; ILIRN; anti-inflammatory; chromosome 2q13; anti-inflammatory; chromosome 2q13; anti-inflammatory; antiarthritic; hepatotropic; osteopathic; gene therapy; arthritis; hepatic inflammation; chronic obstructive pulmonary disease; osteoporosis; ds; IL-IRNic.

Homo sapiens

/standard_name= "Single nucleotide polymorphism" Location/Qualifiers replace(11,T) /*tag= a variation

WO2003064600-A2

07-AUG-2003

27-JAN-2003; 2003WO-US002232.

25-JAN-2002; 2002US-0351951P

(INTE-) INTERLEUKIN GENETICS INC.

Kornman K, Kolpin MR, Hsieh C, Nicklin M, Duff G, Aziz N;

Govindaraju R;

WPI; 2003-618359/58.

Determining whether the subject has or is predisposed to developing a disease or condition that is associated with an IL-1 inflammatory haplotype, useful for treating inflammation, comprises detecting an IL-1 allele

Claim 18; Fig 10A; 96pp; English.

c. This invention relates to the identification and use of general including the structure and organisation of movel IL-1 like genes found within the the structure and organisation of movel IL-1 like genes found within the the structure and organisation of movel IL-1 like genes found within the IL-1 locus as well as polymorphisms (single nucleotide polymorphisms; C. SNPs) and associated haplotypes within these genes. The invention also relates to the use of these polymorphisms and haplotypes for predicting including the structure and specificated to the use of these polymorphisms and haplotypes for predicting inflammatory disease) and for treating IL-1 associated inflammatory phenotypes. IL-1 is a primary inflammatory cytokine and has been implicated in mediating both acute and chronic pathological inflammatory completed in mediating both acute and chronic pathological inflammatory completed in mediating molecules, IL-1 alpha and IL-1 beta, are encoded by genes ILhA and ILIBA, an anti-inflammatory non-encodes IL-1 receptor antagonist (IL-1RA), an anti-inflammatory non-encodes IL-1 ceceptor antagonist (IL-1RA), an anti-inflammatory non-encodes IL-1 alpha and IL-1 gene cluster is on the long arm of chromosome (IL-1RA may have antiinflammatory, antiarthritic, hepatotropic or of proteins may be useful for gene therapy. The methods and polymucleotide proteins may be useful for gene therapy. The methods and polymucleotide proteins may be useful for diagnosing and treating an inflammatory chicageses, for example arthritis, hepatic inflammation, chronic obstructive in the and including a single nucleotide polymorphism of the including a single nucleotide polymorphism of the including and including a single nucleotide polymorphism of the including and including a single nucleotide polymorphism of the including and including a single nucleotide polymorphism of the including and including a single nucleotide polymorphism of the including and including a single nucleotide polymorphism of the including and present sequences This invention relates to the identification and use of genetic invention in the human ILIRN gene. 8888888888888888888888888888888

Score 20.2; DB 1; Length 25; Sequence 25 BP; 0 A; 1 C; 11 G; 13 T; 0 U; 0 Other; .5%; Query Match Best Local Similarity 88.09 ****rheg 22; Conservative

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Gaps

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3; Indels

5.4e+02

Pred. No.

88.0%;

0; Mismatches

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RESULT 318 AAX34894/

AAX34894;

ВР

AAX34894 standard; DNA; 20

(first entry) 28-JUN-1999 PCR primer used to amplify FGFR3.

Immortalized human hair papila cell; HPC; screening; hair growth; SV40 viral Large T-antigen gene; deleted replication initiation point; hair growth stimulating agent; PCR primer; ss.

Synthetic.

JP11089565-A.

06-APR-1999.

97JP-00271927. 19-SEP-1997; 97JP-00271927 19-SEP-1997;

(SHIS) SHISEIDO CO LTD.

WPI; 1999-281045/24.

Immortalised human hair papila cells used for evaluation of hair growth agent - are prepared by transformation of human hair papila cells with gene with deleted replication initiation point.

Example 2; Page 7; 23pp; Japanese.

The specification describes the preparation of immortalized human hair papila cells (HPC). The method comprises transformation of HPC with an SV40 viral Large T-antigen gene with deleted replication initiation

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point. The immortalized HPC can be used in a screening method for a hair growth agent, by culture of immortalized HPC in the presence of a substance to be rested and observation of the growth of the immortalized HPC. HPC is also used in development of hair growth stimulating agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer used for detecting mutant fibroblast growth factor receptor 3.
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                                                                                                                                                                                                                                                                                                                                    Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                             of the invention
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of coloractal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                           /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                           Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothioate, ss.
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/note=_"2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not\overline{e} = "2 - methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                Human FGFR-3 antisense oligonucleotide, ISIS #125165.
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                                                                                                                                                                                                                                                                                                                                                       are 5-methylcytidines"
1. .5
/*tag= b
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                                BP
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                                AAD55461 standard; DNA; 20
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/*tag= c
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modified_base
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                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                  Synthetic.
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                                                                AAD55461;
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RESULT 320
                  AAD55461
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Length 20;

0.5%; Score 20; DB 1; Li 100.0%; Pred. No. 4.4e+02;

Query Match Best Local Similarity

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Gaps

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0; Indels

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02;

100.0%; Pred. wc.

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Local Similarity

Query Match Best Local & Matches 20 557 CCAACCAGACGGCGGTGCTG 576

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Gaps

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Length 20; Indels

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AAD55428;

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                 Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
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/note= "2'-methoxyethyl (2'-MOB) nucleotides"
16. .20
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                                                                                                                                                                                                                                                                                                                                                                                Human FGFR-3 antisense oligonucleotide, ISIS #125118.
Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
                                           Score 20; DB 1; L. Pred. No. 4.4e+02;
                                 0.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                          127 CTGTGCCACTTCAGTGTGCG 146
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/mod_base=
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                                                                                     Conservative
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                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                           AAD55435;
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                                                 Query Match
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AAD55435/c
                                                                                         Matches
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/note= "Phosphorothioate backbone; All cytidine residues
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                Indels
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                  Mismatches
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                                                          3690 CTTGGGGCCCAGTGCATGGT 3709
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/mod_base= OTHER
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Synthetic

Homo

Monia BP,

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Gaps

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/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human PGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                     Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                            1688 TGGCCCGGGACGTGCACAAC 1707
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Matches
                                                                                                                                                                                                                                                                                    RESULT 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
 patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note== "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                     0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Human FGFR-3 antisense oligonucleotide, ISIS #125135
                                                              Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
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/note= "2'-methoxyethyl (2'-MOE)
16. .20
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/mod base= OTHER
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                                                                                                      Local Similarity 100.
ses 20; Conservative
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Matches
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AAD55440/c
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molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR.3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR.3 such as developmental disorders or conditions. hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                            Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human FGFR-3 antisense oligonucleotide, ISIS #125190.
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100.0%; Pred. No. ...
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/mod_base= OTHER
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JUK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breach or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
116. .20
/*tag= c /*tag= c
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100.0%; Pred. No: 4.4e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                  Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                            471 CAAGITIGGCAGCATCCGGC 490
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/*tag= a
/mod_base= OTHER
      Claim 3; Page 79; 120pp; English.
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/note= "2
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Best Local Similarity 100.
Matches 20; Conservative
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Monia BP,
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                                                                         The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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                                                      Claim 3; Page 79; 120pp; English.
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                                  disorder
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/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_bass= OTHER
/mote= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2 -methoxyethyl (2'-MOB) nucleotides"
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100.0%; Pred. No. 4.46+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                   Claim 3; Page 79; 120pp; English.
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ID AAD55432 standard; DNA; 20
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Best Local Similarity 100.
Matches 20; Conservative
Wyatt JR;
                                                     WPI; 2003-313244/30.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (PGF) receptor 3 (also known as FGRR-3, ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRR-3 such as developmental disorders or the hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, broadents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to chucidate expression in differential and/or combinatorial analyses to chucidate expression. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1. .5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                          Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
/*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human FGFR-3 antisense oligonucleotide, ISIS #125157.
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                                                                                                                                                                                                                                                            Claim 3; Page 79; 120pp; English.
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                            06-SEP-2002; 2002WO-US028549.
                                                          10-SEP-2001; 2001US-00953047.
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                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                       Monia BP, Wyatt JR;
                                                                                                                                                       WPI; 2003-313244/30.
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20-MAR-2003.
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                                                                                                                                                                                                                                   The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRP-3) ACH, JTK4 and CRK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRP-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGPR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotiģes"
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/note== "2'-methoxyethyl (2'-MOE) nucleotides'
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                               Claim 3; Page 78; 120pp; English.
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      10-SEP-2001; 2001US-00953047.
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/*tag= b
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Best Local Similarity 100.
Matches 20; Conservative
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                                      (ISIS-) ISIS PHARM INC.
                                                                       Monia BP, Wyatt JR;
                                                                                                     WPI; 2003-313244/30.
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0; Indels

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02;

100.0%; Pred.

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRE-3) ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophlylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression
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/note= "Phosphorothioate backbone; All cytidine residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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                                                                             /note= "2 -methoxyethyl (2'-MOE) nucleotides"
"2'-methoxyethyl (2'-MOE) nucleotides'
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense oligonucleotide targetted to human FGFR-3
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                                                            /mod_base= OTHER
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3, ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, crevical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 4.4e+02;
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100.0%; Pred. No. ..
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AAD55456/
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3. ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, broagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues of antisense oligonucleotide targetted to human FGFR-3
                /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
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developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                                                                                                                        /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                      are 5-methylcytidines"
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/note= "2
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                 mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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              are 5-methylcytidines"
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues.
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/note= "Phosphorothioate backbone; All cytidine residues
                    developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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  Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 4.4e+02;
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/note= "2'-methoxyethyl
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                                                                                                                                   /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides'
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/mod base= OTHER
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/note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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                                                                                                                                  Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                  Human FGFR-3 antisense oligonucleotide, ISIS #125209
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AAD55503 standard; DNA; 20
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                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                         Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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16. .20
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100.0%; Pred. No. 4.40+02;
tive 0; Mismatches 0; Indels
                                           Human FGFR-3 antisense oligonucleotide, ISIS #125193.
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             07-AUG-2003 (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
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modified_base
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Synthetic.
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Monia BP,

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                                                      The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRR-3 such as developmental disorders or the hyperprise of coloredtal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to chucidate expression in differentian and/or combinatorial analyses to chucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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Claim 3; Page 79; 120pp; English.
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RESULT 337 AAD55503/c

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGPR-3, ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues.
                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                                                                                                     Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compound targeted to a nucleic acid molecule encoding fibroblast
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "2 -methoxyethyl (2'-MOE) nucleotides'
                                                                                                                         Human FGFR-3 antisense oligonucleotide, ISIS #125146.
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 78; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           base= OTHER
                             AAD55445 standard; DNA; 20 BP.
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                                                                                          07-AUG-2003
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RESULT 338
                AAD55445,
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or
                                                                                                                                                                                                                                                                                                      /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                         Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                       (2'-MOE) nucleotides"
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                                                                                                                            Human FGFR-3 antisense oligonucleotide, ISIS #125164.
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/note= "2'-methoxyethy1 (7
16..20
/*teg= c
/mod_base= OTHER
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                            AAD55460 standard; DNA; 20
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/*tag= b
                                                                                            (first entry)
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                                                            AADS5460;
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RESULT 339
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               AAD55460/
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Gaps ö

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; Live 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 20; Conservative

Query Match

Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 0 Other;

sequence is an

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WO2003023004-A2.
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AAD55490/c
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                                                                                                                                                                                                   Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                  nucleotides
             Length 20;
           0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.48+02;
ive 0; Mismatches. 0; Indels
                                                                                                                                                                                 Human FGFR-3 antisense oligonucleotide, ISIS #125166.
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/note= "2'-methoxyethyl (2'-MOE)
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                                   Conservative
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                          Similarity
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modified_base
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                                                                                                                                                                                                                                                            Synthetic.
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                  Query Match
                            Best Local
                                                                                                          340
                                     Matches
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AAD55462/
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16..20
/*reg= CTHER
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                                                                                                                                         Length 20;
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They are also useful in antisense therapy. The present antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human FGFR-3 antisense oligonucleotide, ISIS #125196.
                                                                                Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                      0.5%; Score 20; DB 1; Lo
100.0%; Pred. No. 4.4e+02;
:ive 0; Mismatches 0;
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/*tag= a
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                                                                                                                                                                                                                                                      3767 TCCGAAAATAAAGACACCT 3786
                                                                                                                                                                                                                                                                                         20 TCCGAAAATAAAGACACCT
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Best Local Similarity
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Location/Qualifiers
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Matches
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AAD55447/C
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are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tool in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                             0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                              Human FGFR-3 antisense oligonucleotide, ISIS #125145.
                                                                         Sequence 20 BP; 7 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                     100.0%; Prec. ...
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                                                                                                                                       929 TGTTCATCCTGGTGGTGGCG 948
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                                                                                                                                                                                                                                                                                                                                                                                                           base= OTHER
                                                                                                                                                       20 TGTTCATCCTGGTGGTGGCG 1
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modified_base
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                     AAD55444;
                                                                                              Query Match
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                                                                                                                                                                                           RESULT
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as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1. .5 /
/*tag= b
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developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3; ACH, JTK4; CEK2; cancer, phosphorothioate, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/*tag= c
/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 20; 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                     antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 6 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
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Monia BP,
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                                                                                                                                                                                                                                                                                                     RESULT 345
AAD55479/c
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Matches
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                  The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3). ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRF-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                 Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                       Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                               Human FGFR-3 antisense oligonucleotide, ISIS #125161.
                                                                                                                                                     Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note = "2'-methoxyethyl (2'-MOE)
                                                                                                                                                                                    Best Local Similarity 100.0%; Pred. No. 4.4 Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                  2798 CTATAATAGATGCTGTA 2817
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'mod base= OTHER
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     Claim 3; Page 79; 120pp; English.
                                                                                                                                                                                                                              20 CTATAATAGATGCTGTGTA 1
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*tag=
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                                                                                                                                                                                                                                                                      RESULT 344
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, broagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to clucidate expression in differentian and/or combinatorial analyses to clucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/mod= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothioate, 88.
growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/*tag= c
/mod_bag= OTHER
/mod_e= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-WOE) nucleotides"
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                                                                                                                            Claim 3; Page 79; 120pp; English.
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*tag=
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Best Local Similarity
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modified_base
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20-MAR-2003
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                                                                                                       The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorated. bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Phosphorothioate backbone, All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                             Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides
                                                                                                                                                                                                                                                                         0.5%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 4.4e+02; ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                       110 GGCTCACGCAGCGCGTACTG 129
                                                                                    Claim 3; Page 79; 120pp; English.
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Best Local Similarity 100.
Matches 20; Conservative
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          WPI; 2003-313244/30
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AAD55481/c
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/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                       Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/*tag= b
/mod_base= OTHER
16. .20
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Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                              Example 15; Page 79; 120pp; English.
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100.0%;
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Best Local Similarity 100.
Matches 20; Conservative
(ISIS-) ISIS PHARM INC.
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                                                        Wyatt JR;
                                                                                                                 WPI; 2003-313244/30.
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                           The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, teagents, they are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/noce= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                       Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FGFR-3 antisense oligonucleotide, ISIS #125154.
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/mod_base= OTHER
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/mod_base= OTHER
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AAD55452 standard; DNA; 20 BP.
                      06-SEP-2002; 2002WO-US028549.
                                                    10-SEP-2001; 2001US-00953047
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                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                  Wyatt JR;
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, WITK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, brospone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
                                                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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06-SEP-2002; 2002WO-US028549
                                                                          10-SEP-2001; 2001US-00953047
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07-AUG-2003 (first entry)
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Best Local Similarity 100.
Matches 20, Conservative
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/mod_base= OTHER
/mod="Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                      /mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense oligonucleotide targetted to human FGFR-3
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            /*tag= c
/mod_base= OTHER
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                                                                                                         06-SEP-2002; 2002WO-US028549
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Best Local Similarity
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modified base
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/*tag= c
/*tag= c
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//note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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WO2003023004-A2
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Synthetic.
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
              /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                                                                                          Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                                                             /note= "2'-methoxyethyl (2'-MOE) nucleotides"
16...20
                                                                                                                    /note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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                                   are 5-methylcytidines"
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                                                                                                             /mod_base= OTHER
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AAD55438 standard; DNA; 20 BP.
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Best Local Similarity 100.
Matches 20, Conservative
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                                                          *tag=
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                                                                       /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 4.4e+02;
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Location/Qualifiers
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/mod base= OTHER
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Best Local Similarity 100.
Matches 20; Conservative
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/*tag= a /mod base= OTHER /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers

modified base

sapiens

Ношо

Synthetic.

/mod_base= OTHER 10ce= "2'-methoxyethyl (2'-MOE) nucleotides" (-20 '*tag= c ______

1..5 /*tag= b

modified base

modified base

/mod_base= OTHER /note= "2 -methoxyethyl (2'-MOE) nucleotides"

WO2003023004-A2

20-MAR-2003

Human, antisense, fibroblast growth factor receptor 3, prophylaxis, developmental disorder, hyperproliferative disorder, antisense therapy, FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothioate, ss.

Human FGFR-3 antisense oligonucleotide, ISIS #125153.

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophlaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3.
                                                                                                                                                                 /note= "Phosphorothioate backbone; All cytidine residues
developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                               Location/Qualifiers
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modified base
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                                                   Homo sapiens
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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2211 CCAACAATGTGAGGGGTCCC 2230

Best Local Similarity 100. Matches 20; Conservative

20 CCAACATGTGAGGGTCCC

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AAD55451 standard; DNA; 20 BP

RESULT 354 AAD55451/c

07-AUG-2003 (first entry)

AAD55451;

Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental

disorder.

10-SEP-2001; 2001US-00953047. 06-SEP-2002; 2002WO-US028549.

(ISIS-) ISIS PHARM INC Monia BP, Wyatt JR; WPI; 2003-313244/30. RESULT 356

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGPR-3) ACH, TYR4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of coloractal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophlaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                Human, antisense, fibroblast growth factor receptor 3; prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH, JTK4; CEK2; cancer; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                     Human FGFR-3 antisense oligonucleotide, ISIS #125156
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                                           (first entry)
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Best Local Simi
Matches 20;
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                                         07-AUG-2003
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              AAD55454;
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/mod_base= OTHER /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers

/*tag= b /mod base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. 20

/*tag= c /mod_base= OTHER /note= "2 -methoxyethyl (2'-MOE) nucleotides"

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The invention relates to antiense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known ass FGFR-3; ACH, JUTK4 and CEK2) to inhibit its expression. Antiesnes compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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//mod base= OTHER
/mod base= OTHER
/mode= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                    Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "2 -methoxyethyl (2'-MOE) nucleotides"
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                        Human FGFR-3 antisense oligonucleotide, ISIS #125191.
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                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/mod_base= OTHER
            BP.
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          AAD55485 standard; DNA; 20
                                                                             (first entry)
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                                                                                                                                                                                                                                   Synthetic.
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AAD55485,
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Gaps ö

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels

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Conservative

Similarity

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Gaps

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Length 20; Indels

0.5%; Score 20; DB 1; Le llarity 100.0%; Pred. No. 4.4e+02; Conservative 0; Mismatches 0;

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Best Local Similarity
Matches 20; Conserv
  Query Match
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are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                        Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                        Human FGFR-3 antisense oligonucleotide, ISIS #125195
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GTGGGCCCGGACGCCACACC 686
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                                 20 GTGGGCCCGGACGGCACACC
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Synthetic.
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667
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AADS 55

AADS
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit tes expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial mallyes to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an

antisense oligonucleotide targetted to human FGFR-3 Sequence 20 BP; 6 A; 9 C; 5 G; 0 T; 0 U; 0 Other;

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or byperporliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breasf or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial nantyes to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                               Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/*tag= b
/mod_base= OTHER
16. .20
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                   Human FGFR-3 antisense oligonucleotide, ISIS #125198.
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825 CTCTGCGTGGTGGTGC 844
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                                                                                                          AAD55492 standard; DNA; 20
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modified_base
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
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reagents, therapeutics, prophylaxis, kits and diagnostics, and as tool in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                     Gaps
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                 0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FGFR-3 antisense oligonucleotide, ISIS #125116.
                                                                                                                 Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                             197 CTGAGGACACAGGTGTGGAC 216
                                                                                                                                                                                                                                                CTGAGGACACAGGTGTGGAC 1
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Best Local Similarity 100.
Matches 20; Conservative
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*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                Gaps
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/note= "2'-methoxyethyl (2'-MOB) nucleotides"
16. .20
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                                                                                              Length 20;
                                                                                                                                0; Indels
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                      antisense oligonucleotide targetted to human FGFR-3
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                                                          Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                          0.5%; Score 20; DB 1; Lv
100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                        1434 GCTGGTGGAGTACGCGGCCA 1453
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/mod_base= OTHER
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                                                                                                      Query Match
Best Local Similarity
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Monia BP,

RESULT 35

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disorder

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Gaps

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0; Indels

0.5%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 4.4e+02;

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 20; Conservative
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compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                     ch 0.5%; Score 20; DB 1; Length 20; 1 Similarity 100.0%; Pred. No. 4.4e+02; 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                     antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                       Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
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1. .20
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/mod_base= OTHER
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/mod_base= OTHER
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                                                                                                                                                                                                                        Best Local Similarity
Matches 20, Conserv
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Synthetic.
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/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
arc 5-methylcytidines"
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developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH, JTK4; CEK2; cancer, phosphorothioate; ss.
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-methoxyethyl (2'-MOE) nucleotides"
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100.08; Pred. ...
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/note= "2'-methoxyethyl
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                                                                                                                           2572 GGGACATCACAGGGTGCGCT 2591
                                                                                                                                                                                               20 GGGACATCACAGGGTGCGCT 1
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/note= "2 -
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Claim 3; Page 78; 120pp; English

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WPI; 2003-313244/30.
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                                                 The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, theraputics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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                                                                                                                                                                                                                                                                                                                                                                                                           Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3; ACH, JTK4, CEK2, cancer, phosphorothloate, ss.
                                                                                                                                                                                                                                   Gaps
   receptor and for treating an animal having cancer or developmental
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                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Human FGFR-3 antisense oligonucleotide, ISIS #125152
                                                                                                                                                                    antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                        Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                           ch 0.5%; Score 20; DB 1; Le 1 Similarity 100.0%; Pred. No. 4.4e+02; 20; Conservative 0; Mismatches 0;
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/*tag= a
/mod_base= OTHER
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/note= "2 -metho
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                                  Claim 3; Page 79; 120pp; English.
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Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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/note= "2 -methox
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/mod_base= OTHER
                                                                                                                                                                     Claim 3; Page 79; 120pp; English.
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AAD55480 standard; DNA; 20 BP.
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/*tag= b
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hes 20; Conservative
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1. .5
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                                                                                                                                                                                                               Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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  06-SEP-2002; 2002WO-US028549.
                                        10-SEP-2001; 2001US-00953047.
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/*tag=
                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                              Monia BP, Wyatt JR;
                                                                                                                                                                        WPI; 2003-313244/30.
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH, JTK4, CEK2, cancer, phosphorothioate, 88.
                                                                                                                         Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
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Matches 20; Conservative
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*tag=
(ISIS-) ISIS PHARM INC.
                                             Wyatt JR;
                                                                                   WPI; 2003-313244/30
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                                          Monia BP,
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/*tag= a
/mod_base= OTHER
/mod_e= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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                                                                                                                       06-SEP-2002; 2002WO-US028549.
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nes 20; Conservative
                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
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Matches
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developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH, JTK4; CEK2, cancer, phosphorothioate, ss.
                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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Pred. No. 4.4e+02;
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                                                                                           10-SEP-2001; 2001US-00953047.
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRPA.3 ACH, JUTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or byperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3; ACH, JTK4; CEK2; cancer, phosphorothioate, 88.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 4.4e+02;
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100.0%; Pred. No. *..
... 0; Mismatches
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3) ACH, "TK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
      /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                                                                                 /*tag= b
/mod_base= OTHER
/mod_base= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/mod base= OTHER
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AAD55502/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colocral, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                      /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                            not\overline{e} = "2 - methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
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/*tag= c
/mod_base= OTHER
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                                                                 modified base
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FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                 Synthetic
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Matches
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                                  /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy;
                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                         'note= "2 -methoxyethyl (2'-MOE) nucleotides'
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                                                                   are 5-methylcytidines"
             Location/Qualifiers
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               Key
modified base
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or
                                                                                                                                                         /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
:ive 0; Mismatches 0;
                                                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 78; 120pp; English.
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ID AAD55441 standard; DNA; 20
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Homo sapiens
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/mod_base= OTHBR
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                    Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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16. .20
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                                                                    Human FGFR-3 antisense oligonucleotide, ISIS #125150.
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Matches 20; Conservative
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modified_base
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                                                                                                                                                                                                   Synthetic.
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 AAD55448;
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                                                                                                                                                                                                                                /note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                             Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3, ACH, JTK4; CEK2, cancer, phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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16. .20
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Human FGFR-3 antisense oligonucleotide, ISIS #125142.
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/mod base= OTHER
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                                                                                                        Homo sapiens
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                                                                                                                          Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperporliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense oligonucleotide targetted to human FGFR-3
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AAD55448 standard; DNA; 20 BP

RESULT 373 AAD55448/c ID AAD554 XX

Matches

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20 TATTTGTTGTAGACTTAACA

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGRR-3) ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                            /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                     Human, antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                         Human FGFR-3 antisense oligonucleotide, ISIS #125207
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AADS5501 standard; DNA; 20
                                                             (first entry)
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modified_base
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRPA.3 AGH, JUTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeuties, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to abucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                                                                                                      Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                         Human FGFR-3 antisense oligonucleotide, ISIS #125200.
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/mod base=
                               AAD55494 standard; DNA; 20
                                                                                               (first entry)
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*tag=
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                                                                                                                                                                                                                                           Synthetic.
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                                                                 AAD55494;
RESULT 375
                    AAD55494/
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0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 20; Conservative

Query Match

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Gaps ; 0

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AAD55491;
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3; ACH, JTK4; CEK2; cancer; phosphorothioate, ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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16. .20
   Pred. No. 4.4e+02;
   ilarity 100.0%; Pred. No. 4.4
Conservative 0; Mismatches
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/mod_base= OTHER
                                                                                                                                              20 TACCGTGACGTCCACCGACG
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Best Local Similarity
Matches 20; Conserv
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                     Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                       0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
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AAD55491 standard; DNA; 20
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Best Local Similarity 100.'
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Synthetic.
Sequence 20
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Gaps .; 0

Length 20; 0; Indels

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/note= "Phosphorothicate backbone; All cytidine residues are 5-methylcytidines"
Appropriated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0;
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*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-313244/30.
                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD55496;
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                                                                                                                                                                                                                                                                                                                                                                        RESULT 379
AAD55496/c
                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
                    in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /\text{not}\overline{e}= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotides
                                                                                                                                            0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FGFR-3 antisense oligonucleotide, ISIS #125199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "2'-methoxyethyl (2'-MOE)
                                                                                                            Sequence 20 BP; 0 A; 7 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                      1260 CAAGGACCGGCCGCCAAGC 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 79; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                AAD55493 standard; DNA; 20
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                                                                                                                                                                  Local Similarity 100.
nes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monia BP, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-313244/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                   AAD55493;
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                RESULT 378
AAD55493/c
                                                                                                                                                                                          Matches
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nucleotides"

vivlemore401-10.rng

BP.

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The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                  human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 1049; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                        (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                       11-DEC-2001; 2001JP-00377637.
                                                                                                                                                                                                                                                                                                                        11-DEC-2001; 2001JP-00377637
                                  ADH93212 standard; DNA; 20
                                                                                                                                    Human gene PCR primer #57.
                                                                                                   (first entry)
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                                                                                                                                                                                                                        Homo sapiens.
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                                                                    ADH93212;
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   RESULT 381
                   ADH93212
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breact or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences which can be used to detect single nucleotide polymorphisms (SNPB). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises isolated human gene sequences and PCR primer
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; ss; PCR; primer.
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                                                                                                                                                                                                                                                     Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                         2557 CTGCCTTTGCACCACGGGAC 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 TGGAGAACAAGTTTGGCAGC 483
                                                                                                                                                                                                                                                                                                                                           20 CTGCCTTTGCACCACGGGAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene PCR primer #65.
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                                                                                                                                                                                                                                                                                       20; Conservative
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                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Matches
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Gaps
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                                                                                                                                                                                                                                              human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; 88; PCR; primer.
Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                     1824 GCTCTGGGAGATCTTCACGC 1843
                                                                  1 GCTCTGGGAGATCTTCACGC 20
                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2001; 2001JP-00377637
                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2001; 2001JP-00377637
                                                                                                                                  ADH93215/c
ID ADH93215 standard; DNA; 20
                                                                                                                                                                                              22-APR-2004 (first entry)
                                                                                                                                                                                                                       Human gene PCR primer #60.
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1 TGGAGAACAAGTTTGGCAGC 20

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JP2002272474-A.
                                                        sapiens
                                                               24-SEP-2002.
                                              27-AUG-2003
                                                        Homo sapie
Synthetic.
                                          ACC79688;
                       Query Match
                          Matches
                                      RESULT
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WO2003083046-A2.
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30-MAY-2002;
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08-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                       ADK51119;
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                                                                                                                 Query Match
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epithelial cells in which it is judged that flat epithelial cells
ceptated from an organism can proceed to flat epithelial cancer when the
calsath base in fibroblast growth factor receptor (FGFR) gene of the cells
calsath base in fibroblast growth factor receptor (FGFR) gene of the cells
calsath base in fibroblast growth factor receptor (FGFR) gene of the cells
calsath cancer in the complete substance of treating agent for flat epithelial cancers in
which a candidate subtence of treating agent for flat epithelial cancer
calsath (exon 17) amino acid in FGFR3 gene is mutated from
which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from
candidate substance is selected by using the facts that
capterine and said candidate substance is selected by using the facts that
the 2128th base in the flat epithelial cell FGFR3 gene after the
che 2128th order to quanine and that the 697th amino acid of FGFR3
capterion returned to guanine as the indices. The method is used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                      The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                       Polymucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, fibroblast growth factor 3, FGF3, flat epithelial cell; cancer;
flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                             0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                         Claim 2; SEQ ID NO 1052; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                    462 CGTGGAGACAAGTTTGGCA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 6; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZERI ) ZERIA SHINYAKU KOGYO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACC79688 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                               20; Conservative
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                          WPI; 2003-819215/77.
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for the inspection of flat epithelial cells. The present sequence represents a PCR primer for human FGFR3, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Furtak K;
Spytek KA;
( M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
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                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                         0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.40+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                 Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NOVX protein-related PCR primer SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example C; SEQ ID NO 140; 433pp; English.
                                                                                                                                                                                                                                                                                                                       2188 CGGACGTGAAGGGCCACTGG 2207
                                                                                                                                                                                                                                                                                                                                                                                cedacercaaceccacree 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-00115479.
2002US-0370349P.
2002US-0370969P.
2002US-0372019P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 -WAY - 2002; 2002US - 0384543P.
03 -UUN - 2002; 2002US - 00166619.
15 -AUG - 2002; 2002US - 0040748P.
04 - NOV - 2002; 2002US - 002T828.
31 - MAR - 2003; 2003US - 00403161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK51119 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-812539/76.
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DNA preparation; 5' mRNA; linker synthesis; primer synthesis; gene regulation; gene expression; ss; tag. 5' mRNA DNA preparation method related tag DNA sequence #8

1 CCTACGTTACCGTGCTCAAG 20

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ADK70840 standard; DNA; 20

06-MAY-2004

ADK70840;

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                                                                                                                                                                                                                                                                                                      cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DW, Bento P, Boldog FL, Burgess CE, Casman SJ, Furtak K, Gorman L, Gould-Rothberg BE, Gunther E, Heyes MP, Li L, Spytek KA; Stone DJ, Zhong M, Malyankar UM, Edinger SR, Patturajan M;
                                  Gaps
                                ö
   Length 20;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
0.5%; Score 20; DB 1; Le
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                        Human NOVX protein-related PCR primer SegID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example C; SEQ ID NO 143; 433pp; English.
                                                                686 CCTACGTTACCGTGCTCAAG 705
                                                                                  1 CCTACGTTACCGTGCTCAAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-2002; 2002US-00115479.
08-APR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370569P.
12-APR-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0384543P.
03-JUN-2002; 2002US-0160619.
15-AUG-2002; 2002US-0160619.
04-NOV-2002; 2002US-0160619.
                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smithson G;
                                                                                                                                                                            20
                                                                                                                                                                                                                                           (first entry)
                                  Conservative
                                                                                                                                                                            ADK51122 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-812539/76.
                  Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                     WO2003083046-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothenberg ME,
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                            ADK51122;
    Query Match
                                                                                                                                             RESULT 385
                                                                                                                                                             ADK51122
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Harbers MT

Carninci P,

Hayashizaki Y,

(RIKE) RIKEN KK. (DNAF-) DNAFORM KK.

WPI; 2004-082194/08.

12-JUN-2003; 2003WO-JP007514. 12-JUN-2002; 2002JP-00171851. 12-AUG-2002; 2002JP-00235294.

WO2003106672-A2.

24-DEC-2003.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a method for preparing a DNA fragment corresponding to a nucleotide sequence of a 5' end of an mRNA. The method is useful for synthesising a nucleotide sequence to be used as a linker or primer and selectively collecting multiple nucleic acid fragments containing information on the nucleotide sequences at the 5' end of multiple mRNA in a sample. The method is also useful for identifying regions in the genome, which are required for gene regulation and gene expression. The present DNA sequence was used in an example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer #6, used for amplification of pear plant microsatellite DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Preparing DNA fragment corresponding to nucleotide sequence of 5' end region of mRNA, by preparing nucleic acid corresponding to nucleotide sequence of 5' end of mRNA, cleaving nucleic acid with restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pear plant, microsatellite DNA; DNA marker; species discrimination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 1 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; SEQ ID NO 40; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2319 GTGTGTGTGTGTGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK50766 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK50766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK50766/
EXEXEXEXE
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686 CCTACGTTACCGTGCTCAAG 705

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Gaps

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0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; ve 0; Mismatches 0; Indels

100.0%; Prec. nctive 0; Mismatches

20; Conservative

Matches

Local Similarity

Query Match

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The present invention relates to a new microsatellite DNA comprising a fully defined sequence of 389 base pairs as given in the specification. The microsatellite DNA can be used as a DNA marker effective for discriminating the species and grades, selecting useful species and isolating useful species and of a collection (ABK50761-ABK50766) of PCR primers used in the methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simple sequence repeat; SSR; single site amplification; SSA; disease;
                                                                                                                                                                                                             Microsatellite DNA of Pyrus, useful as DNA marker for discriminating
                                                                                                                                                                                                                                                                                                                                                         the invention for amplification of pear plant microsatellite DNA
                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 1; Length 27; Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
grade discrimination; species selection; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSA primer 2 for amplifying A. thaliana and Z. mays DNA
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 7 Other;
                                                                                                                                                          (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2332 TGCGTGTGTGTGTGTGTGCACA 2355
                                                                                                                                                                                                                                                     Example 36; Page 27; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 TGTGTGTGTGTGTGTGTGTGTWVM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ89470 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00915609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00915609
                                                                                                          21-JUL-2000; 2000JP-00220340
                                                                                                                                   21-JUL-2000; 2000JP-00220340
                                                                                                                                                                                                                                                                                                                                                                                                            0.5%;
Local Similarity 79.2%;
Les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-328353/28.
                                                                                                                                                                                      WPI; 2002-366818/40.
                                                                                                                                                                                                                           species and grades.
                                                     JP2002034562-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ackendree WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS6054300-A
                                                                                05-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; ss
                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ89470;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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Sequence 28 BP; 2 A; 1 C; 13 G; 12 T; 0 U; 0 Other;
 Example 1; Col 9-10; 11pp; English.
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Gaps ö Query Match
0.5%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 6.5e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 2314 GGTCTGTGTGTGTGTGTGTGTGTG 2341

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1 genatrcererererererererere AAH39005 standard; DNA; 23 BP AAH39005; RESULT 389 유

14-AUG-2001 (first entry)

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss. SNP specific upper PCR primer SEQ ID 1801.

13-OCT-2000; 2000WO-US028436. WO200129262-A2. Homo sapiens 26-APR-2001.

99US-0160096P.

15-OCT-1999;

(ORCH-) ORCHID BIOSCIENCES INC.

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nepatic necrosis; PCR primer; ss.
                                                                                                                                                                                                                                                                            Claim 1; Page 59; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG82642 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIGF gene reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2003; 2003WO-US017591
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                                                      Pohl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                          WPI; 2001-290930/30
                                                      Picoult-Newburg L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003103581-A2.
                                                                                                                                                                                                                        acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG82642;
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XX
AC ADG826
XX
DT 11-MAR
XX
XY
DT 11-MAR
XX
XY
Ilver
XW 11ver
XW 11ver
XW 11ver
XW Medica
XW M
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide

Craites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the cligonucleotides of the invention. The PCR primers are used to amplify a SNP primer is used as a genotyping primer.

Craited by a single-nucleotide primer extension reaction. The performing a single-nucleotide primer extension reaction. The cligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g.

Caused by one or more SNPs. Phenotypic traits include diseases e.g.

Caused by one or more SNPs. Phenotypic traits include disease, mechanism, diabeter and acute intermitten porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune confesses, including, rheumatoid arthritis, multiple solerosis, crifiammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and part in a number of part in the present sequence represents a PCR primer specific New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic for a human SNP containing DNA sequence

ö Gaps ; Score 19.8; DB 1; Length 23; Pred. No. 5.5e+02; 2; Indels Sequence 23 BP; 0 A; 0 C; 10 G; 13 T; 0 U; 0 Other; 0; Mismatches

2311 TITGGICTGTGTGTGTGTGTG 2333

liver growth, hepatocyte proliferation, pathological liver condition, liver damage; vascular endothelial growth factor receptor modulator; VEGFR modulator; hepatotropic; antiinflammatory; liver growth promoter; liver failure; hepatitis; liver cirrhosis; toxic liver damage; medicamentary liver damage;

(GETH) GENENTECH INC.

Le Couter J; Ferrara N, Hillan KJ,

WPI; 2004-071254/07

Promoting liver growth or promoting hepatocyte proliferation in liver of subject, treating pathological liver condition e.g. cirrhosis in subject, by administering vascular endothelial growth factor receptor modulator.

Example 4; Page 44; 64pp; English.

The present invention describes a method for promoting (M1) liver growth or promoting (M2) hepatocyte proliferation in the liver of a subject, or promoting (M3) a pathological liver condition in a subject, or protecting (M3) liver from damage in the subject due to exposure to a hepatotoxic (M3) liver from damage in the subject due to exposure to a hepatotoxic growth factor receptor (VEGFR) modulating agent (I). Also described: (I) an article of manufacture comprising a container composition contained within the container and a label on the container instructing uses of the composition for promoting liver growth, where the composition comprises a VEGFR modulating agent in the amount effective to promote liver growth, where the composition comprising a first container, a LABEL on the first container, and a composition contained within the first container, where the composition comprises a VEGFR modulating agent in the amount ceffective to promote liver growth, a second container comprising a buffer and an instruction for using the kit for promoting liver growth. (I) has modulator, and a liver growth promoter. (I) can be used for promoting liver growth or hepatocyte proliferation in the liver of a subject, creating a pathological liver condition in a subject used as liver for failure, hepatitis, liver firmoidamage in a subject due to exposure to character and a liver growth promoter. (I) can be used for promoting cor for protecting liver firmoidamage in a subject due to exposure to character acceptor activation, which is much more potent and beneficial in promoting negation and liver growth than systemic (dalivery of the principal liver mitogen, hepatocyte growth factor (HGF). nvention.

Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

Gaps .; 0 Length 23; Indels Score 19.8; DB 1; Pred. No. 5.5e+02; Query Match
0.5%; Score 19.8; C
Best Local Similarity 91.3%; Pred. No. 5.5e
Matches 21; Conservative 0; Mismatches

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2002 CAGCTGGTGGAGGACCTGGACCG 2024

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23 CAGTTGGTGGAAGACCTGGACCG 1 ADG82637 standard; DNA; 23 (first entry) 11-MAR-2004 ADG82637; RESULT 391 ADG82637/c g

liver growth; hepatocyte proliferation; pathological liver condition; liver damage; vascular endothelial growth factor receptor modulator; VEGFR modilator; hepatotropic; antiinflammatory; liver growth promoter; liver failure; hepatitis; liver cirrhosis; toxic liver damage; medicamentary liver damage; hepatic encephalopathy; hepatic coma; hepatic necrosis; probe; ss

bFGF gene probe.

Synthetic

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The present invention describes a method for promoting (M1) liver growth or promoting (M2) hepatocyte proliferation in the liver of a subject, treating (M3) a pathological liver condition in a subject, or protecting (M4) liver from damage in the subject due to exposure to a hepatotoxic agent, which involves administering to the subject a vascular endothalial growth factor receptor (VEGFR) modulating agent (I). Also described: (I) an article of manufacture comprising a container, composition contained within the container and a label on the container, composition comprises a VEGFR modulating agent in the amount effective to promote liver growth, and (2) a kit comprising a first container, a LABEL on the first container, and a composition container and a liver growth, a second container to promote liver growth, a second container comprising a buffer and an instruction for using the kit for promoting liver growth. (I) has hepatotropic and antinflammatory activities, and can be used as a VEGFR andulating a pathological liver growth promoter. (I) can be used for promoting liver growth or hepatocyte proliferation in the liver of a subject treating a pathological liver condition in a subject such as liver intention the hearth of promoting liver damage, mediametry liver growth benefit and a liver condition in a subject such as liver liver damage hearth or promoting liver damage, mediametry liver growth benefit and a liver condition in a subject such as liver liver damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoting liver growth or promoting hepatocyte proliferation in liver of subject, treating pathological liver condition e.g. cirrhosis in subject, by administering vascular endothelial growth factor receptor modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or for profecting liver from damage in a subject due to exposure to hepatotoxic agent. The VEGFR modulator create a local cascade of signaling events originating in sinusoidal endothelial cells following VEGF receptor activation, which is much more potent and beneficial in promoting hepatocyte proliferation and liver growth than systemic delivery of the principal liver mitogen, hepatocyte growth factor (HGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver damage, hepatic encephalopathy, hepatic coma or hepatic necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.8; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002 CAGCTGGTGGAGGACCTGGACCG 2024
                                                                                                                                                                                                                                                                                                                                                                                                    Le Couter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 cagriderecaacacciedacce 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 43; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                           05-JUN-2003; 2003WO-US017591.
                                                                                                                                                                                                                                     05-JUN-2002; 2002US-0386637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ,
                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-071254/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
WO2003103581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present
                                                                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH70580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH70580/c
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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers pecifically priming and allowing amplification of each 'Dete agene, 'DetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, infeatious diseases, and neoplastic diseases. Autoimmune diseases include Addison's disease, and neoplastic diseases. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include multiple sclerosis and Alzheimer as contact with allargens that lead to allergies, Type II hypersensitivities such as those present in coodpasture's syndrome and Type IV hypersensitivities such as those caused by infections diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by such as lukaemias, limphomas and cancers such as suche as the parain, and a lukaemias, limphomas and cancers such as senser of the brain, and a senser of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                      allergy, type II hypersensitivity, Goodpasture's syndrome, type IV hypersensitivity, leprosy, infectious disease, viral infection, HIV, fungal infection, Candida, parasitic infection, schistosome,
                              Addison's disease, atrophic gastritis;
degenerative nervous system disease; multiple sclerosis;
Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
                                                                                                                                                                                    filaria, bacterial infection; Mycobacterium; neoplastic disease;
lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast. The present sequence represents a Vbeta gene repeat sequence.
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hypersensitivity disease; infectious disease; neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 12 A; 10 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 774; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGTGTGT 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00263959
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                                                                                                                                                                                                                                              breast cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hood LE, Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOOD/) HOOD L E (ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                     US2002150891-A1.
                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-1994;
19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vbeta gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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AAZ98498/c
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Length 23; 2; Indels AAZ98498;

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acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each gene specific primer has a sequence complementary to a distinct mRNA, and each labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of labeled NAs which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                                   The present invention relates to protein 9.90, which contains characteristic histone and hexokinase sequences (see ABF59132). The protein can be used for treating various diseases (e.g. malignant tumours, heemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in example from the invention. Note: The present sequence is the SEQ ID 3 shown in the sequence listing. This sequence differs from the SEQ ID 3 shown in the disclosure (see ABZ70123)
                                                                                                                                                   Characteristic sequence protein 9.90 containing histone and hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to producing a sub-population of labeled nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer; 88; DNA microarray; differential expression analysis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19.8; DB 1; Length 24; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 2 A; 2 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                   Example 3; Page 24 (Disclosure); 30pp; Chinese.
                                                                                                                                                                          and polynucleotides encoding this polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chenchik A, Jokhadze G, Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 1107; 11pp; English
                  CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2328 TGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene specific PCR primer #1107
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Best Local Similarity 91.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK67019 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLON-) CLONTECH LAB INC
                    (BODE-) BODE GENE DEV
                                                                                                     WPI; 2002-751599/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-314699/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK67019;
                                                              Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ99483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein 9.90; histone; hexokinase; tumour; cytostatic; haemopathy; PCR; HIV infection; anti-HIV; immunological disease; inflammation; primer; ss.
                                                                                                Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 0.5%; Score 19.8; DB 1; Length 24; 1 Similarity 91.3%; Pred. No. 5.7e+02; 21; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 8 A; 12 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2329 GTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 14; 35pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 GCGCGCGTGTGTGTGTGTGTGTG
                                                              discus derived sequence #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 24 BP
                                                                                                                                                                                                                                                                                                           99WO-JP003551
                                                                                                                                                                                                                                                                                                                                                    98JP-00232153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer #1
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sekino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-224692/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ70117 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
                                                                                                                                                                        Haliotis discus.
                                                                                                                                                                                                                 WO200011156-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein 9.90
                                                                                                                                                                                                                                                                                                        01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                    18-AUG-1998;
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                    19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Local

Matches

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Gaps

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different physiological sources, where the method comprises producing subpopulation of labeled NAs for the different physiological sources, comprising the populations for each physiological source to identify differences in the population, where the comparison is preferably performed by hybridising the labeled NAs for each of the distinct physiological sources to an array of probe NAs stably associated with the surface of a substrate to produce a hybridisation pattern for each of the sources, where sources, and comparing the patterns for each of the sources, where cafferential gene expression assays are utilised in differential expression analysis of diseased a normal tissue e.g. neoplastic a normal tissue, or different tissue or subtissue types. The present sequence is a fundament gene specific PCR primer used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
for analysing the differences in the RNA profiles between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
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Sequence 26 BP; 2 A; 9 C; 6 G; 9 T; 0 U; 0 Other;

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ch 0.5%; Score 19.8; DB 1; Length 26; 1 Similarity 91.3%; Pred. No. 6.3e+02; 21; Conservative 0; Mismatches 2; Indels
                                                                     2546 TGGCTCGGCCTCTGCCAC 2568
                                                                                       1 TGGGTCGGCCTCTACCTTGCAC 23
                    Local Similarity
      Query Match
Best Local S
                                        Matches
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Gaps

Simple sequence repeat; SSR; single site amplification; SSA; disease; SSA primer 1 for amplifying A. thaliana and Z. mays DNA. AAZ89469 standard; DNA; 27 BP (first entry) 16-JUN-2000 primer; 88 AAZ89469;

97US-00915609. 21-AUG-1997; US6054300-A. 25-APR-2000 Zea mays.

Arabidopsis thaliana.

97US-00915609 21-AUG-1997;

(USDA) US SEC OF AGRIC.

Mckendree WL;

WPI; 2000-328353/28.

Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.

Example 1; Col 7-8; 11pp; English.

This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distinguishing between species, strains or varieties within species or identifying the presence of a disease

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export regulation, variety and ecotype identification, marker development, forensic DNA fingerprinting, etc. The method can also be used to generate a linear DNA molecule containing two target sequences from one sequence within a single stranded DNA template and flanking containing two target sequences. It can also be used for e.g. for regions for these target sequence. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. Cloning cDNA or genomic DNA which flanks any known short target sequence. Cloning cDNA or genomic DNA which flanks any known short target sequence. Consing and sequence darived from amino acid sequence back translation using a polymerase having strand displacement capability which can synthesize up to 10 kb fragmants. This is especially useful for obtaining synthesize up to 10 kb fragments. This is especially useful for obtaining carelerated development of high resolution DNA markers that may be allows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue than 1 mug). It also allows the production of a PCR template of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with consuming steps, typically requiring no less than three months, with the primers used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant expression cassette comprising a promoter that is functional in plants, operably linked with a coding sequence and a non-plant 3' termination sequence, useful for gene expression in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heterologous gene; expression cassette; gene expression; PCR; primer; ss.
condition. It also provides a marker for use in areas such as import and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer #4 used to construct heterologous 3'-termination DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 0.5%; Score 19.8; DB 1; Length 27; Local Similarity 91.3%; Pred. No. 6.5e+02; Local Si, Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 12 A; 11 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2331 GTGCGTGTGTGTGTGTGCA 2353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 crererererererererea 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2002; 2002US-0390529P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilkinson JQ, Mcbride K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WILK/) WILKINSON J Q. (MCBR/) MCBRIDE K. (BERT/) BERTAIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-374960/35.
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polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention
                                                                                        Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forenaic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting the presence of
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                                                     Human inflammatory bowel disease associated polymorphic site #452
                                                                                                                                                                                                                                          /*tag= a
/note= "SNP, optionally T or A at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 0.5%; Score 19.6; DB 1; Length 27; I Similarity 81.5%; Pred. No. 6.9e+02; 22; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rioux J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGTGTGTGT 2342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WHED ) WHITEHEAD INST BIOMEDICAL RES (BLLI-) ELLIPSIS BIOTHERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene specific PCR primer #350.
                                                                                                                                                                                    Location/Qualifiers
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daly M, Hudson TJ, Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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10-APR-2000; 2000US-0196046P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2316 TCTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367874/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                WO200142511-A2
                                                                                                                                                                                                     Key
misc_feature
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6352829-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
is a PCR primer used to construct DNA. This sequence is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel set of inter-simple sequence repeats
                                                                                                                            Gaps
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                                                                                      Score 19.8; DB 1; Length 27;
Pred. No. 6.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.6; DB 1; Length 23; Pred. No. 5.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID 5 alternative.
                                                   Sequence 27 BP; 14 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 0 A; 1 C; 9 G; 11 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                 2317 CTGTGTGTGTGTGTGTGTG 2339
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                                                                                                                                                                                      27 CTGTGTGTGTTTGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                         (ISSR) - PCR primer
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                                                                                        Query Match 0.5%;
Best Local Similarity 91.3%;
Matches 21; Conservative
cells. The present sequence heterologous 3'-termination
                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH91377 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                inter-simple séquence rep
animal; Basmatí rice; ss
                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                              ADD69512 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animal systems
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                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                           5' anchored
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16-OCT-2003

Synthetic.

ADD69512;

Nagaraju JG,

Query Match

AAH91377

RESULT 399
AAH91377/C
ID AAH913
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AC AAH913

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Gaps

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The invention relates to producing a sub-population of labeled nucleic acids (NAS) comprising concacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAS, where each gene specific primer has a sequence complementary to a distinct mRNA, and each labeled NA is generated using a single gene specific primer. The method is useful for analysing the differences in the RNA profiles between several different physiological sources, where the method comprises producing subpopulation of labeled NAS for the different physiological sources, comprising the population, where the comparison is preferably differences in the population, where the comparison is preferably by solological sources to an array of probe NAS stably associated with the surface of a substrate to produce a hybridisation pattern for each of the sources, where sources, and comparing the patterns for each of the sources, where control assays are utilised in differential gene expression assays are utilised in differential expression analysis of diseased a normal tissue e.g. neoplastic a normal comparing the PCR primer used in the method of the pivention. Note: The sequence data for this patent did not form part of the printed specific approach.
                                                                                                                                                                                                    Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
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Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28 BP; 7 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
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                                                                                                                                       Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1765 GAGGCCTTGTTGACCGAGTCTACAC 1790
                                                                                                                                                                                                                                                                                Example 3; SEQ ID NO 350; 11pp; English
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                               99US-00225928
                                                                  97US-00859998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                         Chenchik A, Jokhadze G,
                                                                                                      (CLON-) CLONTECH LAB INC
                                                                                                                                                                          WPI; 2002-314699/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                 05-JAN-1999;
                                                                      21-MAY-1997;
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02-FEB-1993
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05-MAR-2002.
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AAQ33891
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Matches
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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
construction and (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
connstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
concomically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 selection; primers; OPTIPRIM; breeding; cattle; parentage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2318 TGTGTGTGTGTGTGTGTGT 2338
                                                                                                                                                                                             rable 7; Page 286; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGTGTGTGTGTGTGTGTGT 21
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92WO-US000340.
                              91US-00642342.
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                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-284684/34.
                                                                                                                   WPI; 1992-284684/34.
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Matches 20; Conserv
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                                                          (GENM-) GENMARK.
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 15-JAN-1992;
                               15-JAN-1991;
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02-FEB-1993
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AAQ34015
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                                                                                                                  The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MooI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MooI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connectant traits esp. in cattle, to allow selective or program of the connectant of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene
  Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB 1; Length 21;
Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2319 GTGTGTGTGTGTGTGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 281; 517pp; English.
                                                                          Table 7; Page 336; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33879 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               field.)
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in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sepecification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                                                                                                                                                               0.5%; Score 19.4; DB 1; Length 21; ilarity 95.2%; Pred. No. 5.5e+02; Conservative 0; Mismatches 1; Indels
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Pred. No. 5.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide RTC05 used in an Example from US5932556.
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                                                                                                                                                                                                                 Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           2318 TGTGTGTGTGTGTGTGTGT 2338
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Best Local Similarity 95.2%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                 Local Similarity
wes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD28; inhibition;
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                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 404
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The present sequence is that of a synthetic oligonuclectide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3 '-OH' synthetic oligonuclectide which comprises multiple crepats of dinuclectides such as GT. TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, crivation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (ITMF)-alpha by immune system cells, in an animal having and secondary sarcoma such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, lenkemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                       Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 17; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2000; 2000US-0228925P.
                                                                           Synthetic oligonucleotide 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH46014 standard; DNA; 21
                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phillips NC,
                                                                                                                                                                                                                        lymphoma; ss
                          12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf37 which contains the repeat sequence is from the marker clone Mdf37 which contains the repeat sequence is from formula: (AC)10A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGTGTGT 2338
     GTGTGTGTGTGTGTGTGTG 2339
                                   GIGIGIGIGIGIGIGIG 21
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91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00222177
                                                                                                                                                                                                   AAT65738 standard; DNA; 21
                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                               25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
     2319
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                                                                                                                                                                                                                                                           AAT65738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                            RESULT 409
AAT65738/
XX
XX
AAT65738/
XX
AAT65738/
AAT6678/
AAT6678/
AAT6678/
AAT67/
AAT6
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Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
                                                              0; Gaps
                             0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; tive 0; Mismatches 1; Indels
Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                             2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                         21
                                                                                                                                                                                                                                                                                               Synthetic oligonucleotide 14.
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AAH46013 standard; DNA; 21 BP

RESULT 406

g ઠ

AAH46013

AAH46013 ID AAH4 XX AC AAH4

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vivlemore401-10.rng

05-APR-2001

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Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a synthetic oligonucleotide useful to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention. The invention relates to a composition, comprising a 2 to 20 base 3-OH, 5'-OH synthetic oligonuclectide which comprises multiple repeats of dinuclectides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, perimary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence
tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 17; 77pp; English.
                                                                                                                                                                                                                                                                         (BION-) BIONICHE LIFE SCI INC.
                                                                                                                                                                           12-DEC-2000; 2000WO-CA001467
                                                                                                                                                                                                                13-DEC-1999; 99US-0170325P, 29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                Filion MC;
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-398150/42.
                                                                                              WO200144465-A2.
                      lymphoma; ss
                                                                                                                                                                                                                                                                                                              Phillips NC,
                                                                                                                                  21-JUN-2001.
                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         caspases
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Gaps
                               .
Score 19.4; DB 1; Length 21;
Pred. No. 5.5e+02;
0; Mismatches 1; Indels
                                                            2319 GTGTGTGTGTGTGCGTGTG 2339
   0.5%;
                               20; Conservative
                  Best Local Similarity
      Query Match
                                  Matches
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Immunostimulatory nucleic acid #818.
    AAF99702 standard; DNA; 21 BP
                       12-JUN-2001 (first entry)
              AAF99702;
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Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection; baceerial infection, fungal infection; parasitic infection; cancer, asthma, infections allergy; immune deficiency; phosphorothioate; ss.

Synthetic

WO200122972-A2

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy, retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                    Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.4; DB 1; Length 21; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis inhibitory oligonucleotide #907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                              Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                          Krieg AM, Schetter C, Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 rererererererererer 21
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                                                                        25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                  25-SEP-2000; 2000WO-US026383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 95.2%;
Matches 20; Conservative
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                                                                                                                                                (IOWA ) UNIV IOWA RES FOI
(COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                                                  WPI; 2001-273485/28
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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; cytochrome P450 02E; CYP45002E1; LTF; adranged receptor beta1; ADBR1; aryl hydrocarbon; ARNY; cathepsin S; CYS2; aryl hydrocarbon; ARNY; cathepsin S; CYS2; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; epoxide hydroxylase 2; EPHXZ; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HNMY; Kallikrein 2; KLKZ; nicotinamide-N-methyl transferase; NNMT; UDP-glucuronosyl transferase 2; NGO2; sulfotrandserase thermolabile; STM; UGT2B7; UDP-glucuronosyl transferase; UGT2B1; urokinase receptor; uPA; multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
                                                                                                                                                                                                                                                                           The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lession, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplassis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                       Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 35; 276pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS97830 standard; DNA; 21 BP
                                           (COLE-) COLEY PHARM GROUP INC.
14-DEC-2000; 2000US-025534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid of the invention
                                                                                                                                  WPI; 2002-566690/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200257410-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-2002
                                                                                      Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS97830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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This invention relates to the sequence of an isolated mucleic acid

molecule comprising at least one base variation from that of a known

molecule comprising at least one base variation from that of a known

mulecule comprising at least one base variation from that of a known

mulecule comprising at least one base variation from that of a known

mulecule comprising at least one base variation from that of a known

mulecule control (ARN), and plants, addensive, diazepam binding

(ARN), cathepsin S (CTSS), cyclooxgenase 2 (CDX2), diazepam binding

control (FLAP), gluethione-S-transferase 12 (GST12), histenmine-N-methyl

transferase (HNWT), NADPH quinone Sardorducase 1 (MO21), histenmine-N-methyl

cransferase (HNWT), NADPH quinone Sardorducase 2 (MO22),

culfocransferase (HNWT), NADPH quinone Sardorducase 2 (MO22),

confort I, 2, 3, 4, or 5 (CHMT), CHMR3, CHMR4 or CHMR5) sequence

confort tracting and responsible for a variety of disorder-related

confort reading the disorders. The nucleic acid molecules comprising the

confort reading the disorders. The nucleic acid molecules comprising the

confort reading the disorders. The nucleic acid molecules comprising

confort reading the disorders. The nucleic acid molecules of career for a career for Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for The present sequence represents a Gaps .. 0 0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; ve 0; Mismatches 1; Indels Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other; polymorphic DNA sequence of the invention Example 16; Page 130; 714pp; English nervous system function. 2324 TGTGTGTGTGCGTGTGTGT 2344 21 TATGTGTGCGTGTGTGTGT 1 28-NOV-2001; 2001WO-US044838. 28-NOV-2000; 2000US-00724389. 95.2%; Query Match Best Local Similarity 95.2 Matches 20, Conservative disorder-related traits. (DNAS-) DNA SCI LAB INC. VPI; 2002-698522/75 Guida M, Hall J; ð

; 0

0.5%; Score 19.4; DB 1; Length 21; 55.2%; Pred. No. 5.5e+02; ve 0; Mismatches 1; Indels

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RESULT 411 ABS97832/c ID ABS97832 standard; DNA; 21

(first entry)

23-DEC-2002 ABS97832;

HXXXH

25-JUL-2002.

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Adrenegic receptor beta1; ADBA1; aryl hydrocarbon; AHR; MRP3; NR11Z;

W adrenegic receptor nuclear translocator; ARMY; cathepsin S; CTSS;

CYClooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

W epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

W HUMT; kallikrein 2; KLK2; incotinamide-N-methyl transferase;

W HUMT; kallikrein 2; KLK2; incotinamide-N-methyl transferase;

W HUMT; kallikrein 2; KLK2; incotinamide-N-methyl transferase;

W HUMP; W HUMD world oxidoreductase 28; UQC2; sulfotransferase; NNMT;

W UDP-glucuronosyl transferase; UGT2B15; urokinase receptor;

W ultidrug resistance 1; lactotransferrin; orphan nuclear receptor;

W acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

Altered drug metabolism; cardiovascular function; colorectal tumour;

W central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism

Homo sapiens.

WO200257410-A2.

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC

Guida M, Hall J;

WPI; 2002-698522/75

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

29-MAR-2002; 2002US-00112653. 29-MAR-2001; 2001US-0279642P.

KRIE/) KRIEG A M. BERG D J.

BERG/)

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
cc molecule comprising at least one base variation from that of a known
cc human cytochrome P450 Al (CTP4501Al), cytochrome P450 A2 (CTP4501Al),
cytochrome P450 O2E1 (CTP4500E1), adrenergic receptor betal (ADBR1),
caryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
(ARNY), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
cinhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
crotein (FLAP), glutathione-S-transferase 12 (GST12), histemmine-N-methyl
cc transferase (HNWT), MADPH quinone oxidoreductase 2 (MOC2),
culfotransferase thermolabile (STM), UDP-glucuronosyl transferase (HWBI),
cc transferase (HOT2B1S), urokinase receptor (UPA), multidrug resistance 1
cc (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
cc (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
cc (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
cc (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
cc receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR4), CHMR5) sequence.
cc receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR4), CHMR5 or cHMR5) sequence
cc receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR4), CHMR5 or custing direction are useful of their esponsible for avariety of disorder-related
ctraits as a result of their e.g., overexpression, constitutive
cc and/or traating the disorders. The nucleic acid molecules comprising the
cc and/or traating the disorders. The nucleic acid molecules comprising the
cc and/or traating the disorders. The nucleic acid molecules comprising the
cc and/or mutation or underexpression, which may be used in diagnosing
cc and/or traating the disorders. The nucleic acid molecules
companies. The polymorphic sequences contained in CYP4501Al, CYP4501Al,
cyPARS, MRN, MRN, and/or MDR3 are useful for screening individuals for succeptibility to cancer. Polym

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Gaps

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Score 19.4; DB 1; Length 21; Pred. No. 5.5e+02; 0; Mismatches 1; Indels

Query Match 0.5%; Best Local Similarity 95.2%; Matches 20; Conservative (

Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psortasis, eczema, allergic contect dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid

Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.

WPI; 2003-521815/49. Krieg AM, Berg DJ;

Disclosure; Page 32; 229pp; English.

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used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or naematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHWR3, CHWR4 or CHWR5 for altered central and peripheral nervous system function. The present sequence represents a
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory, antiinflammatory, dermatological, antipsoriatic, antiulcer; gene therspy, vaccine; non-allergic inflammatory disease, psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease, ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                   ö
                                                                                                                                            Length 21;
                                                                                                                                                                   1; Indels
                                                                                                                Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                         Score 19.4; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                   0; Mismatches
                                                                                       polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory nucleic acid #876.
                                                                                                                                                                                             2344
                                                                                                                                                                                                                    21 rerarerecerererer 1
                                                                                                                                                                                             2324 TGTGTGTGTGCGTGTGTGT
                                                                                                                                                                                                                                                                                    ACH03241 standard; DNA; 21 BP
                                                                                                                                          0.5%;
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                                                                                                                                                                  Matches 20; Conservative
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                             ACH03241;
                                                                                                                                                                                                                                                         RESULT 412
                                                                                                                                                                                                                                                                        ACH03241
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gene therapy; PCR primer; ss.
                                      WO2003066840-A2.
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                                                         14-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                  Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stem cell; dental follicle; tooth; membrane structure; periodontal ligament; pluripotent mesenchymal stem cell; osteopathic; antiinflammatory; stem cell therapy; tissue replacement; tissue repaitransplantation; periodontal tissue; periodontitis; dental cementum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                             ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor receptor 3-IIIC reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                      hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                             Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 17; 221pp; English.
                                                                                                                           Immunostimulatory nucleic acid #818.
 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2318 TGTGTGTGTGTGTGCGTGT 2338
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                   21
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                                                                                                                                                                                                                                  02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%;
                                                                                                                                                                                                                                                                                                             Bratzler RL, Petersen DM,
                                                                  ADB37204 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC64706 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                       (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                              WPI; 2003-657977/62.
                                                                                                                                                                                            US2003087848-A1
                                                                                                         04-DEC-2003
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                                                                                                                                                                          Synthetic.
                                                                                      ADB37204;
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  2318
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The present invention describes a stem cell (A) that is obtained from non-embryonic tissue isolated from the dental follicle of a (wisdom) tooth which can differentiate in vitro into a membrane structure that resembles periodontal ligament. Also described: (1) a stem cell (A1), derived from con-embryonic or post-natal animal cells or tissue, that is capable of self-remewal and differentiation to cells of ando-, ecto- or meso-dermal lineages, and (2) pluripotent mesenchymal stem cells (A2) obtained from (A). (A) has osteopathic and antiinflammatory activities, and can be used con stem cell therapy, and in tissue replacement. (A), and cells differentiated from them, can be used to prevent or treat cellular defects, dysfunction and/or disease, e.g. tissue repair or transplantation. They can especially be used to rebuild periodontal tissue (in cases of periodontitis) or dental cementum, and to improve the challing of tooth extraction or skin lesions. They can also be used in associated bone) or association with a scaffold, for growing teeth (or associated bone) or arterial/venous vessels in the mouth or as gene therapy carriers. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; ss; short interfering RNA; siRNA; anglogenesis; vascular endothelial growth factor; VBGF; VBGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pluripotent embryonic-like stem cells derived from dental fuseful e.g. for engineering teeth or dental tissue, and for transplantation.
                                                                                                                                                                                                                                                              Schierholz J, Brenner N, Zeilhofer F, Hoffmann KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 23; 68pp; English.
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05-FEB-2003; 2003WO-EP001131.
                                                                                    06-FEB-2002; 2002US-0354152P.
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                                                                                                                                                                              CAES-) STIFTUNG CAESAR
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99WO-EP010209. 98EP-00204291

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Porcine; pig; wild boar; quantitative trait locus; QTL; chromosome 2; mapping; 2pl.7; select breeding; genotype; phenotype; muscle mass; fat deposition; IGF2; insulin-like growth factor 2; microsatellite; ds.
                                                                                                                                                                                                                                                                                                                                                   Porcine microsatellite PIGQTL1 oligonucleotide #29.
                                                                                                                                                                                                                                                                           1609 AAGTGCATCCACAGGGACCTG 1629
                                                                                                                                                                                                                                                                                 1 AAGTGTATCCACAGGGACCTG 21
                                                                                                                                                                                                                                                                                                                  AAA65560 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                                                                                                                WO200036143-A2
                 29-JAN-2004.
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The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises cresting the animal for the presence of a parentally imprinted quantitative trait locus (QTL). The pig QTL is located at chromosome 2, mapping at around position 2pl.7. Also described are: (1) an isolated and/or recombinant nucleic acid (M1) comprising a parentally imprinted QTL or its functional fragment; (2) an isolated and/or recombinant nucleic acid (M2) comprising a synthetic parentally imprinted QTL derived and/or recombinant comprising a synthetic parentally imprinted QTL derived from at least one chromosome or its functional fragment; (3) an animal cuch as pig selected for having desired genotypic or potential phenotypic properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its fragment is an embryo desired genotypic or potential phenotypic properties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in breeding animals destined for slaughter. The present sequence represents a microsatellite oligonucleotide, which is given in an example from the present invention for the identification of the present sequence represents in the IGF2 (insulin-like growth factor 2) and
                                                                                                                                                                                                                                                                                                                                                                     Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
                                                                                                                                                                                                                                               Georges M, Spincemaille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 10; 107pp; English.
                                                                                                                                                                                    (SEGH-) SEGHERSGENTEC NV
                                                                                                                                                                                                                                                                                                             WPI; 2000-431612/37.
                                                                                                                         UYLI-) UNIV LIEGE.
                                                                                                                                                      MELICA
16-DEC-1999;
                                                                                                                                                                                                                                                     Andersson L,
                                                       16-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deposition.
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Matches
interfering RNA (sirRNA) molecules, which can be used to inhibit angiogenesis. Specifically, it refers to sirNAs that target and cause RNA1-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Fit-1) and the Fik-1/KDR (kinase domain region) genes, as well as mutants derived thereof. The present invention describes sense and antisense RNA strands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with angiogenesis and the carget the overexpression of VEGF, which include diabetic retinopathy, ageraleated macular degeneration, inflammatory disease, psoriasis and crheumatoid arbitis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, Wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antiinflammatory, antipsoriatic, antidhebmatic and antiarthritic activities. This oligonucleotide is a human FIk-1/KDR DNA oligo, a target for siRNA inhibition of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic retinopathy and cancer.
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                                                                                                                                                   18-JUL-2003; 2003WO-US022444
                                                                                                                                                                                                                 24-JUL-2002; 2002US-0398417P
14-NOV-2002; 2002US-00294228
                                                                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
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                                                       Gaps
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                       / Match 0.5%; Score 19.4; DB 1; Length 22; Local Similarity 95.2%; Pred. No. 5.8e+02; Local Sol, Conservative 0; Mismatches 1; Indels
Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   Porcine microsatellite PIGQTL1 oligonucleotide #29.
                                                                                   2824 ATATATACATATATATA 2844
                                                                                                           1 ATATATATATATATA 21
                                                                                                                                                                                AAA65560 standard; DNA; 22 BP
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RESULT 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises testing the animal for the presence of a parentally imprinded quantitative trait locus (QTL). The pig QTL is located at chromosome 2, mapping at around position 2pt. 7. Also described are: (1) an isolated and/or recombinant nucleic acid (N1) comprising a parentally imprinted QTL or its functional fragment; (2) an isolated and/or recombinant nucleic acid (N2) comprising a synthetic parentally imprinted QTL cucleic acid (N2) comprising a synthetic parentally imprinted QTL derived from at least one chromosome or its functional fragment; (3) an animal such as pig selected for having desired genotypic or potential phenotypic properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its fragment is cusful for selecting an animal destined for slaughter or a breeding animal having desired genotypic or potential phenotypic properties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in Dreeding animals destined for slaughter. The cyresent sequence represents a microaatellite oligonucleotide, which is given in an example from the present invention for the identification of flambing location of slaughter 2) and chiral of the second of slaughter 2 and 2 a
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                                                                                                                                                                                                                                                                       Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
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                                                                                                                                                                  Spincemaille G;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 10; 107pp; English.
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     98EP-00204291
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                                                       (UYLI-) UNIV LIEGE.
(MELI-) MELICA HB.
(SEGH-) SEGHERSGENTEC NV.
                                                                                                                                                                     Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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     16-DEC-1998;
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                                                                                                                                                                        Andersson L,
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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(COLE-) COLEY PHARM GMBH.
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Best Local Similarity 95.2
Matches 20, Conservative
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(COLE-) COLEY PHARM GMBH
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                               Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                    Claim 101; Page 56; 338pp; English
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WPI; 2001-273485/28
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous leason, rheumatcoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
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ABS78426/c
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1 ATATATATATATATA 21

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diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases. The method is psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                    Gaps
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                                                                                                                                               BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
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Pred. No. 5.8e+02;
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                                                                                                                                                                                  Query Match 0.5%;
Best Local Similarity 95.2%;
Matches 20; Conservative
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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                                                                  Immunostimulatory nucleic acid #879.
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         BP.
                                                                                                                                                                                                                                                                                                     29-MAR-2002; 2002US-00112653.
                                                                                                                                                                                                                                                                                                                               29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.2%;
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         22
                                                                      (first entry)
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           ACH03244 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                                                                                                              Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                         JS2003050268-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
                                                                        25-SEP-2003
                                                                                                                                                                                                                                                                        13-MAR-2003.
                                                                                                                                                                                                              Synthetic.
                                         ACH03244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 424
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ACH03244,
            0 x 2 x 5 x 5 x 5 x 5 x
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Query Match
0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels

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Gaps

Gaps

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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; 88.
                                                                                                                     The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                    preventing allergy or asthma using an immunostimulatory one or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                      Score 19.4; DB 1; Length
Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP specific lower PCR primer SEQ ID 1870.
                                                                                   Disclosure; Page 17; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               2824 ATATATACATATATATATA 2844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH39074/c
ID AAH39074 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-290930/30
                    and/or pre
acid alone
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                    Treating nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH39074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB 1;
Pred. No. 5.8e+02;
hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #821
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                                                                                                                                                                                                                                                                                                                                                  Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB37207 standard; DNA; 22
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Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                         (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M. (FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-657977/62.
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                                             Synthetic
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(FOUR/)
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assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterchaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune disease, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of the target sequence #8 which was used in an experiment to determine the in vitro cleavage of target duplexes to evaluate the lengths of purine and pyrimidine tracts which are useful in obtaining oligonucleotides capable of triple helix formation with target nucleic acids. The complementary strand overhangs the 3' end by the sequence CTAG and the sense strand overhangs the complementary strand by the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide(s) forming triple helix with target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purine; pyrimidine; tracts; therapeutic; diagnostic; control; gene expression; mRNA synthesis suppression; ds.
                                                                                                                                                                                                                                                                                               Score 19.4; DB 1; Length 24;
Pred. No. 6.4e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                               Sequence 24 BP; 12 A; 11 C; 0 G; 1 T; 0 U; 0 Other;
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ilarity 95.2%;
Conservative (
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Target sequence #8.
                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 20; Conserv
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21-JAN-1992;
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28-OCT-1993
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Matches
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0.5%; Score 19.4; DB 1; Length 26;

Query Match

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determn, of coat colour genotype in pigs by analysis of the KIT gene for duplication or deletions, or analysis of KIT protein, used to establish breeding programmes for pigs of selected colour.
           Gaps
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                                                                                                                                                                                                                         KIT gene primer KITDEL2-FOR for pig coat colour determination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plastow GS;
             Indels
                                                                                                                                                                                                                                                   KIT gene; pig; coat colour; pigmentation; primer; PCR; polymerase chain reaction; ss.
             <u>;</u>
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95.2%; Pred. No. 7e+02;
           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the desired, usually white, coat colour
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                                         2319 GIGIGIGIGIGIGIGCGIGIG 2339
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                                                            6 GTGTGTGTGTGTGTGTG 26
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95GB-00025364.
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                                                                                                                                        AAT84434 standard; DNA; 26
                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson L, Moller MJ,
             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DALG-) DALGETY PLC.
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nes 20; Conserv
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           WO9705278-A1
                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-1996;
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12-DEC-1995;
                                                                                                                                                                                              13-NOV-1997
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                                                                                                                                                                                                                                                                                                 Synthetic.
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Matches
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                                                                                                            RESULT 428
                Matches
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neuroepithelial stem calls, which are capable of self-renewal in adherent feeder-cell-independent (AFCI) culture medium and differentiation to central nervous system (CNS) neuronal or glial cells and to neuronal crest stem calls. Also described is an isolated population of mammalian CNS glial-restricted precursor (GRP) cells which can self-renew in the AFCI culture medium and can differentiate to CNS glial cells but not to CNS neuronal cells. The stem cells can be used to generate a population of mammalian motor neurons by incubating the stem cells by incubating the stem cells of mammalian motor neurons by incubating the stem cells in a medium comprises laminin-coated plates and NEP medium lacking chick embryo extract. The stem cells can also produce neural crest stem cells by inducing the cells on differentiate in vitro. The inducing step comprises comprises antioned mitogen (preferably fibroblast growth factor; FGF) and chick embryo extract. Inducing can also comprise adding a dorsalizing agent to the cells, preferably a bone morphogenetic protein (BMP) such as BMP-2, -4 or -7. The stem cells and inducing the stem cells of the corrier of the cells of the cells on a laminin-coated by stem cells to differentiate in vitro to neural crest stem cells, and inducing these cells to differentiate. AAX00039 to AAX00034 represent PCR primers which are used in an example from the present invention to amplify different FGF and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an isolated, pure population of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian neuroepithelial stem cells and glial restricted precursor - car
self renew and differentiate into central nervous system cells, used for
generating various types of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS; central nervous system; glial cell; FCR primer; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 0.5%; Score 19.2; DB 1; Length 24; Local Similarity 87.5%; Pred. No. 6.7e+02; es 21; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 4 A; 9 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayer-Proschel M, Mujtaba T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                984 GAAAGGCCTGGGCTCCCCCACCGT 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 26; Page 58; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 GAAGGCTTGGGCTCGCCCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. discus derived sequence #23.
                                                                                                                                                                                                                                                                      98WO-US009630.
                                                                                                                                                                                                                                                                                                                                                    98US-00073881,
                                                                                                                                                                                                                                                                                                                                                                                                    (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ98505 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070093/06
                                                                                                          Homo sapiens
                                                                                                                                                               WO9850526-A1
                                                                                                                                                                                                                                                                      07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                    06-MAY-1998;
                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ98505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rao MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ98505,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           # X B X B X B X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      products according to breed origin; (b) determining or testing the breed origin; (b) determining or testing the breed origin; (c) relidating an animal product. The method contign of a product a sample of the product for the allele(s) of at least comprises analysing a sample of the product for the allele(s) of at least one breed-determinant (BD) gene. The present invention also describes: (1) methods for determining the coat colour genotype of a pig by determining; (i) the allele(s) of the alpha melanocyte-stimulating confidence of the protein at positions associated with coat colour, or the size of the alpha-MSHR protein; (ii) the amino acid sequence of an alpha-MSHR protein; (iii) detecting which microsatellites (or other linked marker alleles), linked to the alpha-MSHR gene, or particular alleles of it, are present; and (iv) analysing nucleic acid to determine if the KIT care present; and (iv) analysing nucleic acid to determine if the KIT method of the invention is applied to samples from fish, birds and manmals, especially pigs. Particular applications are confirming stated origin of meats; in quality control; for maintaining stock purity, and in the present process can be made quantitative. The present sequence inexpensively. The process can be made quantitative. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic acid or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuroepithelial stem cell; lineage restricted intermediate precursor; oligodendrocyte; astrocyte; self-renewal; neuron; differentiation;
                                                  Porcine, wild boar; meishan; pietrain; large white; hampshire; duroc; differentiation; breed origin; alpha-MSHR; coat colour; stock purity; alpha melanocyte-stimulating hormone receptor; KIT; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plastow GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wales R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 BP; 6 A; 3 C; 8 G; 7 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
  KIT gene PCR forward primer KITDEL2-FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1796 AGAGTGACGTCTGGTCCTTTGGGGT 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 14; Page 53; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giuffra E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAAGTGAYGTCTGGTCCTATSGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PIGI-) PIG IMPROVEMENT CO UK LID.
                                                                                                                                                                                                                                                                                                                                                                           97GB-00011214.
                                                                                                                                                                                                                                                                                                                        98WO-GB001531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGFR-3 PCR antisense primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX00036 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson L, Kijas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-070222/06.
                                                                                                                                                                                                              WO9854360-A1
                                                                                                                                                                                                                                                                                                                        27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-1998;
                                                                                                                                                                                                                                                                      03-DEC-1998
                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX00036,
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                                                                                                                                                                                                                                                                                                     Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-2 macroglobulin-like polypeptide variant;
antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozozacide; neuroprotective; antibacterial; fungicide; anticorvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; RGFR4; complement factor I precursor; matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 19.2; DB 1; Length 24;
87.5%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 10 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOV1 TET/TAMRA labelled probe SEQ ID NO:147.
                                                                                                                                                                                                     (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2328 TGTGTGCGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 TGCATGCATGTGTGTGTGTGTGTG 1
                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 14; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL57202 standard; DNA; 24 BP
                                                                                                                                 99WO-JP003551
                                                                                                                                                                     98JP-00232153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                      Sekino M;
                                                                                                                                                                                                                                                                        WPI; 2000-224692/19.
 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Haliotis discus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                               Haliotis discus
                                                                   WO200011156-A1
                                                                                                                                                                                                                                      ľakahashi H,
                                                                                                                                     01-JUL-1999;
                                                                                                                                                                     18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004
                                                                                                   02-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL57202;
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ADL57202
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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the gecification. A polypeptide of the invention has antidiabetic.

C anorectic, cardiant, Mypotensive, antiatreriosclerotic, anorectic, anorectic, antiatation. Hypotensive, antiatreriosclerotic, anorectic, antiatation, fungicide, protozoacide, nootropic.

C antilipamatory, dermatological, antiasthmatic, and antilpodies antiatreriotic, antiatrerior, antiparkinsonian, anticonvulsant, osteopathic, antilatematory. The polypeptides, nucleic acid molecules and antibodies in gene therapy. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder.

C are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder.

The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases (wiral, bacterial, fungal, dispetens), and protozoal), anorexia, cancer, cardiavascular diseases (wiral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiavascular diseases (costeoarthritis) hematopoletic disorders, inflammatory skin disorders, cathma, and various dyslipidaemias. The nucleic acids and polypeptides for the identification of small molecules may also be used as targets for the identification of small molecules proliferation, haematopolesis, wound healing and anglogenesis, in generation of antibodies that bind immunospecifically of proliferation, haematopolesis, wound healing and expenses for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, completens NOVIA-1 tehow homology to complement factor I precursor; NOVA shows homology to matrix metalloproteinser, and pharmacogenomics. The procusor; NOVA show homology to alpha-2 macroglobulin-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane protein-like, NOV12a-12c show homology to beta-neoendorphin-dynorphin precursor. The present sequence represents a probe used in the
                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections
                                                                                                                                                                                                                                                                                                                                    Padigaru M, Rieger DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; SEQ ID NO 147; 214pp; English.
                                                                                                                                                                                                                                                                                                                                  Zhong M, Guo X, Anderson DW, Ort T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the invention.
                                                                                                                                                  23.SEP-2002; 2002US-0412766P.
23.SEP-2002; 2002US-0412825P.
24.SEP-2002; 2002US-0412767P.
25.SEP-2002; 2002US-0413342P.
                       09-SEP-2003; 2003WO-US028141.
                                                                                   2002US-0409544P.
2002US-0410320P.
2002US-0411060P.
                                                                2002US-0409145P
                                                                                                                                                                                                                                              2002US-0414832P
                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-315567/29.
                                                                                     10-SEP-2002; 212-SEP-2002; 216-SEP-2002; 2
                                                                                                                                                                                                                                                 30-SEP-2002;
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Gaps

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ch 0.5%; Score 19.2; DB 1; Length 24; I Similarity 87.5%; Pred. No. 6.7e+02; 21; Conservative 0; Mismatches 3; Indels

Query Match Best Local Similarity

Matches

WO2004022723-A2

18-MAR-2004.

Homo sapiens

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1317 CACTGACAAGGACCTGTCGGACCT 1340

Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

vivlemore401-10.rng

RESULT 434

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring or family members of a gene and a cross-species comparison. Each of the nucleic acide further comprises at ag sequence. The array of nucleic acide for probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of many has hear has been been and a cross-species comparises by primer extensions or in screening content of the primer extensions or in screening content or probes and the sequence or specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 80269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 3 A; 8 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 80269; 9pp; English.
ACI80278 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2002; 2002US-00098263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cross-species comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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ACI80278/X

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       Score 19.2; DB 1; Length 25; Pred. No. 7e+02;
                              3; Indels
0.5%; Sco...
87.5%; Pred. No. /c...
                                                     2569 CACGGGACATCACAGGGTGCGCTC 2592
                                                                          21; Conservative
    Query Match
Best Local Similarity
Matches 21; Conservat
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RESULT 435 AAD40532/c

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population with an agent which increases fibroblast growth factor receptor 3 (FGFR3) expression or activity, where increase in FGFR3 protein expression or activity, where increase in FGFR3 protein expression or activity results in differentiation of the stem cells into osteoblast cells. The method is useful for stimulating the population of stem cells increases bone density. The method is useful for accening the agent increases bone density, or ameliorates the effects of osteoporosis. The method is useful for diagnosing a condition characterised by abnormal stem cell differentiation, bone density or rate of osteoblast formation and treating a patient with a condition characterised by an abnormal rate of osteoblast formation condition characterised by an abnormal rate of osteoblast formation of seteblast formation of seteblast formation, bone density or osteoporosis. The sequence is a RT-PCR primer used for human FGFR3 expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                                                            Human; stem cell; fibroblast growth factor receptor 3; FGFR3;
osteoblast cell; bone density; osteoporosis; osteopathic; receptor;
RT-PCR; primer; ss.
                                                                                                                                   Forward RT-PCR primer used for FGFR3 expression in human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Axelrod DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cook JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 3 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jaiswal N, Houghton A, Mertz L,
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                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001; 2001US-0285691P.
23-JUL-2001; 2001US-0306879P.
10-SEP-2001; 2001US-0317974P.
                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001; 2001WO-US048270.
                                                                                                                                                                                                                                                                                                                                                                                                                L8-DEC-2000; 2000US-0255882P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                  AAD40531 standard; DNA; 19
                                                                                            (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                             WO200250246-A2.
                                                                                              30-OCT-2002
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                                                       AAD40531;
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AAD40531
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19-NOV-2002 (first entry)

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population with an agent which increases fibroblast growth factor receptor 3 (FGFR3) expression or activity, where increase in FGFR3 protein expression or activity results in differentiation of the stem cells into osteoblast cells. The method is useful for stimulating the population of stem cells to differentiate into osteoblast cells. The method is useful for screening the agent increases bone density. The method is useful for screening the agent threases bone density, or ameliorates the effects of osteoporosis. The method is useful for diagnosing a condition characterised by abnormal stem cell differentiation, bone density or rate of osteoblast formation and treating a patient with a condition characterised by an abnormal rate of osteoblast formation, bone density or osteoblast. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                        Human; stem cell; fibroblast growth factor receptor 3; FGFR3;
osteoblast cell; bone density; osteoporosis; osteopathic; receptor;
RT-PCR; primer; ss.
                                                                                                 Reverse RT-PCR primer used for FGFR3 expression in human tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.4e+02; ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000US-0255882P.
24-APR-2001; 2001US-0288591P.
21-ZUL-2001; 2001US-038879P.
10-SEP-2001; 2001US-0317974P.
                                                                                                                                                                                                                                                                                                           18-DEC-2001; 2001WO-US048270.
                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
AAD40532 standard; DNA; 19
                                                                (first entry)
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                                                                  30-OCT-2002
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                                  AAD40532;
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ABQ81991
ID ABQ81995
XX
AC ABQ8199
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Cook JS, Axelrod DW;

Ji D,

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                                                                0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.4e+02; rive 0; Mismatches 0; Indels
                               Sequence 19 BP; 7 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma tag PCR primer, SEQ ID No 143.
                                                                                                                                               1702 CACAACCTCGACTACTACA 1720
                                                                                                                                                                                                                                                                                ADC13476 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                         18-DEC-2003 (first entry)
                                                                        Query Match 0.5
Best Local Similarity 100.
Matches 19; Conservative
present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                           RESULT 437
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has a tumour cell or site of anglogenesis, or if a treatment is effective in changing angiogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of siglec in a cell. Peripheral blood monouclear cell (PBMC)-expressed Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as an indicator of angiogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ82006 represent nucleotide sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; anglogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for determining if an individual
                                                                                                                                                                                                                                                                                                                                                                                                      Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
                                                                88
                                                            Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer;
                              Kaposi's Sarcoma TAG PCR primer SEQ ID NO:141.
                                                                                                                                                                                                                                                                                                     (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Page 24; 38pp; English
                                                                                                                                                                                                                                                                                                                                         Cornelissen M;
                                                                                                                                                                                                                                23-JAN-2001; 2001EP-00200228.
28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
                                                                                                                                                                                                   23-JAN-2002; 2002EP-00075264
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-668396/72.
                                                                                                                                                                                                                                                                                                                                       Van Der Kuyl AC,
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                                                                                                   Ното варіенв
                                                                                                                                  SP1225233-A2
                                                                                                                                                                   24-JUL-2002
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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell (PBMC) expressed Keratin 14, TIE 1, Salioadhesin, or Siglec 1 sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for checting the presence of a tumour cell in an individual. The expression product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This
                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, fibroblast growth factor 3; FGF3; flat epithelial cell; cancer;
flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 143; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1702 CACAACCTCGACTACTACA 1720
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                                                                                                                                                                                                                                                                                                         Van Der Kuyl AC, Cornelissen
                                                                                                 28-SEP-2001; 2001EP-00203703
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                                                                                                                                                                                                                                        (PRIM-) PRIMAGEN HOLDING BV
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Best Local Similarity 100.،
المالية المال
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                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-589342/56.
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                                    02-APR-2003.
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The present invention describes a method for the inspection of flat epithelial cells in which it is judged that flat epithelial cells epithelial cells in which it is judged that flat epithelial cancer when the separated from an organism can proceed to flat epithelial cancer when the case in fibroblast growth factor receptor (FGFR) gene of the cells is mutated from guanine to thymine. Also described is a method for coreaning treating or preventive agents for flat epithelial cancers in which a candidate substance of treating agent for flat epithelial cancer is applied to flat epithelial cancer cells producing FGFR protein in which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from guanine to thymine or the 697th amino acid is mutated from glycine to cysteine and said candidate substance is selected by using the facts that the 2128th base in the flat epithelial cell FGFR3 gene after the application returned to glycine as the indices. The method is used for the inspection of flat epithelial cells. The present sequence Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer. inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer. represents a PCR primer for human FGFR3, which is used in an example from Human, fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88. Gaps ö Query Match 0.5%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 19; Conservative 0; Mismatches 0; Indels Human fibroblast growth factor 3 exon 17 PCR primer #1. Seguence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other; 2048 ACGAGTACCTGGACCTGTC 2066 Example; Page 6; 18pp; Japanese. (ZERI) ZERIA SHINYAKU KOGYO KK. Example; Page 6; 18pp; Japanese. (ZERI) ZERIA SHINYAKU KOGYO KK 19 ACGAGTACCTGGACCTGTC 1 ACC79683 standard; DNA; 19 BP 22-MAR-2001; 2001JP-00083352 22-MAR-2001; 2001JP-00083352 27-AUG-2003 (first entry) the present invention WPI; 2003-345602/33. WPI; 2003-345602/33. JP2002272474-A. sapiens. 24-SEP-2002 Synthetic. ACC79683; RESULT 439 Homo 셤 ò

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Gaps ö

Example C; SEQ ID NO 146; 433pp; English.

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The present invention describes a method for the inspection of flat
epithelial cells in which it is judged that flat epithelial cells
separated from an organism can proceed to flat epithelial cancer when the
separated from an organism can proceed to flat epithelial cancer when the
constant pass in fibroblast growth factor receptor (FGFR) gene of the cells
is mutated from guanine to thymine. Also described is a method for
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constant cancers in
constant cancers in
constant constant cancer cells producing FGFR protein in
which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from
constants to thymine or the 697th amino acid is mutated from glycine to
constant cancers and said candidate substantes is selected by using the facts that
constant cancer and said candidate substantes is selected by using the facts that
constant cancer cancer cells FGFR3 gene after the
constant cancer and that the 697th amino acid of FGFR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention
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0.5%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 5.4e+02;
vative 0; Mismatches 0; Indels
                                                                              1777 GACCGAGTCTACACTCACC 1795
                                                                                                                  1 gacceaercracacrcace 19
                                             19; Conservative
                   Best_Local Similarity
Matches 19; Conserv
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Human NOVX protein-related PCR primer SeqID.
                             ADK51125 standard; DNA; 19 BP.
                                                                                                      (first entry)
                                                                                                      17-JUN-2004
                                                                   ADK51125;
RESULT 440
                    ADK5112
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cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; 88.

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05-ARR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-03720PP.
22-APR-2002; 2002US-037473P.
30-MAX-2002; 2002US-0384543P.
                                                                          01-APR-2003; 2003WO-US010142
                                                         WO2003083046-A2
                                                                                    02-APR-2002;
05-APR-2002;
                                                Homo sapiens
                                                                  09-OCT-2003.
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Casman SJ, Furtak K; MP, Li L, Spytek KA; Patturajan M; Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, 04-NOV-2002; 2002US-00287226. Smithson G; (CURA-) CURAGEN CORP. Rothenberg ME,

2002US-0403748P

15-AUG-2002;

The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cycosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotocxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.

Sequence 19 BP; 7 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

WPI; 2003-812539/76.

New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.

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                                                                                                                                                                                                                                                                                                                                                                                                                detection; RNA interference; siRNA; gene silencing; gene expression;
            This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                .
0
                                                                                                                                                                    0.5%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                             Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 61; 325pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                          RNA interference target sequence #47.
                                                                                                                                                                                                                           1283 TCACCGTAGCCGTGAAGAT 1301
                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-2003; 2003WO-JP014893.
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                                                                                                                                                                                                                                                                                                                  ADQ27139 standard; DNA; 19
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                                                                                                                                                                                                    19; Conservative
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                                                                                                                                                                             Query Match
Best Local Similarity
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(SAIG/) SAIGO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEIK/) TEI K. (NAIT/) NAITO Y.
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                                                                                                                             invention.
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The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3 'terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                   ss; detection; RNA interference; siRNA; gene silencing; gene expression;
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                   RNA interference target sequence #48.
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                                                                      26-AUG-2004 (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
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(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; RNA interference; siRNA; gene silencing; gene expression;
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                                                                      Gaps
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                         Length 19;
                                                                    0; Indels
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                      DB 1; Le
5.4e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                      CACAACCTCGACTACTACA 1720
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                                          Local Similarity 100.
nes 19; Conservative
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(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
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WO2004048566-A1 Homo sapiens.

ADQ27140 standard; DNA; 19 BP

RESULT 443

ADQ27140 ID ADQ2

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The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine,
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                                                                                                                                                                           The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is quanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
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                                       Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
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Pred. No. 5.4e+02;
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                                                                                                                                                Disclosure; SEQ ID NO 60; 325pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA interference target sequence #50.
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nes 19; Conservative
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            WPI; 2004-487423/46.
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(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
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Matches
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
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(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
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(NAIT/) NAITO Y.
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8 셤 ö

Gaps ö

0; Indels

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thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                    ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                                                                    ö
                                                                                              Score 19; DB 1; Length 19;
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stephen S;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                               Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:722.
                                                                         Sequence 19 BP; 6 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        William M,
                                                                                                   100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 12; SEQ ID NO 722; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devin L,
                                                                                                                                        1934 CACACGACCTGTACATGAT 1952
                                                                                                                                                   1 CACACGACCTGTACATGAT 19
                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-2003; 2003WO-US036787
                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002; 2002US-0426137P.
10-SEP-2003; 2003US-0502050P.
                                                                                              0.5%;
                                                                                                                                                                                                                ADQ61020 standard; RNA; 19
                                                                                                                                                                                                                                                          09-SEP-2004 (first entry)
                                                                                                                   19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angela R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DHAR-) DHARMACON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-420527/39.
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                              RNA interference.
                                                                                                                                                                                                                                                                                                                                                        WO2004045543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anastasia K,
                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004.
                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                     ADQ61020;
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siRNA and a second optimised siRNA. The method is useful in selecting siRNA for generating a gene silencing reagent. The present sequence is used in the exemplification of the invention. The sequence is shown in
                                                                                    Gaps
                                                                                                                                                                                                                                                   gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                                    ö
                                                                 Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                       William M, Stephen S;
                                                                                   0; Indels
                                                                                                                                                                                                                                Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:724.
                                              Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                             the specification as DNA, but described as siRNA
                                                                 Score 19; DB 1; L. Pred. No. 5.4e+02;
                                                                      100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; SEQ ID NO 724; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Devin L,
                                                                                                       383 GCATCAAGCTGCGCCATCA 401
                                                                                                                         1 GCATCAAGCTGCGGCATCA 19
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10-SEP-2003; 2003US-0502050P.
                                                                 0.5%;
                                                                                                                                                                        ADQ61022 standard; RNA; 19
                                                                          Local Similarity 100.
Les 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Anastasia K, Angela R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the target sequence.
                                                                                                                                                                                                                                                                                                                                                                                     (DHAR-) DHARMACON INC
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-420527/39.
                                                                                                                                                                                                                                                    ss; siRNA; gene s
RNA interference.
                                                                                                                                                                                                                                                                                                 WO2004045543-A2.
                                                                                                                                                                                                             09-SEP-2004
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                                                                                                                                                                                                                                                                               Synthetic.
                                                                 Query Match
Best Local Si
Matches 19;
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                                                                                                                                                     RESULT 448
                                                                                                                                                                 ADQ6102;
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used in the exemplification of the invention. The sequence is shown in the specification as DNA, but described as siRNA.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene silencing; Bcl-2; optimised; short interfering RNA;
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0
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                                                                                                               Length 19;
                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:721.
                                                                Sequence 19 BP; 6 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                  Score 19; DB 1; Lo
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      William M,
                                                                                                    0.5%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                          1700 TGCACACCTCGACTACTA 1718
                                                                                                                                                                                                                                                     1 recachactrosactacta 19
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                                                                                                                                                                                                                                                                                                                                                                       ADQ61019 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                     Sest Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; siRNA; gene s
RNA interference.
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                                                                                                                         Query Match
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AD061019

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DE ANTI-FR

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The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of sequences of 19-25 nucleotides in length that are substantially complementary to a stretch of nucleotides of the target sequence, where the functionality is dependent upon non-target specific sequence, where the functionality is dependent upon non-target specific sequence; where the functionality is dependent upon non-target specific sirana also claimed are methods for gene-silencing, developing an sirana algorithm for selecting sirana, selecting an sirana with improved functionality, selecting hyperfunctional sirana, a sirana molecule comprises a sequence substantially similar to sirana. The sirana molecule compress a sequence substantially similar to sirana. The sirana of GAGAGUUGGUUGAUU, GAAGUAGUGAUU,

CAUGAGGCCUUGUUUGA, UGCGGCCUUGUUGAUU, GAAGUAGUGAUUGAUU,

CAUGAGGCCUUGUUUGA, UGCGGCCUUGUUGAUU, GAAGUAGUGAUU,

CAUGAGGCCUUGUUUGA, UGCGGCCUUGUUGAUU, GAAGUAGUGAUU,

CAUGAGGCCUUGUUUGA, UGCGGCCUUGUUGAUU, GAAGUAGUGAUACAGUUCA,

CAUGAGGCCUUGUUGAUU, GAAGAUUGCUUGCUUGAUUGAUU, GAAGUAGUGAUGAUACAGUUCA,

CAUGAGGGCCUUGUUUGA, UGCGGCCUUGUUUGAUU, GAAGUAGUGAUGAUACAGUUCA,

CAUGAGGGCCUUGUUUGA, UGCGGCCUUGUUUGAUU, GAAGUAGUGAUGAUGAUACAGUUCA,

CAUGAGGGCCUUGUUUGA, UGCGGCCUUGUUUGAUU, GAAGUAGUGAUGAUGAUACAGUUCA,

CAUGAGGGCCUUGUUUGA, UGCGGCCUUGUUUGAUUU, GAAGUAGUGAUGAUGAUACAGUUCA,

CAUGAGGGCCUUGUUUGA, UGCGGCCUUGUUUGAUUU, GAAGUAGUGAUGAUACAGUUCA,

CAUGAGGCCUUGUUUGA, UGCGGCCUUGUUUGAUUU, GAAGUAGUGAUGAUACAGUUCA,

CAUGAGGGCCUUCUUUGA, UGCGGCCUUCUUGUUCAGUUCA,

CAUGAGGGCCUUCUUGAUUA,

CAUGAGGGCCUUCUUGAUUA,

CAUGAGGGCCUUCUUGAUUA,

CAUGAGGGCCUUCUUGAUUA,

CAUGAGGGCCUUCUUGAUUA,

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CAUGAGGGCCUUCUUGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene silencing; Bcl-2; optimised; short interfering RNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stephen S;
                                                        Score 19; DB 1; Length 19;
Pred. No. 5.4e+02;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:723.
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            Sequence 19 BP; 2 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devin L, William M,
                                                                                      ilarity 100.0%; Pred. No. 5.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; SEQ ID NO 723; 199pp; English
                                                                                                                                                              1331 TGTCGGACCTGGTGTCTGA 1349
                                                                                                                                                                                                            1 reredakerereka 19
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                                                                                                                                                                                                                                                                                                                                    ADQ61021 standard; RNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2002; 2002US-0426137P.
10-SEP-2003; 2003US-0502050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the target sequence.
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                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; siRNA; gene a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004045543-A2
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                                                                                                                                                                                                                                                                                                                                                                                       ADQ61021;
                                                                                                                                                                                                                                                                                         RESULT 450
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The present invention describes using a leukotriene synthesis inhibitor

(I) for the manufacture of a medicament for the treatment of myocardial infraction in an individual.

Also described is a method (MI) for the treatment of acute coronary

Also described is a method (MI) for the treatment of acute coronary

antiatherosclerotic, cardiant and antianginal activities, and can be used

as a leukotriene biosynthesis inhibitor, and a leukotriene receptor

antiatherosclerotic, cardiant and antianginal activities, and can be used

as a leukotriene biosynthesis inhibitor, and a leukotriene receptor

cantagonist. (I) can be use for the manufacture of a medicament for the

treatment of myocardial infarction or susceptibility to myocardial

infarction in an individual who has at least one risk factor chosen from

an at-risk haplotype for myocardial infarction, an at-risk haplotype in

the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a

cc flap nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-

CD) gene promoter; in an individual who has at least one risk factor

chosen from diabetes, hypertension, hypercholesterolaemia, elevated

chosen from diabetes, hypertension, hypercholesterolaemia, elevated

inflammatory marker chosen from Creactive protein (CRP), serum amyloid

A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue

necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukotriene synthesis inhibitor; myocardial infarction; antianginal; acute coronary syndrome; antiatherosclerotic; cardiant; antianginal; leukotriene biosynthesis inhibitor; leukotriene receptor antagonist; 5-lipoxygenase activating protein; FiAP; human; chromosome 13; chromosome 134; polymorphism; 5-lipoxygenase gene promoter; 5-LO gene promoter; diabetes; hypertension; hyporrohiserscholesterolaemia; obesity; inflammatory marker; low density lipoprotein; cholesterol; high density lipoprotein; angina; atherosclerosis; microsatellite marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of leukotriene synthesis inhibitor for manufacture of a medicament for treatment for myocardial infarction or susceptibility to myocardial infarction in individual.
                                                                              Gaps
                                                                              ;
0
   Length 19;
                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FLAP related microsatellite marker SEQ ID NO:394
   DB 1; Le
5.4e+02;
   0.5%; Score 19; DB
100.0%; Pred. No. 5.4
ive 0; Mismatches
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                                                                                                                                                    GGACGCCCCCTACGTT 693
                                                                                                                                                                                                                           1 GGACGCCACACCTACGTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2003; 2003WO-US032556
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADNO6744 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004 (first entry)
                                                                              19; Conservative
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Query Match
Best Local Similarity
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soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-1, matrix metalloprotease type-9, in an metalloprotease type-9, in an individual having increased low density lipoprotein (IDL) cholesterol in and/or decreased high density lipoprotein (HDL) cholesterol, in an individual having increased leukotriene synthesis; in an individual having previous myocardial infarction or acute coronary syndrome (ACS) event, stable angina; or in an individual who has atherosolerosis or who receive myocardial infarction of low in arteries (MI) is useful for treating an individual suffering from acute coronary syndrome chosen from unstable angina, non-ST-elevation myocardial infarction (STEMI). The human FLAP gene is located on chromosome 13, more specifically to 13q12. The present sequence represents a microsatellite marker used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a composition comprising a polypeptide having a first domain with carbohydrate binding activity and a second domain with kinase activity, a first domain with discoidin-type ligand binding characteristics and a second domain with tyrosine kinase activity. The invention is useful to diagnose, prognose and treat a patient having surface. The present sequence represents a tyrosine kinase antisen oligonculectide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new polypeptide has a discoidin-type ligand binding domain and a yrosine kinase domain and is useful to diagnose and treat a patient naving tumors of epithelial type cells which express the polypeptide on
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; antisense; tyrosine kinase; epithelial type cell tumour.
                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 19; DB 1; Length 20;
100.0%; Pred. No. 5.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 9 A; 10 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine kinase antisene oligonculeotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGCGT 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 rerererererererecer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE79941 standard; cDNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson JD, Rutter WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JOHN/) JOHNSON J D. (RUTT/) RUTTER W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-009136/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EDMA/) EDMAN J C.
                                                                                                                                                                                                                                                                               present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE79941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE79941/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8
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AAF63628 standard; DNA; 27 BP.

RESULT 454 AAF63628/

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of 500

CC clones cross-hybridised. Assuming independent distribution of 500

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 210 such bovine microsatellites is summarised in the

Specification and indexed herein (see below). The sequences upstream and

CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence waset to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify important traits esp. in cattle, to allow selective

CC connomically important traits esp. in cattle, to allow selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                              PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                   / Match 0.5%; Score 19; DB 1; Length 24; Local Similarity 69.6%; Pred. No. 7.1e+02; les 16; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 BP; 2 A; 1 C; 12 G; 11 T; 0 U; 0 Other;
     Seguence 24 BP; 1 A; 6 C; 7 G; 4 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                               Sequence of a microsatellite from clone TGLA70B.
                                                                                                             1618 cacagegaccigecigcocceca 1640
                                                                                                                               24 CAYCGSGAYCTGGCYGCYCGSAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 383; 517pp; English.
                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00642342.
                                                                                                                                                                                                                                    AAQ34131 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1992;
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                                                                                                                                                                                                                                                                                                      25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus.
                                                                                                                                                                                                                                                                       AAQ34131;
                                              Query Match
                                                                                                                                                                                                   RESULT 453
                                                                                Matches
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The present invention describes a method for the production of isogenic transgenic plant lines (A) by transforming cells of a hybrid with T-DNA transgenic plant lines (A) by transforming cells of a hybrid with T-DNA vector containing a transgene (I), the hybrid being derived by crossing a vector containing a transgene (I), the hybrid being derived by crossing a containing transformation (LT).

Inc of interest (LI) and a line suitable for transformation (LT) in the products only, then back-crossed with LI and selection of T-DNA into the LI cenome only, then back-crossed with LI and selection of products until contained. The method is used for introgenession of several cransgenic characteristics into a plant. (I) may express an antisense transgenic characteristics into a plant. (I) may express an antisense cond/or improves some agronomic or nutritional property. By selecting primary transformatts, the method allows introduction of genes without confinence in it makes possible production of truly isotransgenic lines which (I) can be transferred to a plant genome is increased, since the which (I) can be transferred to a plant genome is increased for mumber of backcrossings required is reduced and the genetic sources for moduction of commercial hybrids is significantly broadened. The present sequence (I,e, a GSPLB oligonucleotide) in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of transgenic plant lines, useful for producing elite hybrids with transgenic characteristics, includes selection for incorporation of transgene into particular parent.
                                                                                                                                          Isogenic transgenic plant; line; T-DNA; transformation; cross-breeding;
hybrid; plant; characterisation; amplification; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 0.5%; Score 19; DB 1; Length 27; Local Similarity 81.5%; Pred. No. 8e+02; Conservative 0; Mismatches 5; Indels
                                                                                                    Isogenic tranagenic plant line related GSPLB4 SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 BP; 5 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3639 GGGCAGCTGTCCTTGCTTGCAG 3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 36; 44pp; French.
                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1999; 99FR-0009990.
                                                                                                                                                                                                                                                                                                                                                   25-JUL-2000; 2000WO-FR002130.
                                                                     04-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-168557/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez P, Garcia D;
                                                                                                                                                                                                                                                                        WO200107632-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (RHOB-) RHOBIO.
                                                                                                                                                                                                                                                                                                                  31-FEB-2001.
                                                                                                                                                                                                                                Synthetic.
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                                   AAF63628;
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Matches
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GAGCAGCTGAAGCTTGCATGCCTGCAG 1

AAQ33888 standard; DNA; 22 BP.

RESULT 455 AAQ33888 ID: AAO3

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0; Gaps

2333 GCGTGTGTGTGTGTGTG 2351 7 ccercrerererererere

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comnstream of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
bredging. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroepithelial stem cell; lineage restricted intermediate precursor; oligodendroyte; astrocyte; self-renemal; neuron; differentiation; neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS central nervous system; glial cell; PCR primer; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.8; DB 1; Length 22;
Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     rable 7; Page 216; 517pp; English
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                                                                                                                                                       92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.5
Best Local Similarity 90.9
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                         Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                              GENM-) GENMARK.
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                                                               WO9213102-A1
                                                                                                                                                       15-JAN-1992;
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                     Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACI)5 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information converted the microsatellite sequence were used to generate the required for prince for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                       PCR; selection; primers, OPTIPRIM; breeding; cattle, parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 18.8; DB 1; Length 22; ilarity 90.9%; Pred. No. 6.7e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA135.
                                                                                                                               Microsatellite sequence from clone TGLA306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2330 TGTGCGTGTGTGTGTGTGTG 2351
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                                                             (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                           WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1992;
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                                                             25-MAR-2003
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02-FEB-1993
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                                                                                       02-FEB-1993
                                                                                                                                                                                                                                                                                                                                        06-AUG-1992
                                                                                                                                                                                                                                              Bos taurus
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                     AAQ33888;
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RESULT 456
AAQ33716
XX
XX
AC AAQ3371
DT 25-MAR.
DT 25-MAR.
DT 02-PBB.
XX
DE Micross
XX
XX
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XX
GER, 56

Best Loc Matches

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Gaps

Ohlsen KL;

Bussey H,

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Example 26; Page 58; 78pp; English.
                                                                                                                                                                                                                                                26-DEC-2001; 2001WO-US049486.
             (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                   ABZ29984 standard; DNA; 22
                          WPI; 1999-070093/06.
                                                                                                                                                                                                                            Candida albicans
                                                                                                                                                                                                                                   WO200253728-A2.
  07-MAY-1997;
06-MAY-1998;
                                                                                                                                                                                                 30-JAN-2003
                                                                                                                                                                                                                                          11-JUL-2002.
                                                                                                                                 FGFR genes
                                                                                                                                                                                          ABZ29984;
                    Rao MS,
                                                                                                                                                                             RESULT 458
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The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by a large one allele by insertion, of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter, (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells maying both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal adent, an antifungal agent that inhibits the growth of a fungus to an antifungal and for identifying a therapeutic agent for treatment of a mammalian disasse. (MI) is useful for identifying a compound which modulates the cativity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, cativity. The method is useful for identifying a compound having the cativity. The method is useful for identifying a compound having the cativity of inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a per primer used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based or perfect this patent is not represented in the printed specification but is based or construction.
                                                                                                                                                                                                                      Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma; bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 18.8; DB 1; Length 22; 90.9%; Pred. No. 6.7e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ASTH11 5' region polymorphic site, SEQ ID NO:103 (a).
                                                                                                                                                                                                                                                                                                                    Claim 36; SEQ ID NO 4135; 167pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 9 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2322 TGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 reracerererecerererere 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA80357 standard; DNA; 23 BP
                                                                                                                                  Boone C,
              20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                  Roemer T, Jiang B,
                                                                                                                                                                                 WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA80357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA80357
%X6666666666666666666666668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTFXSXXWWWWXXBXTXTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                         Mammalian neuroepithelial stem cells and glial restricted precursor - can self renew and differentiate into central nervous system cells, used for generating various types of cells.
                                                                                                                                                                                                                                                                                                                                                                          present invention describes an isolated, pure population of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an example from the present invention to amplify different FGF and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.5%; Score 18.8; DB 1; Length 22; Best Local Similarity 90.9%; Pred. No. 6.7e+02; Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans GRACE strain PCR primer SEQ ID NO 4135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 5 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                          Mayer-Proschel M, Mujtaba T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 AGCCTGGTCATGGAAAGCGTGG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agcrrregreardeanage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                        97US-00852744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Gaps

; 0

replace(12. .13, TGTGTA) /*tag= a

variation

Location/Qualifiers

Homo sapiens

US6087485-A 11-JUL-2000.

vivlemore401-10.rng

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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
                                                                           repeat; ISSR; SSR; PCR; primer; genotyping; plant;
88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligodeoxyribonucleotide; intersubunit linkage; phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 18.8; DB 1; Length 23; 90.9%; Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 23 BP; 1 A; 1 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified DNA oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                5' anchored (ISSR)-PCR primer - SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 Grandrerererererer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2315 GTCTGTGTGTGTGTGTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                    09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                                                                                                                                                                               08-APR-2002; 2002IN-CH000260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic disorder; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX59719 standard; DNA; 24
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                inter-simple sequence
animal; Basmati rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-804317/75.
                                                                                                                                                                                                                    WO2003085133-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9525814-A1
15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagaraju JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1995
                                                                                                                                                                                                                                                                    16-OCT-2003
                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX59719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX59719/
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH1I and ASTH1I ocus, which are suscitated with a genetic predaposition to asthma and bronchial hyperreactivity. The ASTH1I locus, and have similar patterns of expression and common sequence motifs. They are both expressed in trachea, lung and adered of transcription factors, which have been implicated in the est family of transcription factors, which have been implicated in the activation of a variety of genes including the TCRs gene and cytckine genes known to be important in the actiology of asthma. Both ASTH1I and ASTH1I mand ASTH1I mand ASTH1I mand ASTH1I mand ASTH1I will as a variety of genes including the TCRs gene and cytckine crowns involved are all 5' to the start codon in exon b. In contrast, alternative splicing of ASTH1I transcripts results in 3 different ASTH1I incled are all 5' to the start codon in exon b. In contrast, attending a series are useful as diagnostics to identifying ASTH1 related genes, for identifying expression of the gene in a biological specific gene modifications in cell lines. The encoded ASTH1 proteins are useful as immunogens to raise specific antibodies; in drug screening for compositions that minic or modulate activity or expression of ASTH1I and as a therapeutic. The ASTH1 genes or fragments thereof, encoded proteins, and charapeutic additional in the identification of individuals predisposed to development of aethma, and for modulation of gene activity in vivo for prophylactic and therapeutic purposes. The intact ASTH1I and and ASTH1I contrast. ASTH1I and the identification of individuals predise proteins or active fragments thereof may be used to modulate or reduce bronchal hyperreactivity, sequences. The intact ASTH1I and AMAB0264-AB0416 contrast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein. for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent polymorphic sites within the ASTH1J or ASTH1I genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 18.8; DB 1; Length 23; 90.9%; Pred. No. 7.18+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           Cardon L, Buckler A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 1 A; 2 C; 11 G; 9 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Col 41-42; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 rerererererarerecere 23
                                                                                                                                                                                                                                                                                           North M,
                                                                                                                                                                                                                                                                    Miller A, No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD69447 standard; DNA; 23 BP
                                                                                                                    98US-00009913
                                                                                                                                                                    97US-0035663P
97US-0051432P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
                                                                                                                                                                                                                                             (AXYS-) AXYS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-505109/45.
                                                                                                                                                                                                                                                                                           Galvin M, Miller
Brooks-Wilson AR,
                                                                                                                         21-JAN-1998;
                                                                                                                                                                      21-JAN-1997;
                                                                                                                                                                                                01-JUL-1997;
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Gaps .. 0

Indela

95WO-US003575 94US-00210505

20-MAR-1995; 18-MAR-1994;

ADD69447;

RESULT 460
ADD69447
ID ADD6944
XX
AC ADD6944

Query Match

Matches

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95WO-US003575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-130681/12.
                                                                                                                                                                                                                           WPI; 1995-344627/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UROC-) UROCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9804689-A1
                                                                                                                            (LYNX-) LYNX
20-MAR-1995;
                                                                                                                                                                           Gryaznov SM,
                                                  L8-MAR-1994;
                                                                            18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-1998
                                                                                                                                                                                                                                                                                                                                RNA strands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV26338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                             nucleoside subunits joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The closed action with a target nucleic acid molecule. The oligodeoxyribonucleotides has a sequence of nucleoside subunits effective to form a duplex with a target nucleic acid molecule. The oligodeoxyribonucleotides are more resistant to nuclease digestion and have improved RNA and dsDNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cytcoxicity. They may be used in diagnostic and therapeutic applications, e.g., in combatting infections agents such as bacteria, viruses, etc. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, etc. . The present sequence represents an oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                         Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and
                                                                                                                                                                                                                                                                                                                                                             specification describes oligodeoxyribonucleotides having contiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "each base is linked by N3'-P5' phosphoramidate
linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= a
note= "each base is linked by N3'-P5' phosphoramidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified oligonucleotide containing N3'-P5' phosphoramidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 18.8; DB 1; Length 24; ilarity 90.9%; Pred. No. 7.48+02; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 10 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligodeoxyribonucleotide; intersubunit linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2823 TATATATATATATATATA 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Disclosure; Page 54; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 rarararaaaarararara 1
                                                          (LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder; cancer; ss.
          94US-00214599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX59721 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                            Schultz RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                            WPI; 1995-344627/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified base
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             18-MAR-1994;
                                                                                                            Gryaznov SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999
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                                                                                                                                                                                                                                                                   RNA strands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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The specification describes oligodeoxyribonucleotides having contiguous uncleoside subunits are joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The oligodeoxyribonucleotides has a sequence of nucleoside subunits effective consignation with a target nucleic acid molecule. The coligodeoxyribonucleotides are more resistant to nuclease digestion and have improved RNA and dsDNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity in combatting infections agents such as bacteria, viruses, etc. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, etc. The present sequence represents an oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 10 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 57; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralph
                                                                                                                                                                                                                            Chen J;
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                                                                                                                                      THERAPEUTICS INC
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94US-00210505.
94US-00214599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                 Schultz RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
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This primer is used in the relative quantitative RT-PCR to examine the expression of the genes which is used for the identification of markers of human prostate cancer. Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer markers are provided in the specification. The specification also provides methods for identifying markers for human prostate cancer and for detection of prostate cancer calls. The markers can be identified by amplifying human prostate RNA to provide nucleic acid amplification products, separating the products and identifying those RNA that are differentially expressed between human cells in a sample can be detected by detecting a nucleic acid in a sample, the nucleic acid being a prostate cancer marker. Primers and probes derived from this marker can be used for the detection of prostate cancer calls in a sample. Antibodies against the protein encoded by the marker nucleic acid fragments, inhibitors of the protein and olygonucleotides antisense to the markers can be used for the diagnosis of prostate cancer.
Human prostate cancer marker - useful for detection and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                 Example 4; Page 121; 229pp; English.
                              human prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human prostate cancer
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ö 0.5%; Score 18.8; DB 1; Length 24; 90.9%; Pred. No. 7.4e+02; 2; Indels 0; Mismatches 2329 GTGTGCGTGTGTGTGTGTGT 2350 22 GTGTGCATGTGTGTCTGTGT 1 Best Local Similarity 90.9 Matches 20; Conservative Query Match ð g

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Gaps

AAX26085 standard; DNA; 24 BP. AAX26085;

20-MAY-1999 (first entry)

Prostate disease marker gene fragment amplifying RT-PCR primer.

Prostate cancer; benign prostatic hyperplasia; marker gene; tumour; differentiation; Reverse Transcription Polymerase Chain Reaction; diagnostic; progression; cancer; metastasis; RT-PCR; primer; ss.

Homo sapiens. Synthetic

US5882864-A.

16-MAR-1999

96US-00692787 31-JUL-1996; 95US-0001655P 31-JUL-1995;

(UROC-) UROCOR INC.

WPI; 1999-214055/18.

O'hara SM;

An G,

Veltri R, Ralph D,

Diagnosing prostate cancer and benign prostatic hyperplasia cells - using oligonuclectide probes specific for marker genes associated with tumor differentiation and progression in Reverse Transcription Polymerase Chain Reaction analysis.

Example 4; Col 66; 74pp; English

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate till length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer. Ladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in munondetection methods for detecting or quantifying the cancers, and for
               The invention relates to methods for diagnosing prostate cancer or benign prostatic hyperplasia cells in a biological sample. The method uses oligomucleotides specific for marker genes associated with tumour differentiation and progression in Reverse Transcription Polymerase Chain Reaction (RT-PCR) analysis. The methods are diagnossic techniques useful for detecting and monitoring the progression of benign prostatic hyperplasia and human prostate cancer (the most prevalent form of cancer and a major cause of death in males) prior to the tumor undergoing metacasis, therefore allowing the optimal method of treatment to be determined before the condition becomes life threatening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection; diagnosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel RNA biomarkers for diagnosis, prognosis and management of prostate,
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                  Local Similarity 90.9%; Score 18.8; DB 1; Length 24; es 20; Conservative 0; Minmart.
                                                                                                                                                                                                                                                Seguence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer specific for cancer biomarker UC Band #210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An G, O'hara SM, Ralph D, Veltri RW;
                                                                                                                                                                                                                                                                                                                                                                         2329 GTGTGCGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 111; 191pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ87571 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UROC-) UROCOR INC.
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Matches
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22 GTGTGCATGTGTGTCTGTGT 1

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ACI77097 standard; DNA; 25 BP

ACI77097,

RESULT

Human microarray DNA oligonucleotide SEQ ID NO 77088.

(first entry)

14-OCT-2003

ACI77097;

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The sequence represents nucleic acid biomarker UC band 210 primer #1, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including libraries, as hybridisation probes for screening genomic human DNA libraries. The ktts comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                     Biomarker UC band 210 primer #1 used in diagnosis/prognosis of cancer.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Prostate; breast; bladder; cancer; biomarker; probe; diagnostic;
benign prostatic hyperplasia; BPH; therapeutic; human; primer; ss.
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                                                                                    Length 24;
                                                                                                                     2; Indels
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                                                    Sequence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                  Score 18.8; DB 1;
Pred. No. 7.4e+02;
0; Mismatches 2;
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                                                                                                                                                      2329 GTGTGCGTGTGTGTGTGTGT 2350
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                                                                                                                                                                           22 GTGTGCATGTGTGTCTGTGT 1
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96US-0013611P.
96US-00692787.
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Local Similarity 90.9%;
nes 20; Conservative (
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                                                                                                                                                                                                                                                                                                                                           29-AUG-2001 (first entry)
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11-JAN-1996;
31-JUL-1996;
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Matches
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Sector for comparison levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison.

CC remily members of a gene and a cross-species comparison.

CC remily method in in situ hybridisation, in Southern, Northern or dotprobes is useful in in situ hybridisation, in Southern, Northern or dotpropression so fany gene, in mapping the 5' termini of mRNA molecules by primer extensions of any gene, in mapping the 5' termini of mRNA molecules by crimer extensions or in screening solwh or genomic libraries or subclones containing segments of DNA that have been contained probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly crow in sequence. The sequence contains of any end in electronic format directly contained in electronic format directly the sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                   EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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0.5%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 7.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 77088; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2569 CACGGGACATCACAGGGTGCGC 2590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                          cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mittmann MP;
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Gaps

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2329 GIGIGCGIGIGIGIGIGIGI 2350

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Query Match

Best Loca Matches

BP.

AAA95390 standard; DNA; 20

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                              EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 36641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 36641; 9pp; English.
                                                                    ACI36650 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   cross-species comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003104410-A1
                                                                                                                                                                                                   13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2003.
                                                                                                                                  ACI36650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
      468
RESULT 46.

ID AC13 6650

ID AC13 6650

XX AC13 6650

XX BST;

XX BST;

XX BST;

XX HOMC

XX
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are altached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening segments of DNA that have been containing segments of DNA that have been containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from USPTO at sequence.html
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primer; 88.
                                                                                                                                                                          Synthetic.
AAV05313;
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                                                                                                       Gaps
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                                                                   0.5%; Score 18.8; DB 1; Length 25; 90.9%; Pred. No. 7.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                        2334 CGTGTGTGTGTGTGCACA 2355
                                                                                                                                                                          cerererererriecerecaca 22
                                                                                       Best Local Similarity 90.9
Matches 20; Conservative
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The present invention describes the rat Nurrl coding and protein sequences. The Nurrl protein is involved in the induction of tyrosine hydroxylase expression in adult rat-derived hippocampal progenitor cells. The Nurrl gene and protein can be used in the treatment of catecholamine-related diseases such as Parkinson's disease, manic depression and schizophrenia. They can also be used to induce tyrosine hydroxylase expression and identify tyrosine hydroxylase related deficiencies, which are linked to the same diseases. The present sequence is a PCR primer used in a method to differentiate adult neural progenitor cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams syndrome cognitive profile; WSCP; cognition; LIM-kinase 1; LIMK1 gene; supra-vascular aortic stenosis; protein kinase; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase expression useful for treating catecholamine-related diseases such as Parkinson's disease, manic depression and schizophrenia.
                                                                                                                                            Rat; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 18.6; DB 1; Length 20; 90.0%; Pred. No. 6.4e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 6 A; 1 C; 7 G; 4 T; 0 U; 2 Other;
                                                                                                              Rat FGFR coding sequence PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                         (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1345 TCTGAGATGGAGATGATGAA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 20; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCNGAGATGGAGRTGATGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV05313 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                           21-MAR-2000; 2000WO-US007544.
                                                                                                                                                                                                                                                                                                                           26-MAR-1999; 99US-00277078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase domain 5' PCR primer.
                                                                              12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Sakurada K, Palmer T,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-656165/63.
                                                                                                                                                                                             Rattus norvegicus.
                                                                                                                                                                                                                           WO200058451-A1.
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                                                                                                                                                                                                                                                         05-OCT-2000.
                                                AAA95390;
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AAV05313
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ABS75681;
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                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                       This oligonucleotide was designed to amplify the region of homology in the kinase domains of PDGF receptor, HER2, HER3, FGF-FLG, FGF-BEK, insulin receptor and IRR. It was used with another kinase homology domain-based primer (see AAV05314) in the amplification of human LIM-kinase 1 (LIMK1) sequences. The LIMK1 gene is composed of 16 exons (see AAV05315 and AAY99599-T99629) and is located 15.4 kb 3' of elsethin in chromosome 7. It encodes a novel protein kinase (see AAW6576). Williams syndrome cognitive profile (WSCP) is detected by determining zygosity of the LIMK1 locus, with hemizygosity being indicative of impaired visuo-spatial constructive cognition. Chromosome 7 deletion analysis allows discrimination between WSCP, SVAS (supra-vascular aortic stenosis) and Williams syndrome
                                                                                                                        Diagnosing Williams syndrome cognitive profile from hemi-zygosity of LIMX1 - gene on chromosome 7 encoding new kinase, allowing differentiation from classic Williams syndrome and supra-vascular aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZAP-70; Zeta chain-associated protein; treatment; prevention; disease; immunosuppressor; cancer; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                      Score 18.6; DB 1; Length 25;
Pred. No. 8.2e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 4 A; 6 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                               1678 GACTTCGGCTTGGCCCGGGACGTGC 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                  GACTITIGGGCTGGCTCGAGACATGC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV73860 standard; cDNA to mRNA; 25
                                                                                                                                                                          Example 3; Page 22; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian ZAP-70 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-00130952.
                                                                                                                                                                                                                                                                                                                                          ch 0.5%;
1 Similarity 84.0%;
21, Conservative 0
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                              97WO-US011687
                                                96US-00678039
                                                                  (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                     Keating MT, Morris CA;
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                                                                                                          WPI; 1998-101185/09.
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26-FEB-1999
                              07-JUL-1997;
                                                 10-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32-DEC-1998
           15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                           stenosis.
                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                       AAV73860-V73865 are PCR primers used in the amplification of a mammalian zeta chain-associated protein, ZAP-70. This protein can be used for the prevention and the treatment of illnesses having an immunosuppressive component such as cancer and infectious diseases. (Updated on 27-AUG-2003
Immune activator comprising membrane-localised ZAP-70 - useful for the prevention and the treatment of conditions exhibiting immunosuppression such as cancers and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 18.6; DB 1; Length 25; 34.0%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 3 A; 11 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PAPP-Ea associated 25-mer SEQ ID 1207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1625 ACCTGGCTGCCCGCAATGTGCTGGT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGGCGGCCCGCAACGTCCTGCT 25
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                                                                                                                                                                      Example 1; Page 16; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Gaps

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0.5%; Score 18.6; DB 1; Length 25; 84.0%; Pred. No. 8.2e+02; ive 0; Mismatches 4; Indels

Conservative

Best Local Similarity Matches 21; Conserv

Query Match

AAQ34170 standard; DNA; 20

RESULT 474 AAQ34170

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Gaps

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridiantion to a DNA library, in analysis of genetic variation or in hybridiantion of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the cucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotter the hybridisation to identify or detect the sequence or specific metations of any gene, in mapping the 5, terminio of mutations of any gene, in mapping the 5, terminio of mutations of any gene, in mapping the 5, terminio of mutations of any gene, in mapping the 5, terminio of mutations of any gene, in mapping the 5, terminio of mutations of any gene, in mapping the 5, terminion of mutations of any gene, in mapping the 5, terminion of mapping the 5, terminion of mutations of any gene, in mapping the 5, terminion of mapping the 5, terminion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                Length 25;
                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human microarray DNA oligonucleotide SEQ ID NO 44261
Sequence 25 BP; 2 A; 0 C; 10 G; 13 T; 0 U; 0 Other;
                                                                            Score 18.6; DB 1;
Pred. No. 8.2e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                           2321 GIGIGIGIGIGIGIGIGIGIGIGIG 2345
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                                                                            0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACI44270 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-2003 (first entry)
                                                                                                                                                                      21; Conservative
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                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                               Matches
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AC144270/C

ID AC144270/C

XX AC144

XX AC144

XX AC144

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KW EST;

KW EST
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

WO9213102-A1.

Bos taurus.

06-AUG-1992

Sequence of a microsatellite from clone TGLA86.

(revised)
(first entry)

25-MAR-2003 02-FEB-1993

AAQ34170;

bp with an (AC)15 and a (TC)15 oligomuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 a 0.5%; Score 18.4; DB 1; Length 20; illarity 95.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 1; Indels Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGCGTG 2337 Local Similarity nes 19; Conserv Query Match Matches à d primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly

and 500

used in genetic identification, gene

Table 7; Page 397; 517pp; English

Polymorphic bovine DNA markers - mapping, and selective breeding.

91US-00642342. 92WO-US000340.

15-JAN-1991; 15-JAN-1992;

Georges M, Massey JM; WPI; 1992-284684/34.

GENM-) GENMARK.

Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;

from USPTO at segdata.uspto.goc/seguence.html

RESULT 475

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Gaps

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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                     GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                               15-JAN-1991;
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24-FEB-1998
                                                                                                                  409213102-A1
                                                                                                                                                                                                    15-JAN-1992;
                                                                                                                                                            06-AUG-1992
                                                                       Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT93829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT93829
        T#X8XXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a bovine microsatellite sequence obtd. by

conscienting a library of bovine MboI DNA fragments of between 250 and 500

constant an (APC)15 and a (TPC)15 oligonucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

conscient a penome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

construer of the microsatellite sequence waset to generate the

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program opriperIM). The microsatellites may be

microsatellity individuals, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

conomically important traits esp. in cattle, to allow selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                        PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                       Microsatellite sequence from clone TGLA22.
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                                      AAQ33816 standard; DNA; 20
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(first entry)
                                                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
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02-FEB-1993
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02-FEB-1993
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                                                                                  AAQ33816;
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                 AAQ33816

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and whost microsatellites is summarised in the sequence information of for ca. 230 such bovine microsatellites is summarised in the sequence used to specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connecting in microsatellite is a marker for the Weaver condition and the QTL trait of enhanced milk prodn. in Brown Swiss condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antitumoural phosphodiester oligonucleotide 19 with cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rable 7; Page 198; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Grererererererer
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92WO-US000340.
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Oligo:nucleotide which binds to retroviral nucleocapsid protein with high affinity - used in targeted molecules, transduced cells and gene therapy vectors for treatment of retroviral infections such as those caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid binding, and for purification of retroviral NC proteins. In particular, the targeted molecules, the transduced cells and gene therapy vectors based on the oligonucleotides can be used for treatment and prevention of retroviral infections such as those caused by HIV
                                                                                                                                                                                                                                         This sequence represents an oligonucleotide which binds to a retroviral nucleocapsid (NC) protein with high affinity. The invention relates to a targeted molecule which binds to a retroviral nucleocapsid protein with high affinity and comprises the oligonucleotide and a fusion partner. Retroviral nucleocapsid proteins, such as NC and the Gag precursors, bind to specific nucleic acid sequences with high affinity. This binding is dependent upon the zinc fingers of the NC protein and has a strong are useful as molecular decoys for retroviral NC proteins, for making fusion proteins which inactivate retroviral NC proteins, in screening assays for detecting molecules which inactivate retroviral NC proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Displacement chromatography for purification of peptide samples by homogeneous application of sample components to chromatography bed.
                                                     Fisher R, Fivash M, Henderson LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.4; DB 1; Length 20;
Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Displacement chromatography; purification; separation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
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Best Local Similarity 95.0
Matches 19; Conservative
                                                     Rein A, Casas-Finet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARS/) MARSDEN J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-339759/29
                                                                                      WPI; 1998-018230/02
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                                                                                                                                                                                                                                                                                                                                                                                                   The present phosphodiesteric oligonucleotide is based on the generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-

(GcTo')c''-(GdTd')d''-(GeTe')e''-(GTTE')f''-(G-TG')g''-N', where: N and G'' = T or G, equal or different from each other; a' b', c', d', e', f', and g' = 0-10, equal or different from each other; a', b', c', d', e', f', and g' = 0-30, equal or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-10, equal or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-10, equal or different from each other; oligonucleotides of this generic sequence (see also AAT93811-27) are believed to selectively bind and sequence (see also AAT93811-27) are believed to selectively and growth of tumoural cell line. They have specific and selective cytocoxic activity against tumour cells, and can be used for treating tumours of the liquid type, in particular of lymphoblastic origin, and of solid type, in particular of lymphoblastic origin, and of solid type, in particular lymphomas. The present oligonucleotide is known, but no biological activity has been reported until the reported cytotoxic antitumour activity. (Updated on 25-WAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retroviral nucleocapsid protein; NC; high affinity; viral replication; gene therapy; retroviral infection; HIV; transduced cell; 88.
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                  /note= "phosphodiester oligonucleotide"
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                                                                                                                                                                                             (SAIC-) SAICOM SRL.
                                                                                                                                                                                                                                                                                                                                        liquid tumours
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ប្រក្រង់និ ઠ ò 셤 The present invention describes a method (I) for sample displacement chromatography separation. The method comprises applying a multicomponent sample along the bed by passing non-eluting mobile solvent phase over the bed, and recovering a desired component of the sample from at least portion of the bed by passing non-eluting mobile solvent phase over the bed, and recovering a desired component of the sample from at least portion of the bed. The sample components are applied in a non-homogeneous manner to bed. The sample components are applied in a non-homogeneous manner to and/or high affinity for the stationary phase material, respectively, and/or high affinity for the stationary phase material. The method sample components at significantly higher concentrations and recovery of sample components at significantly higher concentrations and recovery of sample components at significantly higher concentrations and recovery of sample components at significantly higher concentrations and separation, it involves minimal use of costly HPC solvents and fraction analysis, avoids the use of displacer solution during actual separation analysis, avoids the use of displacer solution during actual separation of analysis, avoids the use of displacer solution during actual separation of the purification of an oligonucleotide by sample displacement invention ö from the human melanocortin-1 receptor (MCIR) gene upstream controlling sequence. Also described is a method for detecting a substance affecting synthesis of melanin in which a host transformed by an expression vector, comprising a control active polynucleotide derived from MCIR, is cultured in the presence of a sample to be tested and a signal formed by the expression of said reporter gene is detected. The control-active polynucleotide is used for the detection of a substance affecting The present invention describes a control-active polynucleotide derived Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection; melanin; ds. Gaps Upstream controlling sequence of melanocortin1 receptor and its ö Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15. Score 18.4; DB 1; Length 20; Pred, No. 6.7e+02; 0; Mismatches 1; Indels Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other; Disclosure; Page 4; 21pp; Japanese. 2318 TGTGTGTGTGTGTGCGTG 2337 Example 2; Page 22; 37pp; English. 1 TGTGTGTGTGTGTGTG 20 98JP-00345881 98JP-00345881 0.5%; 95.0%; AAA73096 standard; DNA; 20 (first entry) Local Similarity 95.0 (SHIS) SHISEIDO CO LTD WPI; 2000-485552/43

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eguences or metanin. The present sequence represents a human melanocortin-1 receptor gene TATA box oligonucleotide, which is given in the exemplification of the present invention
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Matches 19; Conservative
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tendemly repeated nucleotides core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2 included are a nucleic acid primer 2 includes in length. Also included are a nucleic acid primer 3 includes or fescue genomic DNA enriched for SSRs by preparing a clentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profilling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal species varieties by sessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties.
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                                                                                                                                                                   Simple sequence repeat, plant, ds, SSR, ryegrass, fescue, tandem repeat, cereal profiling, grass profiling; seed batch purity testing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYSC-) UNIV SOUTHERN CROSS.
(VACT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
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04-MAY-2000; 2000AU-00007310.
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                                                                    08-MAY-2002 (first entry)
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0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other; Query Match

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2319 GTGTGTGTGTGTGCGTGT 2338

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2318 TGTGTGTGTGTGTGCGTG 2337

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AAH75569 standard; DNA; 20 BP.

RESULT 484
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ID AAH7556
XX
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence copeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer cuitable for amplifying an SSR, identifying (MI) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and cidentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing contained for DNA profiling grass or cereal species varieties by assessing seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties and for DNA profiling to establish the sequence is a ryegrass or fescue SSR
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                                                                                                                                          Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
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STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                             Simple sequence repeat, SSR, #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                             03-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                                                                                                                                                                                                                                                             24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                             08-MAY-2002 (first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
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  AAS13705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VICT-)
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Unidentified
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                                                                                                                                                                                                                                                                   Query Match
                          Mckay R,
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                                                                                                                                                                                                                                                                                     The invention relates to control of telomere length in a cell by modifying the physiological activity of the Mrell protein in the cell, by transformation of the cell with DNA encoding a foreign Mrell protein which may be modified in the C-terminal and/or nuclease domain. The method is useful in gene therapy of telomere length-related diseases such as melanoma, liver cancer, breast cancer, bladder cancer and brain cancer. The present sequence is that of a Mrell related probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, antiinflammatory, cytostatic, antisense gene therapy,
phosphoenol pyruvate carboxykinase-cytosolic, PEPCK-cytosolic, infection,
inflammation, tumour formation, phosphorothioate, ss.
                                                                                                                                                                                                                                       Controlling telomere length for gene therapy of telomere length related tumors comprises transformation using the modified Mrell protein.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                88;
                                              Yeast; Mre11; telomere length, nuclease; gene therapy; melanoma; a
liver cancer; breast cancer; bladder cancer; brain cancer; probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PEPCK-cytosolic antisense oligonucleotide ISIS 108106.
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                           (RIKE ) RIKEN KK.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                        Example 3; Page 16; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2319 GIGIGIGIGIGIGIGCGIGI 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Grererererererer 20
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            06-NOV-2001 (first entry)
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Matches 19; Conservative
                                                                                                                                                                                                      Ohta K, Shibata T;
                                                                                                                                                                                                                         WPI; 2001-541649/60
                                Mrell related probe
                                                                                                WO200160996-A1.
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                                                                                                                  23-AUG-2001
                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                              invention
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The present sequence is one of a number of antisense compounds of up to 30 nucleobases in langth that are capable of inhibiting the expression of phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics. They are commonly used as research genes. They are distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in antisense therapy, by synthesizing oligonucleotides comprising backbone of alkyl or alkoxy thiourea linkages in solution or on solid phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deoxynucleic S-Methythiourea; DNmt; antisense therapy; cardiovascular disease; inflammatory disease; neurocellular disease; antiviral therapy; human immunodeficiency virus; human-cytomegalovirus; influenza; herpes; infection; ss.
                                                                                                                                                                              Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation.
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                                                              Cowsert
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                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 43; 64pp; English.
                                                              Wyatt J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0111800P.
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(ISIS-) ISIS PHARM INC.
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                                                                     Butler MM,
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hes 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev AP, Bruice TC;
                                                                                                                                 WPI; 2001-190979/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA oligomer #5.
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The present sequence was used to demonstrate the ability of deoxynucleic S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An increase in the C content of the oligos resulted in a large decrease in binding. This experiment was performed as an example of a method for preparing oligonucleotides comprising a backbone of alkyl or alkoxy thiorea linkages. The method is useful for preparing oligonucleotides for use in antisense or antigene therapy, to inhibit production of proteins associated with genetic diseases, cardiovascular, inflammatory and neurocellular diseases, and for antiviral therapy, e.g. to treat numan immunodeficiency virus, human-cytomegalovirus, influenza and herpes infections. The compounds are also useful as diagnostic reagents to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind, and by antagonising the normal biological activity of a target protein, they can be used in the manipulation of tissue e.g. The method provides an efficient and rayor and in ex vivo tissue cultures. The method provides an S-methylthiourea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method of treating systemic lupus erythematosus and lupus nephritis, involving administering a conjugate comprising a non-immunogenic valency platform molecule and 2 double stranded DNA epitopes which specifically bind to dsDNA-binding antibodies. Affinity of the epitopes for the antibody is used as a basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating systemic lupus erythematosus in individual comprises e.g. administering conjugate comprising non-immunogenic valency platform molecule and double stranded DNA epitopes which specifically bind to antibody from individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody affinity; DNA epitope; anti-DNA antibody; lupus nephritis; systemic lupus erythematosus; immunotolerance; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                  Example 7; Fig 16; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody binding oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
for selecting individuals to receive treatment. The present sequence is an antibody binding dsDNA sequence described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                    Simple Sequence Repeat; SSR; clover; microsatallite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                      Gaps
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                                                                                                   0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
                                                                                                                                  Indels
                                                                    Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
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                                                                                                                                      0; Mismatches
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                                                                                                                                                                     2319 GTGTGTGTGTGTGTGTGTGT 2338
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                                                                                                                                                                                                     1 Grererererererer 20
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                                                                                                                   Best Local Similarity 95.0
Matches 19; Conservative
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les 19; Conserv
                    an antibody bi
the invention
                                                                                                                                                                                                                                                                                                                                                                                        SSR motif #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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AAI64445/c
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US2002115097-A1

AAI64449;

489

RESULT 46 AAI64449

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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are gluctronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                                      Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, polymorphism, TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 18.4; DB 1; Length 20; 35.0%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 95.0%; Pred. No. 6.7e
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2823 TATATATACATATATATA 2842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TATATATATATATATA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iyer L, Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                    claim 8; Page 9; 13pp; English.
                                                                                                                                                                                                                      Ratain MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002; 2002US-00061693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00251274
                                                                                             01-FEB-2002; 2002US-00061693.
                                                                                                                                      99US-00251274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALS0667 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ARCH-) ARCH DEV CORP.
                                                                                                                                                                              (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-740095/80
                                                                                                                                                                                                                      Rienzo AD, Iyer L,
                                                                                                                                                                                                                                                               WPI; 2002-740095/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002115097-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rienzo AD,
                                                                                                                                          16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002
                                                         22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL50667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL50667/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                     Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 6.7e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2319 GIGIGIGIGIGIGIGIGI 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIGIGIGIGIGIGIGIGI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 35; 52pp; English.
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                                                   В.
                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2001; 2001NZ-00509194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                   AA164449 standard; DNA; 20
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-431058/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koelliker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2003
                                                                                                                                                                          SSR motif #9
                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                               23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001
                                                                                                                                                                                                                                                                                                                                     NZ509194-A.
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RESULT 490

à 셤 AAL50667

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Gaps

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present sequence is an oligonucleotide produced to demonstrate the method of the invention

Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

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Gaps

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Indels

0; Mismatches

19; Conservative

Matches

Best Local Similarity

Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02;

0.5%;

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                                                                                          The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthesis of polynucleotide useful during fabrication of an array involves coupling nucleoside phosphoramidite and a solid-supported nucleoside and treating the product with an oxidation/deprotection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide synthesis; polynucleotide array; protecting group;
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                              0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caruthers M;
                                                                                                                                                                                                                                                                    Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide synthesis method related DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betley JR,
                                                                                                                                                                                                                                                                                                                                                              2823 TATATATACATATATATA 2842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGIL-) AGILENT TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                               8; Page 9; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL45125 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000US-00627249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2001; 2001EP-00118360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dellinger DJ, Perbost MGM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                       TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-156732/21
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1176151-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL45125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sebesta DP, Leuck M, Latham-Timmons HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    fluorescein label"
                                                                                                                                                                                  Immobilisation; Diels-Alder reaction; ss.
                                                                                                                                                                                                                                   Location/Qualifiers
2318 TGTGTGTGTGTGTGCGTG 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 31; 86pp; English.
            1 TGTGTGTGTGTGTGTGTG 20
                                                                                                                                                                                                                                                           /*tag= a
/mod_base= OTHER
/note= "5' fluore
                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000; 2000US-0201561P.
30-JAN-2001; 2001US-0265020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%;
                                                                                                                                                                                                                                                                                                                                                             01-MAY-2001; 2001WO-US013956
                                                                                                                                                            Oligonucleotide SEQ ID NO 2.
                                                                                   ABA96307 standard; DNA; 20
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.0°
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pieken W, Wolter A,
                                                                                                                                                                                                                                                                                                                                                                                                                         (PROL-) PROLIGO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Husar GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114155/15
                                                                                                                                                                                                                                                                                                            WO200184234-A1
                                                                                                                                                                                                                                                modified base
                                                                                                                                    18-MAR-2002
                                                                                                                                                                                                                                                                                                                                     08-NOV-2001.
                                                                                                           ABA96307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pilon J,
                                                            RESULT 493
ABA96307/c
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2318 TGTGTGTGTGTGTGCGTG 2337

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The present invention relates to a method for the synthesis of a polynucleotide which involves coupling a second nucleoside to a first nucleoside through a phosphite linkage, where the second nucleoside has a non-carbonate protecting group protecting a hydroxyl, and exposing the product to a composition which concurrently oxidizes the phosphite formed to a phosphate and deprotects the protected hydroxyl of the second nucleoside. The method is useful for synthesizing the polynucleotides, for carrying out either 3' to 5' or 5' to 3' synthesis and for fabricating an addressable array of polynucleotides on a substrate. The

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RESULT 494

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The invention relates to a method for immobilising a molecule on a support comparing reacting a derivatised molecule with a derivatised support capable of reacting with the molecule via a cycloaddition reaction. The method is used for immobilising molecules on a support using cycloaddition reactions such as the Diels-Alder reaction. The method shows better chemoselectivity, functional groups do not need to be protected and it is highly efficient for immobilising molecules compared to other methods. The present sequence is that of an oligonucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method for immobilizing a molecule on a support comprises reacting derivatized molecule with a derivatized support via a cycloaddition reaction, shows high selectivity and efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid detection; hybridisation; microarray; thermistor; microcalorimetry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 0.5%; Score 18.4; DB 1; Length 20; Local Similarity 95.0%; Pred. No. 6.7e+02; leg 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide (CA)10 used in nucleic acid hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sebesta DP, Leuck M,
                                                                                                                                                                                                                                                                                         Immobilisation; Diels-Alder reaction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGTGCGTG 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 31; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IGTGTGTGTGTGTGTG 20
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ID ABZ24438 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000; 2000US-0201561P.
30-JAN-2001; 2001US-0265020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2001; 2001WO-US013956
                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2003 (first entry)
                              ABA96306 standard; DNA; 20
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Wolter A,
Husar GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114155/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROL-) PROLIGO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200184234-A1
                                                                                                                                                              18-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pieken W,
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ24438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilon J,
                                                                                                   ABA96306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches
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ABA96306

IID ABA9

AC ABA9

XXX ABA9

XXX ABA9

XXX IMMC

XXX IMMC

XXX WO2C SYNT

YXX WO2C

YXX WPI

XXX WC

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The present sequence is that of a (CA)10 oligonucleotide used to CC illustrate the method of the invention. The invention provides methods illustrate the method of the invention. The invention provides methods CC for detecting specific binding interactions through measurang the heat of binding pairs interact with cach other. The invention also provides methods to detect analytes in a cc solution through measurement of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction generated control devices are provided that consist of spatially addressable control devices are provided that consist of spatially addressable cr arrays of thermistors, which are useful in the multiparallel thermal cr analysis of samples. The methods and devices are particularly in the analysis of mucleic acid, repectablly DNA/DNA, DNA/RNA, DNA/RNA (linear uncleic acid), DNA/SNA (short interfering RNA) and DNA/RNA (pptide comprises part of an enzymatic amplification reaction, especially PCR or primer extension reaction. The detection device provides a real time, comparises part of an enzymatic amplification reaction, using the binding or reaction partner. An example from the invention, using the present oligonucleotide, showed that the thermal detection technique is comparisors.
                                                                                                                                                                                                                                                                                     Detection device useful for detecting binding between members of specific binding pair, and for multiparallel thermal analysis of samples, has an array of addressable thermistors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide (TG)10 used in nucleic acid hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 95.0 Matches 19; Conservative
                                                                                                                                                                                                                             Roach JS, Wolter A;
                                                                                                                                                                                                                                                             WPI; 2003-148685/14.
                                                                                                                                                                                           (PROL-) PROLIGO LLC
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                                                  WO200299386-A2
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                                                                                      12-DEC-2002
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             Synthetic.
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                                      modified base
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                                                                                                                            20-MAR-2003,
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                                                                                                                                                                                                                                                                                                                        disorder.
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Matches
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                                                                                                                                                                                                             The present sequence is that of a (TG)10 oligonuclectide used to illustrate the method of the invention. The invention provides methods for detecting specific binding interactions through measuring the heat of binding generated when members of specific binding pairs interact with each other. The invention also provides methods to detect analytes in a solution through measurement of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction generated arrays of thermistors, which are useful in the multiparallel thermal analysis of samples. The methods and devices are particularly in the analysis of samples. The methods and devices are particularly in the analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/RNA, DNA/RNA, DNA/RNA, DNA/RNA, DNA/RNA, DNA/RNA, DNA/RNA, DSA/RNA (special conditions and its binding partner of nucleic acid). The binding between the analyte and its binding or reaction. The detection device provides a real time, digital profile of the binding or reaction between the analyte and its binding or reaction device provides a real time, digital profile of the binding or reaction between the invention, using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                   Detection device useful for detecting binding between members of specific binding pair, and for multiparallel thermal analysis of samples, has an array of addressable thermistors.
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1..5
                                                                                                                                                                                                                                                                                                                                                                                                                       binding or reaction partner. An example from the invention, using the present oligonucleotide, showed that the thermal detection technique is able to distinguish between perfectly matched and mismatched DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4; DB 1; Length 20;
Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human FGFR-3 antisense oligonucleotide, ISIS #125119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGCGTG 2337
                                                                                                                                                                                         Example 2; Page 36; 60pp; English
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           07-JUN-2002; 2002WO-US018200
                                   07-JUN-2001; 2001US-0296685P
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Best Local Similarity 95.0°
                                                                                      Wolter A;
                                                                                                               WPI; 2003-148685/14.
                                                            (PROL-) PROLIGO LLC
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modified_base
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                                                                                      Roach JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 497
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Systemic lupus erythematosus; SLB; impaired renal function; LJP 394 conjugate; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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0
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                          16. 20
/*tag= c
/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOB) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 TGAATGGCAGCAAGGTGGGC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 78; 120pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monia BP, Wyatt JR;
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Novel polynucleotide useful for detecting single nucleotide polymorphisms

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The present invention relates to a method of treating systemic lupus erythematosus (SLB) in an individual. The method comprises selecting an individual having SLE, significantly impaired renal function, and antibodies with high affinity to a polymuclectide epitope by administering a conjugate comprising non-immunogenic valency platform molecules and two or more double stranded DNA (dsDNA) epitopes that are polymuclectides. Also disclosed is a kit comprising the conjugate, LJP 394. The conjugate is administered in an amount effective to reduce incidence of renal flares in the individual. A medication chosen from corticosteroids and cyclophosphamide is also administered to the individual. The conjugate is administered in an amount effective to reduce content of a corticosteroid or cyclophosphamide selective to reduce the amount of a corticosteroid or cyclophosphamide administered to the individual. The present sequence represents a polynucleotide (dsDNA)
                                                                                                                                                                                                                                                                              Treating systemic lupus erythematosus comprises selecting an individual having significantly impaired renal function and administering conjugate having non-immunogenic valency platform molecule and double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 18; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in the treatment of SLE.
13-AUG-2002; 2002US-00219238
                                           13-AUG-2001; 2001US-0311858P.
22-AUG-2001; 2001US-0314281P.
                                                                                                                                                                                      Linnik MD, Hepburn B;
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                                                                                                               (LINN/) LINNIK M D. (HEPB/) HEPBURN B.
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0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
                                   0; Mismatches
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                Local Similarity 95.0
nes 19; Conservative
   Query Match
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Single nucleotide polymorphism detection primer, SEQ ID No 1671 ADF88088 standard; DNA; 20 BP. (first entry) 26-FEB-2004 primer; PCR ADF88088

human; single nucleotide polymorphism; microarray; side effect; ss;

Homo sapiens. Synthetic.

JP2003235571-A.

12-FEB-2002; 2002JP-00034717 26-AUG-2003

12-FEB-2002; 2002JP-00034717.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2003-820454/77.

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                                                                                        The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1200 fully defined sequences as given in specification, a labelling probe containing the SNP containing oligo. The isolated human a microarray equipped with the SNP containing oligo. The isolated human populymorphisms in human gene. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective polymorphisms in a human gene. This polymorleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; single nucleotide polymorphism; microarray; side effect; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism detection primer, SEQ ID No 2088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.5%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 6.7e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 1 A; 1 C; 10 G; 8 T; 0 U; 0 Other;
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                                                        SEQ ID NO 1671; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
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                                                                                                                                                                                                                                                                                                                                                                                             detection method of the invention.
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                     in human gene.
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                                                          Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; rostoropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; acardiovascular disorder; neurological disorder; se.
                 polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism detection method of the invention.
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                                                                                                                                                                                                                                                           Gaps
the invention is useful for detecting the single nucleotide
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                                                                                                                                                                                                         0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                   Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
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/note= "2'-0-methocyethyls"
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Best Local Si
Matches 19;
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mEGES-1). The human megES-1 gene is located on chromosome 9, more specifically to qqq4.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding meGES-1, which specifically hybridise with the nucleic acid encoding inhibite its expression; (2) a method of inhibiting the expression of meGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cyrostatic, antialabetic, immunomodulator, cardiant, neuroprotective, antinflammatory, neuroprotective, nootropic, antistifica, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mEGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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/note= "2'-0-methocyethyls"
                                                                                                          Claim 4; SEQ ID NO 141; 132pp; English.
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Matches 19; Conservative
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chimeric; antisense oligonuclectide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nootropic; antiathritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; diabetes; cancer; ischaemia; reperfuuion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9g34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibite its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense compounds have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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Best Local Similarity 95.0
Matches 19; Conservative
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WO2004028458-A2
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The thuman mPGES-1 gene is located on chromosome 9, more specifically to operate the present invention also describes: (1) antisense compounds, carbining a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding carbinist its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal carbinase oligonucleotides and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulatory and cardiovascular activities, and can ophthalmological, immunomodulatory and cardiovascular activities, and can obe used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, alternation infinity of the composition is a composition in infinity.
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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/note= "2'-O-methoxyethyls"
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/mod_base= OTHER
/note= "2'-O-methocyethyls"
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               Location/Qualifiers
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Matches 19, Conservative
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01-JUL-2004
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                     Synthetic.
                                                            Gierse JK;
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                    Homo
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microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; notropic; antiarthritic; vasotropic; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "phosphorothioate linkages and all cytidine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric; antisense oligonucleotide; phosphorothioate; human;
                            Score 18.4; DB 1;
Pred. No. 6.7e+02;
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/mod_base= OTHER
/note= "2'-O-methocyethyls"
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                                                                                                                                               2319 GTGTGTGTGTGTGTGTGT 2338
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                               Query Match 0.5
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                                                                                                                chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; osotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder;
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                                                           Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:142.
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/note= "2'-O-methocyethyls"
16. .20
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/note= "2'-O-methoxyethyls"
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(first entry)
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having a sequence comprising 8-30 bp targeted to a nucleic acid encoding medES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibite its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiammatory, neuroprotective, notropic, antidiammatory, immunomodulatory and cardiavascular activities, and can ophthalmological, immunomodulatory and extitovative activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e-g., inflammation, Alzheimer's
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                                                                                                                                                                                                   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                 Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02;
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.6. .20
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/mod_base= OTHER
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Best Local Similarity 95.09
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to gaz4.3. The present invention also describes: (1) antisense compounds, or a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, in cells or tissues; and of inhibiting the expression of mPGES-1 in cells or tissues, and nucleic acid mPGES-1 and missense or condition associated with mPGES-1. MPGES-1 chimeric antidifiammatory, neuroprotective, nouroprotective, antidifiammatory, neuroprotective, notropic, antistrictic, vasotropic, antidifiammatory, neuroprotective, notropic, antistrictic, vasotropic, be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., infilammation, inhum, or condition associated with mPGES-1 e.g., infilammation, inhum, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; yrOstatic; antidiabetic; imcrosomal prostaglandin E2 synthase inhibitor; cyrOstatic; antidiabetic; imcunomodulator; cardiant; neuroprotective; antidiammatory; neuroprotective; antidiammatory; immunomodulatory cardiovascular; gene therapy; inflammation; Alzheimer's a sisease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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                                                                                 New antisense compound, having a seguence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                         Claim 4; SEQ ID NO 600; 132pp; English.
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Best Local Similarity 95.0%;
Matches 19; Conservative
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid mpGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mpGES-1, in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpGES-1. MpGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, ophthalmological, immunomodulatory and cardiovascular activities, and can ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or
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/mod_base= OTHER
/note= "2'-O-methocyethyls"
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/note= "2'-0-methoxyethyls"
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can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetees; cancer; ischaemia; reperfuston injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
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/mod_base= OTHER
/note= "2'-0-methoxyethyls"
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/note= "2'-0-methocyethyls"
16. .20
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGE5-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9d34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibite its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, vasotropic, antidifammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can
                                                                                                                                                                     chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; implibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antidifammatory; neuroprotective; nostropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                   ADM13951 standard; DNA; 20
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be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1, which specifically hybridise with he modelec acid mPGES-1 and inhibits its expression; (3) a method of inhibiting the expression of mPGES-1 in cells or tissues, and an expression of antidiabetic jumunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulatory and cardiavascular activities, and can ophthalmological, immunomodulatory and cardiavascular activities, and can ophthalmological, immunomodulatory and cardiavascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                        Claim 4; SEQ ID NO 317; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM14166 standard; DNA; 20 BP
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ADM14166/A
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ADM1-A
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DDT 01-
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0.5%; Score 18.4; DB 1; Length.20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels 2318 TGTGTGTGTGTGTGCGTG 2337 20 rerererererererere

01-JUL-2004 (first entry)

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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; dene therapy; inflammation; altheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; acardiovascular disorder; neurological disorder; se. Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:353.

Homo sapiens Synthetic.

/mod_base= OTHER /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines" /mod_base= OTHER /note= "2'-0-methocyethyls" /note= "2'-0-methoxyethyls" Location/Qualifiers /*tag= c /mod_base= OTHER 1. .5 /*tag= a Q 16. .20 /*tag= Key modified base modified base modified base

WO2004028458-A2

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to human mpGES-1 gene is located on chromosome 9, more specifically to having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antisialess oligonucleotides and antisense compounds have cytostatic, antiinflammatory, neuroprotective, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mpGES-1 e.g., inflammation, Altheimer's condition associated with mpGES-1 e.g., inflammation, Altheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia or reperfusion injury, or
                                                                                                                                                                                                                                                                               e.g.,
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                                                                                                                                                                                                                                                           compound, having a sequence targeted to a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ophthalmic, immunological, cardiovascular or neurological disorder
                                                                                                                                                                                                                                                                               encoding mPGES-1, useful for preparing a composition for treating inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 353; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2319 GTGTGTGTGTGTGCGTGT 2338
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                                        25-SEP-2003; 2003WO-US030374.
                                                                                   25-SEP-2002; 2002US-0413549P.
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                                                                                                                            (PHAA ) PHARMACIA CORP
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Best Local Similarity
                                                                                                                                                                                                                                                                                 encoding mPGES-1,
  08-APR-2004.
                                                                                                                                                                         Gierse JK;
                                                                                                                                                                                                                                                                                                                               schemia.
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Gaps

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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; imPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antidic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss. Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:176. #X \$\ \colon \co

BP.

ADM13989 standard; DNA; 20

ADM13989/c

01-JUL-2004 (first entry)

ADM13989;

Homo sapiens. Synthetic. Key

Location/Qualifiers

chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mFOES-1; mFOES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; notropic; ophthalmological;

Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:484.

immunomodulatory, cardiovascular, gene therapy; inflammation; Alzheimer's disease, arthritis; diabetees, cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.

note = "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

Location/Qualifiers

'mod_base= OTHER

...20 *tag=

modified base

Homo sapiens.

Synthetic

modified base

/*tag= a /mod_base= OTHER /note= "2'-O-methocyethyls" 16. .20 /*tag= c /mod_base= OTHER

modified_base

/note= "2'-0-methoxyethyls"

WO2004028458-A2.

08-APR-2004.

25-SEP-2002; 2002US-0413549P. 25-SEP-2003; 2003WO-US030374.

(PHAA) PHARMACIA CORP

Gierse JK;

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to pag44.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antisinflammatory, neuroprotective, nootropic, antiaflabetic, immunomodulatory and cardiovascular activities, and can be used as MPGES-1 inhibitors and in gene therapy. The antisense compound of can be used for preparing a composition for treating a disease or condition associated with mPGES-1. Althibitors and in gene therapy. The antisense compound
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                                                 /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound, having a sequence targeted to a nucleic acencoding mPGES-1, useful for preparing a composition for treating inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                            /mod_base= OTHER
/note= "2'-O-methocyethyls"
16. .20
                                                                                                                                                                                                      /mod_base= OTHER
/note= "2'-0-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 176; 132pp; English.
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/mod_base= OTHER
                                     /mod base= OTHER
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Best Local Similarity 95.0'
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gierse JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to human mpGES-1 gene is located on chromosome 9, more specifically to opportunity and sequence compounds, having a sequence compounds, having a sequence compounds 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antishames oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulatory and cardiavascular activities, wasotropic, ophthalmological, immunomodulatory and cardiavascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Altheimer's condition associated with mPGES-1 e.g., inflammation, Altheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g. inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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Gaps

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Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02; 0; Mismatches 1; Indels

0.5%;

2319 GTGTGTGTGTGTGTGTGT 2338

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ADM14297 standard; DNA;

(first entry)

01-JUL-2004

ADM14297;

RESULT 513
ADM14297/C
ID ADM1428
XX
AC ADM1428
XX

0.5%; Score 18.4; DB 1; Length 20;

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                                                                                                                                                                                                                                                                     chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9934.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound, having a sequence targeted to a nucleic acid encoding.mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "phosphorothioate linkages and all cytidine
                                                                                                                                                                                                                                            Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:533.
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                 1; Indels
    Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residues are 5-methylcytidines
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                 0; Mismatches
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                                             2318 TGTGTGTGTGTGTGCGTG 2337
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95.0%;
                                                                                                                                                      ADM14346 standard; DNA; 20
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/mod_base=
                                                                                                                                                                                                              (first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                     RESULT 51
ADM14346/
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inhibits its expression; (2) a method of inhibiting the expression of mPGBS-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. WPGES-1 chimeric antisense oligonuclectides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiantlammatory, neuroprotective, nootropic, antiantitic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                  Score 18.4; DB.1; Length 20; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                      1; Indels
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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/note= "2'-O-methocyethyls"
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Best Local Similarity 95.0%;
Matches 19; Conservative
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/*tag= a
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modified base
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Synthetic.
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19; Conservative
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modified base
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                                                                                                                                                                                                              The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gane is located on chromosome 9, more specifically to human mpGES-1 gane is located on chromosome 9, more specifically to gate an expension of the present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal comparing a disease or condition associated with mpGES-1. MpGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, cardiant, neuroprotective, antidiabetic, immunomodulatory and cardiovascular activities, and can compute an encodition as an experience of can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound con the used as mpGES-1 inhibitors and in gene therapy. The antisense compound con condition associated with mpGES-1 e.g., inflammation, Altheimer's condition associated with mpGES-1 e.g., inflammation, Altheimer's condition associated with mpGES-1 e.g., inflammation, injury, or condition immunological, cardiovascular or neurological disorder.
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                                                               New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/mod_base= OTHER
/note= "2'-0-methocyethyls"
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                                                                                                                                                                              Claim 4; SEQ ID NO 319; 132pp; English
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                           WPI; 2004-305094/28
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGSS-1 gene is located on chromosome 9, more specifically to oppose the present invention also describes: (1) antisense compounds, oppose a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically whybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal comparing a disease or condition associated with MPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antistlammatory, neuroprotective, nootropic, antistrating, vasotropic, antistlammatory, neuroprotective, nootropic, antistrating, vasotropic, antistlammatory, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mPGES-1 e-g., inflammation, Alzheimer's condition associated with mPGES-1 e-g., inflammation, Alzheimer's ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                         /note= "2'-0-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 140; 132pp; English.
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encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                       /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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/mod_base= OTHER
/note= "2'-0-methoxyethyls"
                                                                                                                          /mod_base= OTHER
/note= "2'-0-methocyethyls"
                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 316; 132pp; English
                                                      Location/Qualifiers
                                                                                /mod_base= OTHER
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                             Homo sapiens
                                                                                                                                                                                                           08-APR-2004.
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                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mFGES-1 gene is located on chromosome 9, more specifically to adving a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression, (2) a method of inhibiting the expression of mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression, (2) a method of inhibiting the expression of mPGES-1 in cells or tissues, and an express compounds have cytostatic, antidiabetic immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulatory and cardiavascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alichimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; tive 0; Mismatches 1; Indels
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mFoES-1; mFoES-1; inhibitor; microsomal prostaglandin E2 synthase; imPoES-1; mFoES-1; inhibitor; inticrosomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; assotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se. /mod_base= OTHER /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines" Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:321. /*tag= a /mod_base= OTHER /note= "2'-O-methocyethyls" Location/Qualifiers ADM14134 standard; DNA; 20 BP. 01-JUL-2004 (first entry) 16. .20 /*tag= c *tag= modified_base modified base modified base sapiens. Synthetic. ADM14134; Homo

WO2004028458-A2.

/mod_base= OTHER /note= "2'-O-methoxyethyls"

08-APR-2004

25-SEP-2003; 2003WO-US030374.

25-SEP-2002; 2002US-0413549P.

(PHAA) PHARMACIA CORP

Gierse JK;

WPI; 2004-305094/28.

New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or schemia.

Claim 4; SEQ ID NO 321; 132pp; English.

The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to man medically to mere specifically to mere specifically to mere specifically to mere sequence compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal moving a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antishabetic, immunomodulator, cardiant, neuroprotective, vasotropic, antishammatory, neuroprotective, nootropic, antishammatory, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or

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            or
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condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                  Gaps
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                                                           0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
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                                         Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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/note= "2'-O-methoxyethyls"
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Synthetic.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human medES-1 gene is located on chromosome 9, more specifically to oppose the present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid meGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal condition associated with mPGES-1. MPGES-1 and antisense oligonucleotides and antisense compounds have cytostatic, antistanse oligonucleotides and antisense compounds have cytostatic, antistanse oligonucleotides and antisense compounds have cytostatic, antisflammatory, neuroprotective, nootropic, antistrikitic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound con a use used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or copithalmic, immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                     New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.
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25-SEP-2003; 2003WO-US030374
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Best Local Similarity
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modified base
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding incEES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues, and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antialialamatory, neuroprotective, nootropic, antiarthritic, vasotropic, opthalmological, immunomodulatory and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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                         /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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/note= "2'-O-methocyethyls"
16. .20
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/mod base= OTHER
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modified_base
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Synthetic.
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Location/Qualifiers
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                                      2318 TGTGTGTGTGTGTGTGCGTG
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; notropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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'note= "2'-0-methocyethyls"
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immicrosomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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                                                                                                  Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:482.
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/note= "2'-0-methocyethyls"
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/note= "phosphorothioate linkages and all cytidine
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Matches 19, Conservative
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to oliginal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to oliginal prostage of antisense compounds, baving a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically whbridise with the nucleic acid encoding compGES-1, which specifically hybridise with the nucleic acid encoding mpGES-1 in cells or tissues, and (3) a method of theating an animal compises of disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, vasotropic, antidiabetic, immunomodulatory and cardiovascular activities, and can cophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mpGES-1 e-g., inflammation, Alzheimer's disease, arthritis, immunological, cardiovascular or neurological disorder.
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/mod_base= OTHER
/note= "2'-0-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 175; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2319 GIGIGIGIGIGIGIGCGIGT 2338
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                                                                                                                                                                                              25-SEP-2002; 2002US-0413549P
                                                                                                                                                    25-SEP-2003; 2003WO-US030374
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                                                                                                                                                                                                                                        (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                      WPI; 2004-305094/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 19; Conserv
                                                                    WO2004028458-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-2004
                                                                                                              08-APR-2004
                                                                                                                                                                                                                                                                                  Gierse JK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGSS-1 gene is located on chromosome 9, more specifically to having a sequence comprising 8-10 bp targeted to a nucleic acid encoding marging a sequence comprising 8-10 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid encoding compESS-1, which specifically hybridise with the nucleic acid encoding mpGES-1 in cells or tissues; and (3) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal complete acid encodition associated with meGES-1. MpGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mpGES-1 e- g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or optital mic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound, having a sequence targeted to a nucleic acid
                                                                                                                           /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                   /note= "2'-0-methocyethyls"
16. .20
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                                                                 Location/Qualifiers
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/mod_base= OTHER
                                                                                                                /mod base= OTHER
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nes 19; Conserv
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                                                                                                                                                                                                                                         modified base
                                                                                 modified base
                                                                                                                                                                      modified base
              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gierse JK;
                                Synthetic.
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Matches
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BP.

ADO81052 standard; DNA; 20

RESULT 527

ADO81052/ ID ADO8:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the cow prion protein (PrP) comprising a polymorphic microsatellite locus.
                                                                                                                                                                                                                                                                                                                                                                        Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                    gene typing; polymorphic microsatellite loci; PML; disease; disease predsisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT-blue-vector; cow;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                              Cow prion protein microsatellite locus primer #64.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 27; 64pp; German.
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                                                                                                                                        microsatellite; PCR; primer; ss
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                                    29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 95.0 es 19; Conservative
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                                                                                                                                                                                                                                                                                                (UYHO-) UNIV HOHENHEIM
                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-215730/21
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            ADO81052;
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ADO81097/c
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8X4X5X8
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: Cr a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or predisposition to a disease, associated with a gene that include one or more PML, and predisposition to disease used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to disease and for prediagnosis of such diseases, especially prion diseases to but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion cyptein (PrP) comprising a polymorphic microsatellite locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
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gene typing; polymorphic microsatellite loci; PML; disease; predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                              microsatellite; PCR; primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2002; 2002DE-01036711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYHO-) UNIV HOHENHEIM
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                                                                                                                                                                                                                                                         DE10236711-A1
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Sheep prion protein microsatellite locus primer #68.

(first entry)

29-JUL-2004

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                      The invention describes a new compound, having a sequence comprising 8-80 bp targeted to a nucleic acid encoding CDK9, specifically hybridises with handleic acid encoding CDK9 comprising 708-bp sequence and inhibits expression of CDK9. Also described are: inhibiting the expression of CDK9 in cells or tissues; screening for a modulator of CDK9; a diagnostic method for identifying a disease state; a kit or assay device comprising the compound; and treating an animal having a disease or condition associated with CDK9. The oligonucleotide compound is useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer. This sequence represents a human cyclin-dependent kinase 9 (CDK9) antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                               useful for
                                                  \mbox{note} = "OTHER= Phosphorothioate backbone. All cytidines are 5-methylcytidines"
                                                                                     /*tag= a
/mod_base= OTHER
/mod_base= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
15. .20
                                                                                                                                               /note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                              New oligonucleotide compound that inhibits expression of CDK9, useful preparing a composition for treating hyperproliferative disorder, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; human; non-muscle myosin-family heavy chain protein; MYH14; chromosome 19q13.3; Charcot-Marie-Tooth syndrome; brain; peripheral nerve; ovary; intestine; primer; PCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human myosin heavy chain MYH14 exon 21 PCR primer M21-R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Example 15; SEQ ID NO 15; 49pp; English.
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1675 GCAGACTTCGGGCTGGCCCG 1694
                                                                                                                                                                                                                                                                        Dobie KW;
                                                                                                                                      base= OTHER
                                            /mod_base= OTHER
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                                                                                                                                                                                                                                  09-DEC-2002; 2002US-00315765
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                                                                                                                                                                      US2004110140-A1
                 Key
modified_base
                                                                            modified base
                                                                                                                   modified base
                                                                                                                                                                                                                                                                           Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2004
                                                                                                                                                                                          10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                         cancer.
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This invention describes a novel non-muscle, human myosin-family heavy chain protein, designated MYH14 which maps to chromosome 19q13.3, a region associated with Charcot-Marie-Tooth syndrome. MYH14 is associated with Charcot-Marie-Tooth syndrome. MYH14 is associated with brain, peripheral nerves, ovary and intestines and has closest homology with the myosin family proteins MYH0, MYH10 and MHC11. The product of the invention is used to identify mutations and alteration in product of the invention is used to identify mutations and alteration in chromosomal 19q region with the rat sequence AF13055 (encoding a non-muscle myosin heavy chain B) indicated a potential human homologue. A set muscle myosin heavy chain B) indicated a potential human homologue. A set coff exonic primers was designed and used to amplify chons were sequenced and assembled to form an approximately 6kb sequence that included an open canding frame for MYH14, but lacked the polyadenylation signal. The corresponding gene contains 40 exons (about 100 kb), entirely present within the bacterial artificial chromosomes Acologo6, Acolos51s and Aconomic acontains 40 exons (about 100 kb), entirely present within the bacterial artificial chromosomes Acologo6, Acolos51s and Aconomic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding the human myosin heavy chain protein MYH14, useful for identifying mutations or alterations in nucleic acid, derived from chromosome 19q 13.3.
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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                                                                                        24-JUN-2004.
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The present invention describes a phosphoramidite compound (I) comprising two or more nucleoside moieties linked by one or more internucleoside phosphorus atoms, where the internucleoside phosphorus atoms are phosphorus (III) atoms. Also described: (I) preparing a trivalent phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus multimer derivatised solid support (II); and (3) preparing (II). (I) or (II) can be used for the synthesis of oligonucleotides. The present sequence represents a phosphorothioate 21mer oligonucleotide which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; ss; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic
                                                   Novel phosphoramidite compound, useful for the synthesis of oligonuclectides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
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                                                                                                                                                                                                                                                                                                                     synthesised in an example from the present invention
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                                                                                                                              Example 4; Page 28; 67pp; English
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                                                                                                                                                                                                                                                          Novel phosphoramidite compound, useful for the synthesis of oligonucleotides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
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                                                                                                                            (AVEC-) AVECIA BIOTECHNOLOGY INC. (AVEC-) AVECIA LTD.
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Best Local Similarity 95.0
Matches 19; Conservative
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cc interfering RNA (siRNA) molecules, which can be used to inhibit cangiogenesis. Specifically, it refers to siRNAs that target and cause RNAs-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (FIt-1) and the FIt-1/KDR (kinase domain cregion) genes, as well as mutants derived thereof. The present invention of bind to the target RNAs, such that expression is inhibited and the target captured to the target mannas, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with angiogenesis and the overexpression of VEGF, which include diabetic retinopathy, agence related macular degeneration, inflammatory disease, psoriasis and crheumatoid arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, Wilm's tumour and lymphoma. CC Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antiinflammatory, antipsoriatic, antidiabetic and cantiarthritic activities. This oligonucleotide is a human Flt-1 DNA coligo, a target for siRNA inhibition of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; 88; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rhempatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
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Best Local Similarity 95.09
Matches 19; Conservative
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14-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ98000;
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angiogenesis. Specifically, it refers to siRNAs that target and cause RNA-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Filt-1) and the Fik-1/KDR (kinase domain cegion) genes, as well as mutants derived thereof. The present invention describes sense and antisense RNA strands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target cegent is useful for treating diseases associated with angiogenesis and the overexpression of VEGF, which include diabetic retinopathy, agentheumatoid arthritis. Furthermore, in cambination with a therapeutic related macular degeneration, inflammatory disease, psoriasis and renumatoid arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, Wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antiinflammatory, antipsoriatic, antidheumatic and antiarthritic activities. This oligonucleotide is a human FIk-1/KDR DNA oligo, a target for siRNA inhibition of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.5%; Score 18.4; DB 1; Length 21; Best Local Similarity 95.0%; Pred. No. 7.1e+02; Matches 19; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISSR)-PCR primer - SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1609 AAGTGCATCCACAGGGACCT 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAGTGTATCCACAGGGACCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD69446 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2003.
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(first entry)

05-JUL-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human IL3 receptor. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 18.2; DB 1; Length 23; llarity 87.0%; Pred. No. 8.3e+02; Conservative 0; Mismatches 3; Indels
0.5%; Score 18.4; DB 1; Length 24; llarity 95.0%; Pred. No. 8.2e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     Human IL3 receptor antisense oligonucleotide.
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                                                                   2335 GTGTGTGTGTGTGCAC 2354
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                                                                                                                                                                                   AAT76174 standard; DNA; 23
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nyce JW, Metzger WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-051871/05.
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Best Local Similarity
                  Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reactive airways
                                                                                                                                                                                                                                                                                                                                                                                                       WO9640162-A1
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                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                   AAT76174;
     Query Match
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AAX53971 standard; DNA; 23 BP.

AAX53971

AAX53971;

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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX55180-271) can be used for the antisense treatment of
gecifically AAX55180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, pancreatic metastases,
colon cancer, breast cancer, lung cancer, pancreatic metastases,
ell as all types of cancers which may metastasize or have metastasized
to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                             Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.
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                                     Human IL-3 receptor antisense oligonucleotide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 87.0%; Pred. No. 8.3e
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 48; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US019419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0059160P.
98US-00093972.
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                                                                                                                                                                                                                                                                            prostate cancer; ss
                                                                                                                                                                                                                                                                                                                                                              WO9913886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                        5-MAR-1999
                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nyce JW;
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AAF19538
ID AAF195:
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Gaps

Query Match

respiratory obstruction; pulmonary obstruction; impeded respiration; respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; alrayd disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; Human IL3 receptor polynucleotide fragment #1105. (first entry) WO200062736-A2 Homo sapiens 14-MAR-2001 cancer; ss.

24-MAR-2000; 2000WO-US008020

99US-0127958P.

EAST CAROLINA

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigge adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Claim 14; Page 207; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antisinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhosine molecules and their receptors, cytokine and nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensine, growth factors, vadykinin receptors, central nervous system peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonuclectides may be used in this way to treat disorders including respiratory obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactoral hypoproduction and or associated with a disease or surfactoral protein and or secretors of the lung and or secretors of secretor fragments and antisense oligonucleotides used in the exemplification of infections, bronchitis, condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary emphysema, chronic obstructive pulmonary disease (COPD) pulmonary transplantation rejection, pulmonary infections, bronchion and/or cancer. AAF18434 to AAF21543 represent human polynucleotide hypertension,

Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;

DB 1; Length 23;

0.5%; Score 18.2;

the present invention (UYEC-) UNIV EAST 06-APR-1999; 26-OCT-2000 AAF19538; Nyce JW;

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 0 Indels 87.0%; Pred. No. 8.3e+02; Human IL3 receptor antisense fragment no.1095. 1477 CGGGCGCGCCCCCCGGGCCT 1499 1 cerececedecececeder 23 BP. 24-APR-2001; 2001US-0286137P. 23-APR-2002; 2002WO-US013135. (EPIG-) EPIGENESIS PHARM INC. ABZ95232 standard; DNA; 23 (first entry) 20; Conservative Best Local Similarity WO200285308-A2 Homo sapiens. 17-OCT-2003 31-OCT-2002. ABZ95232; RESULT 539 Matches ABZ95232 셤 ઠ

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the institution coodon, coding region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitificammatory steroid and ubjudinone. A composition of the invention has antiinflammatory articles and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artiflammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubjquinone or receptor, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Disclosure; SEQ ID NO 10474; 872pp; English.

Pharmaceutical composition for treating ailments associated with impaired

Katz E, Pabalan J, Aguilar D;

Shahabuddin S; Sandrasagra A,

Li Y, San Tang L,

Nyce JW, I Miller S,

WPI; 2003-229219/22.

respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid

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Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;

at ftp.wipo.int/pub/published_pct_sequences

Query Match

DB 1; Length 23; Score 18.2; 0.5%;

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This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating cautedrated adenosine sensitivity, levels of adenosine (A) or (A) receptors, cautedrated deposition or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a composition composition are respiratory, lung or malignant disease. The administered composition composition composition of a useful for preventing or treating a respiratory, lung or malignant disease. The administered or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The composition, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, and such altergies and/or surfactant hypoproduction, respiratory inflammation, allergies, asthma, impeded respiration, respiratory
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                                                                                                                                                                                                                                                                                                                                                                                 Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.
                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and
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  Pred. No. 8.3e+02;
0; Mismatches 3;
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                                                                1477 CGGCGCGCGCCCCCGGCCT 1499
                                                                                                                                                                                                                                                                                                                                         Human IL3 receptor DNA fragment 1095.
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Tang L, Shahabuddin
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ilarity 87.0%;
Conservative
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Best Local Similarity
Matches 20; Conserv
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Miller S,
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ABD19194
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distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system
                                                                                                e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAH43222-23 are primers which were used to amplify the cDNA encoding human kelch protein 19. Human kelch protein 19 and its corresponding polymucleotide may be used in the diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, kelch protein 19; diagnosis; malignant tumor; hemopathy; PCR; HIV; inflammation; polymerase chain reaction; primer; amplify; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human kelch protein 19 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammations.
                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                         0.5%; Score 18.2; DB 1; Length 23; 87.0%; Pred. No. 8.3e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                      Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 24 BP; 9 A; 10 C; 5 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                1477 CGGGGGGGGGGCCT 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kelch protein 19 primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2001; 2001WO-CN000057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2000; 2000CN-00111516
                                                                                                                                                                                                                                                                                                                                                                                      AAH43222 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                         Query Match
Best Local Similarity 87.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAH43222;
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Matches
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;

cross-species comparison.

US2003104410-A1. Homo sapiens.

05-JUN-2003

Human microarray DNA oligonucleotide SEQ ID NO 55473.

(first entry)

13-OCT-2003

vivlemore401-10.rng

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The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSSB replicase protein, a linear nucleic acid template and a complementary nucleic acid primar which is annealed to the 3' terminus of the template, where the template is at least three nuclectides and the primar is two or three nuclectides, and the template and primar do not form a stable duplex in solution in the absence of the HCV NSSB protein. The complex is useful for detecting HCV replicase activity and permits establishment of sensitive RNA-dependent RNA polymerase assays to screan and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination.

Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NSSB replication and ultimately in the replicase activity may be used for developing anti-HCV pharmaccuticals. Sequences ABK99271-ABK99296 represent HCV NSSB replicase RNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel replicase complex comprising hepatitis C virus NSSB replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence of HCV NSSB.
                                                                                                                                  Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                          Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 0 A; 20 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.2; DB 1;
Pred. No. 9.1e+02;
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                       ABK99282 standard; RNA; 25 BP
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrari
                                                                                                21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-582330/62.
                                                                                                                                                                                                                                                                                                                                                                                                                             (HONG/) HONG Z.
(FERR/) FERRARI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hong Z,
                                                                                                                                                                                                                                                                                                                                                                                                       ZHON/) ZHONG W.
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                                                                                                                                                                                                                                                                                          30-MAY-2002
                                                                                                                                                                                                                 Synthetic
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                                                             ABK99282;
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

16-MAR-2001; 2001US-0276759P. 15-MAR-2002; 2002US-00098263.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

Claim 1; SEQ ID NO 55473; 9pp; English

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018 500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of geneic variation or in hybridisation to a DNA library, an analysis of geneic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of hybridishing at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallalic markers or polymorphisms, or family members of a gene and a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid brobes are all in situ hybridisation, in Southern, Northern or dottor by the hybridisation to identify or detect the sequence or specific containing any sequence or specific containing only a primer extensions or in screening cDNA that have been
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
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87.0%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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les 20; Conserv
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Gaps

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3; Indels

0; Mismatches

20; Conservative Local Similarity

Best Loca Matches

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2920 GGGCGGGCGTGGGGGGCGTGG 2942 24 dedecededecedecededes

ACISS482 standard; DNA; 25 BP

RESULT 543 ACIS5482 ID ACIS548 XX AC ACIS548

ACI55482

Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; thuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; lenkodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; scleroderma; heemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; paramitic infection; graff-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing; anglogenesis; probe; ss.

Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction;

16-DEC-2002 (first entry) Human NOVX probe Ag3765.

ABS78791;

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The invention describes a multimeric molecular complex comprising at least 2 compounds, each of which has at least one targeting element directed to a ligand that confers transcytctic or paracellular transporting properties to a molecular complex specifically bound to the ligand. Also described are: a compound comprising at least 2 targeting elements directed to the ligand, a protein compusiang a chemical linkage to a biologically active calcitonin polypeptide having a chemical linkage to at least one targeting element directed to the ligand; a pharmaceutical composition comprising the compound; delivering a biologically active agent to an animal; transporting a biologically active agent through an epithelial barrier; treating disease in an animal; and identifying a disease in an animal. The complex is useful for preparing a composition for fagnosing or treating diseases, e.g., osteoporosis, renal failure, collitis, gastroentertiis, inflammatory bowel disease, psoriasis, Alzheimer's disease, optic neuropathy or ophthalmoplegia. This sequence represents a linker associated with the isolation of heavy chain regions compared and reverse transcytosis in epithelial cells, exocytosis and forward and reverse transcytosis in epithelial cells,
                                                             antipsoriatic; antiinflammatory; neuroprotective; ophthalmological; gastrointestinal; ostoopathic; nephrotropic; gene therapy; multimeric molecular complex; transcytotic transport; paracellular transport; calcitonin; osteoporosis; renal failure; colitis; gastroenteritis; inflammatory bowel disease; psoriasis; Alzheimer's disease; optic neuropathy; ophthalmopledia; single chain antibody; sFv5AF; linker; heavy chain region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New multimeric molecular complex, useful for preparing a composition for diagnosing or treating e.g. osteoporosis, renal failure, colitis, gastroenteritis, inflammatory bowel disease, psoriasis or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 18.2; DB 1; Length 25; 13.9%; Pred. No. 9.1e+02; ve 4; Mismatches 2; Indels
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                      Single chain antibody sFv5AF related linker #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 51; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-00949039
                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2001; 2001US-00949039
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HAWL/) HAWLEY S B.
(CHAP/) CHAPIN S.
(SHER/) SHERIDAN P L.
(HOUS/) HOUSTON L L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hawley SB, Chapin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-898076/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYN/) GLYNN J M.
                                                                                                                                                                                                                                                                                     US2003166160-A1.
                                                                                                                                                                                                                                                                                                                              04-SEP-2003
                                                                                                                                                                                                                                            Synthetic
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2001US-0277337P 2001US-0277338P 2001US-0277931P 2001US-0278152P 2001US-027894P 2001US-0279036P 2001US-0279036P 2001US-0279036P

22-MAR-2001; 2 23-MAR-2001; 2 26-MAR-2001; 2

28-MAR-2001; 30-MAR-2001; 02-APR-2001; 02-MAY-2001;

20-MAR-2001; 21-MAR-2001;

2001US-0280802P. 2001US-0288148P.

31-MAY-2001; 2001US-0294821P

2001US-0335302P

04-DEC-2001; 2001US-0338375P 07-MAR-2002; 2002US-00094466

2001US-0274849P. 2001US-0275235P. 2001US-0275579P.

08-MAR-2002; 2002WO-US007283

38-MAR-2001;

WO200272770-A2.

19-SEP-2002.

Homo sapiens.

2001US-0275601P. 2001US-0276000P. 2001US-0277239P.

13-MAR-2001; 2 14-MAR-2001; 2 20-MAR-2001; 2 20-MAR-2001; 2

13-MAR-2001;

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New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or polypeptides and antibodies, seancers, Hodgkin disease, von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerlach VL;
a R, Pena CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Malyankar UM, Gerl
Gusev VY, Kekuda R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example C; Page 231; 266pp; English.
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I, Gangolli EA, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vernet CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-713508/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease.
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Gaps

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2920 GGGCGGGCGTGGGGGGCGTGG 2942

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Best Local Similarity 73.9%; Matches 17; Conservative

ABS78791/c ID ABS78791 standard; DNA; 26 BP. XX

RESULT 545

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palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-
telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
cbesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
cnfertility, inflammatory bowel disease, atherosclerosis, hypertension,
cnfertility, inflammatory bowel disease, atherosclerosis, hypertension,
cnfertility, inflammatory bowel disease, atherosclerosis, hypertension,
cnfertility, or graft-versus-host disease. The nucleic acids and
collypeptides may also be used as targets for the identification of small
molecules that modulate or inhibit e.g. neurogenesis, cell
angiogenesis, in gene therapy, in generation of antibodies that bind
immunospecifically to NOVX substances for use in therapeutic or
diagnostic methods. The nucleic acids are further used as hybridisation
diagnostic methods. The nucleic acids are further used as hybridisation
probes, in chromosome mapping, tissue typing, preventive medicine, and
plarmacogenomics. The present uncleic acid sequence represents a probe
that was used in the methods of the invention for detection of human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tunour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonuclectide primers selected from (i) a nucleotide sequence (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a pyrimidiane selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xYY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
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Pred. No. 9.5e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quantitating genetic instability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00734973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HEAL-) HEALTH RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stoler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357197/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5912147-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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AAX77485/
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AAX7
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements suitable for amplifying an SSR, identifying are a nucleic acid primer suitable for amplifying an SSR, identifying (MI) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSRs in the breeding, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
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                                                                                                                                                                                                                                      Score 18; DB 1; Length 18;
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                              Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
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STATE VICTORIA DEPT NATURAL RES & ENVIRO.
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                                                                                                                                                                                                                                                          Local Similarity 100.0%; Pred. No. 6.6
nes 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple sequence repeat, SSR, #36
                                                                                                                                                                                                                                                                                                                   2316 TCTGTGTGTGTGTGTG 2333
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04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                          0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001
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method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tranagenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-associated chondrodysplasia, particularly FGFR3 achondroplasia, e.g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect human FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chondrodysplasia; achondroplasia; transgenic mouse; therapy; fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;
                                                                                                                                                                                                                    Score 18; DB 1; Length 18;
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human FGFR3 allele detecting antisense PCR primer.
                                                                                                                                                                               Sequence 18 BP; 0 A; 1 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                          0.5%; Scor.
100.0%; Pred. No. o...
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                                                                                                                                                                                                                                                                                                                        1 GTCTGTGTGTGTGTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98IL-00125958
                                                                                                                                                                                                                                                                                                   2315 GTCTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROC-) PROCHON BIOTECH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD34804 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypoplasia or large skull.
                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 0.5%; Score 18; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 6.6e+02; nes 18; Conservative 0; Mismatches 0; Indels
                                 DB 1; Length 18; 6.6e+02;
                                                                  0; Indels
Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                    Kaposi's Sarcoma TAG PCR primer SEQ ID NO:142.
                      0.5%; Sco...
100.0%; Pred. No. c...
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                                                                                                       1048 CTGGAGTCCAACGCGTCC 1065
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                                                                                                                                18 CTGGAGTCCAACGCGTCC 1
                                                                                                                                                                                                                                ABQ81992 standard; DNA; 18 BP
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28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2002; 2002EP-00075264.
                                                                                                                                                                                                                                                                                                    19-NOV-2002 (first entry)
                             Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1225233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-2002
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                                                                                                                                                                                             RESULT 549
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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein certain the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell (PBMC) expressed keratin 14, TIE 1, Salioadhesin, or Siglec 1 sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for detecting the presence of a tumour cell in an individual. The expression product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This
                                                                                                                                                                            marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
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                                                                                                                                          Kaposi's sarcoma tag PCR primer, SEQ ID No 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 144; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Der Kuyl AC, Cornelissen M;
                       ADC13477 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001EP-00203703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRIM-) PRIMAGEN HOLDING BV
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                                                                                                    (first entry)
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                                                                                                    18-DEC-2003
                                                                                                                                                                                                                                                                Unidentified
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                                                               ADC13477;
ADC13477/
ID ADC1
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Gaps ; 0.5%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0; Indels 18; Conservative Best Local Similarity Query Match Matches ઠ

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ADH70777 standard; DNA; 18 BP. ADH70777; RESULT 551
ADH70777/C
ID ADH707
XX
AC ADH707
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TO ADH707
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TO ADH707

25-MAR-2004 (first entry)

degenerative nervous system disease, graft versus host disease, hypersensitivity disease; infectious disease, neoplastic disease; actoring disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease, hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; Hype IV hypersensitivity; infections disease; viral infection; HIV; fungal infection; Candida; parastitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer; human; T-cell associated disease; Vbeta; autoimmune disease; Human Vbeta gene repeat sequence #567. breast cancer; ds

Homo sapiens.

JS2002150891-A1.

17-OCT-2002

99US-00263959. 05-MAR-1999;

19-SEP-1994;

94US-00309335. 95US-00531241. 19-SEP-1995;

LE. (ROWE/) ROWEN L. поор (/поон

Rowen L; Hood LE, WPI; 2004-059052/06.

autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a Kit for diagnozing and treating T-cell associated diseases e.g. Vbeta gene.

Disclosure; SEQ ID NO 971; 164pp; English.

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers of specifically priming and allowing amplification of each Vbeta gene, vbetaRNA or CDNA. The kit is useful for diagnosing organ transplant crejection and diagnosing and treating T-cell associated diseases including autoimmune disease, hypersensitivity diseases, infectious diseases, can neoplastic disease, hypersensitivity diseases, infectious disease, arrophic gastritis Degenerative nervous system diseases include multiple atrophic gastritis Degenerative nervous system diseases include multiple contact in the such as contact with allergens that lead to allergies, Type II hypersensitivities such as those caused by viruses such as those present in the contact with allergens such as those caused by the yeast genus Candida, paramatic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by such as leukaemias, lymphomas and cancers such as those caused by such as leukaemias, lymphomas and cancers such as such as the brain, such as leukaemias, lymphomas and cancers such as sacer of the brain, such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.

Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

Gaps ö Score 18; DB 1; Length 18; Pred. No. 6.6e+02; 0; Indels 100.08; Prec. ... Local Similarity 100. nes 18; Conservative Query Match Matches

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The invention relates to short interfering nucleic acids (siNA) which downregulate expression of the human platelet-derived growth factor receptor (PDGFT) gene by RNA interference. The siNAs may or may not comprise ribonuclectides and may be double or single stranded. They comprise sense and may be double or single stranded. They turther comprise sense oligonuclectide and an antisense oligonuclectide. Specifically, the siNAs include short interfering RNA (siRNA, double-contectide), stranded RNA, micro-RNA (miRNA) and short hairpin RNA (siRNA). The siNAs can be unmodified or chemically modified, can contain contain contain contain contain and representation of the professor. The invention also relates to kits complexes of siRNA; and vectors that express siNA. The siNAs are used to modulate expression of the PDGFT gene in cells, tissue explants or complexes of siRNA; and vectors that express siNA. The siNAs are used to complexes of siRNA; and vectors that express siNA. The siNAs are used to complexes of siRNA; and vectors that express siNA. The siNAs are used to complexes of siRNA; and vectors that express siNA. The siNAs are used to complexes of siRNA; on one contain cells, tissue explants or creating leukaemia and solid tumours, restencist polycystic kidney corpanisms (e.g., by ex vivo gene therapy), or in grafts and transplants of the treatment of a variety of conditions. They may be used for treating leukaemia and solid tumours, restencesis, polycystic kidney disease, bronchiolitis, glomerilonephritis and stroke. The sinAs are also the creating leukaemia and solid tumours, restencesis, studying gene condidation, genetic engineering, pharmacogenomics studying gene function, and gene mapping (e.g., of single nucleotide polymorphisms).

The present sequence represents the lower strand of a human PDGFr transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2002;
                                                                                                               01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2003
                                                                           AD015049;
RESULT 552
                    ADO15049/
ID ADO1
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Sequence 19 BP; 6 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
                                                                 Query Match 0.5
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO14738;
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 553
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                                                                                                                                                                                                                                                                                                                                             cytostatic; vasotropic; nephrotropic; cerebroprotective; treating leukaemia; solid tumors; restenosis; polycystic kidney disease; bronchiolitis; glomerulnonephritis; stroke; RNA interference; short interfering nucleic acid; siNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; mirNA; short hairpin RNA; shRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New short interfering nucleic acid, useful e.g. for treatment and diagnosis of tumors, downregulates expression of the platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification; pharmacogenomics; gene function analysis; gene mapping; human; platelet derived growth factor receptor; POGFr; ss.
                                                                                                                                                                                                                                                                                  Human PDGFr-targeted sinA lower strand SEQ ID NO:480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beigelman L, Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0409378P.
09-SEP-2002; 2002US-040929P.
15-JAN-2003; 2003US-0440129P.
                                                                         ADO15049 standard; RNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor receptor gene.
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The invention relates to short interfering nucleic acids (siNA) which downregulate expression of the human platelet-derived growth factor receptor (PDGFr) gene by RNA interference. The siNAs may or may not comprise ribonuclectides and may be double or single stranded. They further comprise sense and antisense regions, or alternatively are assembled from a sense oligonuclectide and an antisense oligonuclectide. Specifically, the siNAs include short interfering RNA (siRNA, doublestrande RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified, can contain deoxyribonuclectides, and can be chemically synthesised, expressed from a vector or enzymatically synthesised. The invention also relates to kits cort he in vitro or in vivo delivery of siRNA; conjugates and/or complexes of siRNA, and vectors that express siNA. The siNAs are used to modulate expression of the PDGFr gene in cells, tissue explants or
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                                                                                                                                                                                                                                                                                                                                                                                        treating leukaemia; solid tunors; restenosis; polycystic kidney disease; bronchiolitis; glomerulonephritis; stroke; RNA interference; bronchiolitis; glomerulonephritis; stroke; RNA interference; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; micro-RNA; short hairpin RNA; siRNA; expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification; pharmacogenomics; diagnosis; gene function analysis; gene mapping; human; platelet derived growth factor receptor; PDGFr; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New short interfering nucleic acid, useful e.g. for treatment and diagnosis of tumors, downregulates expression of the platelet-derived
                                        Gaps
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0
Score 18; DB 1; Length 19;
Pred. No. 7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            cytostatic; vasotropic; nephrotropic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                               Human PDGFr-targeted siNA upper strand SEQ ID NO:169.
          100.0%; Preα. ...
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                                                                             1820 TCCTGCTCTGGGAGATCT 1837
                                                                                                          18 TCCTGCTCTGGGAGATCT 1
                                                                                                                                                                                                                    ВР
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05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0492939F.
15-JAN-2003; 2003US-0440129P.
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2002US-0386782P.
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                                                                                                                                                                                                                    ADO14738 standard; RNA; 19
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06-JUN-2002;
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organisms (e.g., by ex vivo gene therapy), or in grafts and transplants for the treating leukaemia and solid tumours, restenois be used for treating leukaemia and solid tumours, restenois by polycystic kidney disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also useful for drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying genefunction, and gene mapping (e.g., of single nucleotide polymorphisms). The present sequence represents the upper strand of a human PDGFrtargeted double-stranded siNA, which is identical to the PDGFr transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer - for detecting polymorphism in DNA among highly interrelated rice plants or plants of family Brassicae.
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Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1820 TCCTGCTCTGGGAGATCT 1837
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Best Local Similarity 66.7%;
Matches 12; Conservative
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                      target sequence
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ID AAQ4
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antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGBS-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a gcomposition for treating a disease or condition associated with mpGBS-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
                                                                                                                       chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin B2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin B2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinfammatory; neuroprotective; antiinfammatory; inmunomodulatory; cardiant; gene therapy; inflammation; alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin B2 synthase (mPGBS-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9d34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibite its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.ginflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note = "phosphorothioate linkages and all cytidine
                                                                                   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residues are 5-methylcytidines
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/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "2'-0-methocyethyls"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  mod_base= OTHER
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                                                     (first entry)
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                                                     01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                             Synthetic.
                 ADM14399;
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Gaps

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BP.

ADM14399 standard; DNA; 20

RESULT 555

ADM14399/ ID ADM1

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Query Match
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ID ADK9657
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                                                                                                                                                                                                                       chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antidifiammatory; neuroprotective; notropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                        Gaps
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ophthalmic, immunological, cardiovascular or neurological disorder.
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residues are 5-methylcytidines"
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                                                                                                                                                                                                      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:531.
                                     DB 1; Length 20; 7.4e+02;
                                                      0; Indels
                  Sequence 20 BP; 9 A; 10 C; 1 G; 0 T; 0 U; 0 Other;
                              0.5%; Scor.
100.0%; Pred. No. '...
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/note= "2'-0-methocyethyls"
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/note= "2'-O-methoxyethyls"
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                                                                           2334 CGTGTGTGTGTGTGTG 2351
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                                 Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                    01-JUL-2004
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-2004.
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gierse JK;
                                                                                             20
                                                                                                                                                                ADM14344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ischemia
                                                                                                                          RESULT 556
                                                                                                                                    ADM14344,
SXS
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targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding confinition is the sypression; (2) a method of inhibiting the expression of mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and confidence of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal confidence or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antisinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, antiinflammatory, neuroprotective, nootropic, antiarthritie, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's companion and antible condition associated with mPGES-1 e.g., inflammation, Alzheimer's companion and antible condition associated with mPGES-1 e.g., inflammation, Alzheimer, companion and condition associated with mPGES-1 e.g., inflammation, Alzheimer componing and condition and condition and condition and condition and condition and condition and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 18; DB 1; Length 20;
100.0%; Pred. No. 7.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2334 CGTGTGTGTGTGTGTG 2351
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Best Local Similarity 100.C
Matches 18; Conservative
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ADJ98020 standard; DNA; 21

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ADJ98020;

(first entry) 06-MAY-2004 Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 793

vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic. human; ss; short interfering RNA; siRNA; angiogenesis;

Homo sapiens.

WO2004009769-A2.

29-JAN-2004.

18-JUL-2003; 2003WO-US022444.

24-JUL-2002; 2002US-0398417P. 14-NOV-2002; 2002US-00294228.

(UYPE-) UNIV PENNSYLVANIA.

Tolentino MJ, Reich SJ;

WPI; 2004-203472/19.

Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic retinopathy and cancer.

Disclosure, SEQ ID NO 793; 218pp; English.

This invention relates to novel compositions that comprise short interfering RNA (siRNA) molecules, which can be used to inhibit confinition and solveness. Specifically, it refers to siRNAs that target and cause RNA-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Flt-1) and the Flk-1/KDR (kinase domain CC region) genes, as well as mutuants derived thereof. The present invention describes sense and antisense RNA exrands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with angiogenesis and the overexpression of VEGF, which include diabetic retinopathy, agency related macular degeneration, inflammatory disease, psoriasis and crheumatoid arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antidilammatory, antipsoriatic, antidiabetic and antiarthritic activities. This oligonicleotide is a human Flk-1/KDR DNA coligo, a target for siRNA inhibition of the invention. RESULT 558
ADU98020
XX
ADU98020
ADU99020
ADU9902

Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

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                             Gaps
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0
  0.5%; Score 18; DB 1; Length 21;
100.0%; Pred. No. 7.9e+02;
                            0; Indels
          100.0%; Pred. No.
Query Match
Best Local Similarity 100.0
Matches 18, Conservative
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4 CCAGAGTGACGTCTGGTC 21
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AAX00049

BP. AAX00049 standard; DNA; 22

AAX00049;

(first entry)

FGFR PCR sense primer.

16-MAR-1999

oligodendrocyte; self-renewal; neuron; differentiation; neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS; central nervous system; glial cell; PCR primer; amplification; ss. Neuroepithelial stem cell; lineage restricted intermediate precursor;

Synthetic.

Homo sapiens

WO9850526-A1

12-NOV-1998.

98WO-US009630. 07-MAY-1998;

98US-00073881. 97US-00852744. 07-MAY-1997: 06-MAY-1998;

(UTAH) UNIV UTAH RES FOUND

Rao MS, Mayer-Proschel M, Mujtaba T;

WPI; 1999-070093/06.

Mammalian neuroepithelial stem cells and glial restricted precursor - car self renew and differentiate into central nervous system cells, used for generating various types of cells.

Example 26; Page 61; 78pp; English

The present invention describes an isolated, pure population of mammalian neuroepithelial stem cells, which are capable of self-renewal in adherent cededar-cell-independent (AFCI) culture medium and differentiation to central nervous system (CNS) neuronal or glial cells and to neuronal crest stem cells. Also described is an isolated population of mammalian (CNS) precursor (GRP) cells which can self-renew in the CNS silal-restricted precursor (GRP) cells which can self-renew in the AFCI culture medium and can differentiate to CNS glial cells but not to CNS neuronal cells. The stem cells can be used to generate a population of mammalian motor neurons by incubating the stem cells but not to CNS neuronial cells can also produce neural crest stem cells by inducing the cells can also produce neural crest stem cells by inducing the cells to differentiate in vitro. The inducing step comprises caplating the cells on a laminin-coated substrate and preferably comprises chick embryo extract. Inducing can also comprise adding a doraalizing capant to the cells, preferably fibroblast growth factor; GFC) and cells, preferably a bone morphogenetic protein (BMP) such agent to the cells, preferably a bone morphogenetic protein (BMP) such cells can cells, preferably a bone morphogenetic protein (BMP) such peripheral nervous system, by inducing the stem cells to differentiate in vitro to neural crest stem cells, and inducing these cells to differentiate in vitro to neural crest stem cells, and inducing these cells to capanic and contained the cells of the cells. LILERENCIALE. AAX00029 to AAX00054 represent PCR primers which are uning a example from the present invention to amplify different FGF and

Sequence 22 BP; 8 A; 1 C; 8 G; 5 T; 0 U; 0 Other;

Gaps ; 0.5%; Score 18; DB 1; Length 22; 100.0%; Pred. No. 8.3e+02; tive 0; Mismatches 0; Indels 18; Conservative Best Local Similarity Matches 18; Conserv Query Match

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Genetic proximity, gene expression, cell characterisation, homeobox gene, genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene, protein phosphatase, P450, steroid receptor, cadherin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the pre- or mature RNA transcript of human intracellular adhesion molecule (ICAM), E-selectin or vascular cell adhesion molecule (VCAM) It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  disease;
vascular cell adhesion molecule-1; antisense; inflammatory; disease treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                         Bradley MO, Williams TJ,
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98IL-00126627.
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Matches 19; Conservative
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                                                                                                                   Homo sapiens,
                                                                                                                                                                  W09824797-A1.
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                                                                                                                                                                                                                                                                                                           02-DEC-1996;
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16-OCT-1998;
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                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                         Hoke GD,
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AAZ18102/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation - for treating septic shock, adult respiratory distress syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense to sequences contained in the pre-mRNA or mature mRNA transcript of .human intercellular adhesion molecule-1 (ICAM-1). These oligonucleotides may be used for treating septic shock and the manifestations of septic shock, e.g. inflammation, and vascular and tissue defects. They are also useful in the treatment of septic shock associated diseases, e.g. adult respiratory distress syndrome, multiple organ failure etc. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAT58071-85 represent oligonucleotides which are
                                                                                                                                                                                                                                                                                                                                                                              Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect; human intercellular adhesion molecule-1; ICAM-1; inflammation; adult respiratory distress syndrome; multiple organ failure; GM1594; septic shock; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                 ICAM-1 antisense oligonucleotide #10.
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TGAGATGGAGATGATGAA 1364
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                                            rgagargargarga 22
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                                                                                                                                                                  ВР
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                                                                                                                                                                  AAT58080 standard; DNA; 21
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(first entry)
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                                                                                                                                                                                                                                                          25-MAR-2003
18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5580969-A.
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1347
                                                                                                                                                                                                                AAT58080;
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XX AAT58

AC AAT58

AC AAT58

DT 18-M

DT 18-M

DT 18-M

XX ANT18

XX ANT18

XX SYNT:

PY 03-D

XX C SYNT:

PY 12-O

PY 12-O

XX XX C C TAE

CC TAE
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WPI; 1999-419113/35.
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                                        P-PSDB; AAY14629
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16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer; ss
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Vider B;
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                                                                                                                                                                                         cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell comprises: (a) obtaining the first cell and the second cell the pattern cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterishing cells, e.g. for determining the origin of a cell, its cransformed. They can be used for determining the individual, e.g. a fetus. They can also be used for determining the offect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction gene family. Sequences AAZI7803-Z18342 represent primers that can be used for in the RT-PCR for determining the pattern of gene expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic proximity, gene expression, cell characterisation, homeobox gene; genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR; kinase gene, protein phosphatase; P450; steroid receptor, cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                        gene family can be selected from a set of homeobox genes, kinase genes,
protein phosphatase genes, P450 enzyme genes, steroid receptor
                                                                                                                                                                                  new method for identifying and characterising
                                                                                                              Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  superfamily genes or cadherin superfamily genes
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                                                                                                                                                      Claim 4; Page 42; 102pp; English.
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                                                                     WPI; 1999-419113/35.
P-PSDB; AAY14637.
               (GENE-) GENENA LTD
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                                           Vider B;
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                                                                                                                                        The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for denarcterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for detecting a selected genetic defect in an individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     property. The method uses reverse transcriptors postured in a selected (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequence ANZI/R013-Z18342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, PSO enzyme genes, ateroid receptor
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Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1798 AGTGACGTCTGGTCCTTTGGG 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AGTGATGTCTGGTCCTATGGG 1
                                                                                           Claim 4; Page 42; 102pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTK 14 gene specific primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-1999 (first entry)
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Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                                                                                              and a second cell comprises: (a) obtaining the genetic proximity of a first cell and a second cell; the method for determining the genetic proximity of a first cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (c) determining in the first cell and the second cell; (c) capression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the effect of a selected treatment on a test cell. They can also be used for determining the ceffect of a selected treatment on a test cell. They can also be used for braining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptasse polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AA217803-218342 represent primers that can be used con in the RT-PCR reactions to determine genes, kinase genes, kinase genes, kinase genes, kinase genes, kinase genes, containing the pattern of gene family can be selected from a set of homeobox genes, kinase genes, containing the pattern of gene family can be selected from a set of homeobox genes, kinase genes, containing the pattern of gene family can be selected from a set of protein selected from selected from a set of protein selected from a set of selected selected selected from a set of selected selected from a set of selected selected selected selec
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                                                                                                                                                                              The invention provides a new method for identifying and characterising
                                             Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.38+02; iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1798 AGTGACGTCTGGTCCTTTGGG 1818
                                                                                                                              Claim 4; Page 43; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AGTGATGTCTGGTCCTATGGG 1
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P-PSDB; AAY14645.
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les 19; Conserv
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  P-PSDB; AAY14653.
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16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 565
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell comprises: (a) obtaining the first cell and the second cell the pattern co expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its carnisformed. They can be used for detecting a selected genetic defect in the ransformed. They can be used for detecting a selected genetic defect in ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired cobtaining the pattern of gene expression in a selected compression in a selected compression in the RT-PCR reactions to determine the pattern of gene expression. The containing the pattern of gene expression in the used containing the pattern of gene expression. The containing the pattern of containing the pattern of gene expression. The containing the pattern of containing the pattern of containing the pattern of containing the pattern of containing the containing the pattern of containing the pattern of containing the pattern of containing the containing the containing the pattern of containing the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemokines capable of directing migration of dendritic cells, for treating microbial infections, cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a PCR primer used to amplify the chemokine macrophage inflammation protein 3 beta (MIP 3beta) coding sequence. The PCR product is used in the analysis of dendritic cell response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes, steroid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein phosphatase genes, P450 enzyme
expression in a selected gene family.
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                                                               Claim 4; Page 42; 102pp; English.
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Best Local Similarity 90.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caux C, Vanbervliet B,
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different chemokines. The invention relates to the use of chemokines which are capable of directing dendritic cells, in the manufacture of a medicament for the treatment of a disease state. Wethods are included for treating diseases by facilitating or inhibiting the migration or activation of antigen-presenting dendritic cells. The chemokines can be used to initiate, amplify or modulate an immune response. The chemokines are useful for the treatment of disease states e.g. a bacterial, prain, pancreatic, colon, lung, glioma, hepatocellular, endometrial, gastric, intestinal, renal, protate, thyroid, ovarian, testicular, liver, head and neck, colorectal, oesophagus, stomach, eye, bladder, glioblastoma and metastatic carcinomas), autoimmune disease, tissue rejection or an
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        allergy
                     222222222222222X8
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Score 17.8; DB 1; Length 21; Pred. No. 8.38+02; 0; Mismatches 2; Indels 2319 GIGIGIGIGIGIGIGIG 2339 crerereacrereacrere 1 0.5%; 1 Similarity 90.5
19; Conservative 21 Query Match Best Local Matches à g

Gaps ;

> AAH38434 standard; DNA; 21 (first entry) 14-AUG-2001 AAH38434; RESULT 567 AAH38434

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SNP specific lower PCR primer SEQ ID 1230.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfects; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss. 99US-0160096P. 13-OCT-2000; 2000WO-US028436. WO200129262-A2 15-OCT-1999; Homo sapiens. 26-APR-2001.

Pohl M; Picoult-Newburg L,

(ORCH-) ORCHID BIOSCIENCES INC.

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or Claim 1; Page 56; 83pp; English.

identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. caused by one or more SNPs. Phenotypic traits include diseases e.g. dystrophy, familial hypercholesterolaemia, polycystic kidney disease, dystrophy, familial hypercholesterolaemia, polycystic kidney disease, cotecogenesis imperfects and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases, including, rheumatoid arthritis, multiple sclerosis, cancer, nervous system diseases and infection by pathogenic microcyganism. The method is also useful. An forensic investigations and microcyganism. The method is also useful. An forensic investigations and patentity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence to of 8x888888888888888

ö 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; iive 0; Mismatches 2; Indels Sequence 21 BP; 0 A; 3 C; 8 G; 10 T; 0 U; 0 Other; 19; Conservative Query Match Best Local Similarity Matches

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Gaps

2320 TGTGTGTGTGTGTGTGT 2340 rcrererererecererer 21 g ઠે

ABL44374 standard; DNA; 21 BP. RESULT 568

Human chromosome 1p36-35 PCR primer SEQ ID NO:1418. 11-APR-2002 (first entry)

chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome; PCR primer; ss Human;

JP2001321190-A. Homo sapiens. 20-NOV-2001.

12-MAR-2001; 2001JP-00068285. 10-MAR-2000; 2000JP-00066716.

(RIKA) RIKAGAKU KENKYUSHO. (GENO-) GENOTEX YG.

WPI; 2002-144136/19.

Arraying genome clones.

Claim 4; Page 32; 528pp; Japanese.

The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in compliance numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker compliance is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant complified product to specify the discrimination Nos. of the multiwell complished product to specify the discrimination Nos. of the multiwell complete containing the clones having said marker sequence; (d) the order complished in the specified discrimination Nos. to array the multiwell completes; (e) the clones in the multiwell plates of the specified transmination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the cresultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell

plates are specified from the detected result; and (i) the clones are

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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

W dytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

ary cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

w adrenergic receptor beta1; ADBR1; aryl hydrocarbon; ARR; MRB7; Cathepsin S; CTSS;

cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

W poxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

W glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

M HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase;

W MDP-glucuronosyl transferase 28; UDP-glucuronosyl transferase 2B7;

W UDP-glucuronosyl transferase; UGT2B15; urokinase receptor;

W Wlidrug resistance 1; lactotransferrin; orphan nuclear receptor;

W multidrug resistence associated protein 3; cancer; prostate;

M multidrug resistence associated protein; cransferase;

M altered drug metabolism; cardiovascular function; colorectal tumour;

M central nervous system; pulmonary; immunological; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome py50 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
               reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1936-15 DMA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A2 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 A2 (CYP4501A2), darenergic receptor betal (ADBR1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human acetyl choline muscarinic receptor 3 polymorphic sequence #10.
                                                                                                                                                                                  0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                             Sequence 21 BP; 0 A; 2 C; 9 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                               1 TGTGTGTGTGTGTGTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single nucleotide polymorphism.
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                                                                                                                                                                                Query Match
Best Local Similarity 90.5 Matches 19; Conservative
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ö Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; cytochrome P450 02E; CYP45002E1; LTF; adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRB1; MRB1Z; aryl hydrocarbon receptor nuclear translocator; ARWT; cathepsin S; CTS5; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; epoxide hydroxylase 2; ERHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST1Z; histamine-N-methyl transferase; HNMT; kallikrain 2; KLK2; nicochamide-N-methyl transferase; NNMT; UDP-Glucuronosyl transferase 28; UGP2B1; urokinase receptor; uPA; UGT2B7; UDP-Glucuronosyl transferase; UGT2B1; urokinase receptor; uPA; multidrug resistance 1; lactotransferin; orphan nuclear receptor; uPA; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR4; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism. Gaps Human acetyl choline muscarinic receptor 3 polymorphic sequence #10 .; 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred, No. 8.3e+02; 2; Indels Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other; 0; Mismatches 2824 ATATATATATATATATA 2844 1 ATATATATATATATATA 21 ABS98544 standard; DNA; 21 BP 23-DEC-2002 (first entry) Local Similarity 90.5 hes 19; Conservative ABS98544; Query Match Matches RESULT 570 ABS98544/ ઠ 셤

28-NOV-2001; 2001WO-US044838 28-NOV-2000; 2000US-00724389 (DNAS-) DNA SCI LAB INC. WPI; 2002-698522/75. Guida M, Hall J; WO200257410-A2 Homo sapiens. 25-JUL-2002

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 28; Page 160; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 OZEI (CYP4501A1), detenergic receptor beta1 (ADBR1),
cytochrome P450 OZEI (CYP4500ZEI), adrenergic receptor beta1 (ADBR1),
cytochrome P450 OZEI (CYP4500ZEI), detenergic receptor (ARNY), cathepsin S (CTSS), cyclooxgenase 2 (EDRX2), diazepam binding
cytochrome P450 OZEI (CYP4501A1), detenergic receptor (ARNY), batchilk, detenergic by the cytochrome P450 OZEI (AGC2), diazepam binding
cytochrome P450 OZEI (CYP4500ZEI), diazepam binding
cytochrome P450 OZEI (CYP450ZEI), diazepam binding
cytoc peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels Ouery Match Best Local Similarity 90.5 Matches 19; Conservative

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ABS97829 standard; DNA; 21 BP ABS97829/c

ABS97829;

(first entry) 23-DEC-2002 Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #37.

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF; cytochrome P450 02B; CYP45002E1; LTF; ardineral adrenagic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRB1; NRB1; NRB1; aryl hydrocarbon; ARR; MRB1Z; aryl hydrocarbon; ARR; cathepsin S; CYS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; cyclooxgenase 2; COX2; alazepam binding inhibitor; DB1; haematological; glutathione-S-transferase 12; GST1Z; histamine-N-methyl transferase; HNMT; kallikrain 2; KLK2; nicotinamide-N-methyl transferase; NNMT; UDP-Glucuronosyl transferase 2; MOD2; sulfotransferase thermolabile; GTM; UGT2B7; UDP-Glucuronosyl transferase; UGT2B15; urokinase receptor; uPA; multidrug resistance 1; lactotransferrin; orphan nuclear receptor; uPA; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism.

Homo sapiens.

WO200257410-A2.

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 130; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid

molecule comprising at least one base variation from that of a known

molecule comprising at least one base variation from that of a known

the molecule comprising at least one base variation from that of a known

by the comprising at least one base variation from that of a known

comprising the comprising at least one base variation for transferation (ARR), aryl hydrocarbon receptor nuclear translocator

(ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding

comprising the comprise hydrocarbon receptor nuclear translocator

comprise the comprise hydrocarbon receptor (BENEZ), 5-lipoxygenase activating

protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl

curransferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2),

culfortansferase thermolabile (STM), UDP-glucuronosyl transferase 2B4

(UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

curransferase (UGT2B15), urokinase receptor (UGT2B7), multidrug resistance alsociated protein 3

culfortansferase (UGT2B15), urokinase receptor (URA), multidrug resistance associated protein 3

curransferase (UGT2B15), urokinase receptor (URA), multidrug resistance

curransferase (UGT2B15), urokinase responsible for specific traits within the genome and eventually

currants as a result of their e.g., overexpression, constitutive

currants and result of their e.g., overexpression, constitutive

currants and result of their e.g., overexpression, constitutive

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Example 16; Page 131; 714pp; English.

disorder-related traits.

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polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNWT, NQO2, NR112, STW, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/Or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DB1 or CHMR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KMR2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphic DNA sequence of the invention
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Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

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0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels
                                                                               2316 TCTGTGTGTGTGTGTGCGT 2336
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Query Match
Best Local Similarity 90.5
Matches 19; Conservative
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Gaps ö

RESULT 572

ABS97831 standard; DNA; 21 BP

ABS97831;

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #39. (first entry) 23-DEC-2002

Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 028; CYP4501A1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 028; CYP4501B1;

Adrenergic receptor beta1; ADBR1; aryl hydrocarbon, AHR; MRP3; NRI12;

W adrenergic receptor muclear translocator; ARNT; cathepsin S; CTS5;

Cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

W epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

Glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

W NADPH quinone oxidoreductase 2; NQO2; sulfoctransferase thermolabile; STM;

UDP-glucuronosyl transferase 24; UDP-glucuronosyl transferase 287;

UDP-glucuronosyl transferase 28; UGT2B15; urokinase receptor; uPA;

W multidrug resistance associated protein 3; cancer; prostate;

multidrug resistance associated protein 3; cancer; prostate;

acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR4; CHWR5;

w altered drug metabolism; cardiovascular function; colorectal tumour;

central nervous system; pulmonary; immunological; SNP;

single nucleotide polymorphism.

Homo sapiens

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Hall J; Guida M, WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for

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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A2), cycchrome P450 O2B1 (CYP4501B1), adrenergic receptor betal (ADBR1), cycchrome P450 O2B1 (CYP4501B1), adrenergic receptor betal (ADBR1), cycchrome P450 O2B1 (CYP4501B1), adrenergic receptor butlear translocator (ARNY), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding inhibitor (DB1), epoxide hydrocarbon receptor nuclear translocator (ARNY), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding cransferase (HNWT), NADPH quinone oxidoreductase 2 (NQO2), instandine-N-methyl transferase (HNWT), NADPH quinone oxidoreductase 2 (NQO2), cransferase (HNWT), NADPH quinone oxidoreductase 2 (NQO2), cransferase (UGT2B1S), urokinase receptor (UGT2B1), upp-glucuronosyl transferase (UGT2B1S), urokinase receptor (UGP3B1), upp-glucuronosyl transferase (UGT2B1S), urokinase receptor (NRTI2), or acetylcholine muscarinic (MDR1), lactortansferrin (LTF), multidrug resistance associated protein 3 (NRPS), orphan nuclear receptor (NRTI2), or acetylcholine muscarinic cransferase (UGT2B1S), urokinase receptor (NRTI2), or acetylcholine muscarinic cransferase (MDR1), lactortansferrin (LTF), multidrug resistance associated protein 2 (MDR1), lactortansferrin for locating and characterising the genes teeponsible for avariaty of disorder-related craises a result of their e.g., overexpression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid moleculas comprising the captorial craise and/or treating the disorders. The nucleic acid moleculas contained in CYP4501A1, CYP4501A1, CYP4501A1, CAP4501A1, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system function. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphic DNA sequence of the invention
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Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Gaps . 0 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; Indels 0; Mismatches 90.5%; 19; Conservative Best Local Similarity Matches

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2318 TGTGTGTGTGTGTGCGTGT 2338 21 rérarererererererer 셤 8

ABK47993 standard; DNA; 21 BP ABK47993;

RESULT 573 ABK47993/c

02-JUL-2002 (first entry)

Human MIP-3 beta RT-PCR primer -439/MIP-3 beta.

autoimmune disease; tissue rejection; allergy; cancer; hepatocellular; melanoma; breast; pancreas; colon; glioma; endometrium; intestine; lung; prostate; thyrold; ovary; testis; liver; head; neck; colorectal; bladder; ossophagus; stomach; eye; glioblastoma; gastric; metastatic carcinoma; immunosuppressive; antiallergic; cytostatic; rectum; RT-PCR; primer; reverse transcriptase; macrophage inflammatory protein 3 beta; Human; chemokine; MCP-4; hMCP-4; ss; 6Ckine; dendritic cell; renal; beta. MIP-3

Homo sapiens

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The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polynucleotide in a biological sample comprises hybridising at least one of the polynuclaotide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or diagnosing, or a medicament for treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a primer used to identify genes differentially
                                                                                                                             Predicting, diagnosing or prognosing a cardiovascular disease, e.g. angina, ischemia, myocardial infarction or arteriosclerosis by detection of a polynucleotide in a biological sample comprises detecting a hybridization complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anorectic, cardiant, hypotensive, antiarteriosclerotic; anorectic; virucids; antibacterial; hypotensive; antiarteriosclerotic; anorectic; virucids; antibacterial; fungicide; protozoacide; noctropic; antipaction anticonvulsant; osteopathic; antilipaemic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; occomplement factor I precursor; matrix metalloproteinase-15 precursor; fibroblast growth factor-1; FGF-21; fibroblast growth factor-21; FGF-21; antighnation in the polypeptide variant; harding antipactic fibroblast growth factor-21; FGF-21; antighnation in the polypeptide variant; harding antipactic fibroblast growth factor-21; FGF-21; antighnation factor-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV1 reverse real time quantitative PCR primer SEQ ID NO:148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulated in individuals with cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                      Schmitz
                                                                                                                                                                                                                                                                                              Example 3; Page 107; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1796 AGAGTGACGTCTGGTCCTTTG 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAGCGACGTCTGGTCCTATG 21
                      Wick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 2002US-0409145P.
, 2002US-0410934P.
, 2002US-041032P.
, 2002US-0411060P.
, 2002US-041276F.
, 2002US-0412782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5
Best Local Similarity 90.5
Matches 19; Conservative
                      Gehrmann M,
                                                                           WPI; 2003-403108/38.
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10-SEP-2002;
12-SEP-2002;
16-SEP-2002;
23-SEP-2002;
24-SEP-2002;
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                         Munnes M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Using chemokine MCP-4 or 6Ckine to attract dendritic cells to the site of an antigen is useful to treat disease states, particularly autoimmune disease, tissue rejection, allergy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiovascular disease differential gene expression related primer #163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for enhancing an immune response in a mammal, comprising administering chemokine MCP-4 or 6Ckine or their bologically active fragments. The chemokines are capable of directing the migration of demoratic cells to manufacture a medicament for a disease state. The invention is used to treat disease states, including an autoimmune disease, tissue rejection or an allergy, or a cancer, particularly melanoma, breast pancreatic, colon, lung, gioma, hepatocellular, endometrial, gastric, intestinal, renal, prostate, thyroid, ovarian, testicular, liver, head and neck, colorectal, esophagus, stomach, eye or bladder cancer, glioblastoma or metastatic carcinoma. This sequence represents an RT-PCR primer for metorphage inflammatory protein 3 beta (MIP-3 beta), used in analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris; myocardial infarction; cardiant; antiarteriosclerotic; antianginal; gene therapy; differential gene expression; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 7; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   Laface D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACA90116 standard; DNA; 21 BP
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                                                                                                                                                       24-JAN-2001; 2001US-00768917
                                                                                                                                                                                                               24-JAN-2001; 2001US-00768917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responsiveness to chemokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   Vicari AP, Caux C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-351086/38.
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Best Local Similarity
                                                                                                                                                                                                                                                                           (VICA/) VICARI A P. (CAUX/) CAUX C.
                                                                                                                                                                                                                                                                                                              (CAUX/) CAUX C.
(LAFA/) LAFACE D.
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                                  US2002034494-A1
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                                                                                              21-MAR-2002
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Gaps

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Indels

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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, cardiant, hypotensive, anticonvulsant, onsteopathic, antiparkinsonian, anticonvulsant, onsteopathic, antiathmetic, antiparkinsonian, anticonvulsant, onsteopathic, and antibodies antiarthritic, antimiflammatory, dermatological, antiathmetic, and antibodies antiarthritic, antimiflammatory, preferably a NOVX-associated disorder. In gene threapy. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, treating, preventing or diagnosing diseases such as metabolic disorders, diabete, obesity, infectious diseases (viral, bacterial, fungal, albetten, obesity, infectious diseases (viral, bacterial, fungal, disease, barkinson's disease, epilepsy, immune disorders, Alzheimer's disease, barkinson's disease, epilepsy, immune disorders, and various dyslipidaemias. The nucleic acids and polypeptides as targets for the identification of small molecules therapy, in generation of antibodies that bind immunospecifically to NOVX subpeptides of the invention show homology to certain known human proteins: NOVIa shows homology to fibror in processor; NOVIa shows homology to fibror antient factor I precursor; NOVIA shows homology to rellumner factor I precursor; NOVIA and antient human proteins: when the part of the physical antiends of the invention show homology to effect I precursor; NOVIA and antient human proteins: NOVIA shows homology to effect I precursor; NOVIA and antient factor I precursor; NOVIA and antient human proteins: NOVIA and when the proteins antient and antient factor I precursor; NOVIA and antient factor I precursor in the prote
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                                                                                                                                                                                                                                                               New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                  Ort T, Padigaru M, Rieger DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 5 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; SEQ ID NO 148; 214pp; English.
                                                                                                                                                  Zhong M, Guo X, Anderson DW,
25-SEP-2002; 2002US-0413342P.
30-SEP-2002; 2002US-0414832P.
                                                                                        (CURA-) CURAGEN CORP.
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Query Match 0.5%; Score 17.8; DB 1; Length 21; Best Local Similarity 90.5%; Pred. No. 8.3e+02; Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                              1351 ATGGAGATGATGAAGATGATC 1371
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New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or

Example C; Page 231; 266pp; English.

Parkinson's disease.

Vernet CA, Tchernev VT, Malyankar UM, Gerlach VL; 19en BD, Patturajan M, Gusev VY, Kekuda R, Pena CEA; 10golli EA, Taupier RJ;

Zerhusen BD, Pat 1, Gangolli EA,

Spytek KA, Zhong M, WPI; 2002-713508/77.

The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. ONVX mucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Wuntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiatelangiectasia, leukodystrophies, addiction, anxiety, depression, pain,

ABS78792 standard; DNA; 22 ABS78792 RESULT 576 ABS78792 ID ABS7 XX AC ABS7 XX

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Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obsestly; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; sathma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; angiogenesis; PCR; primer; ss.
                     Human NOVX reverse primer Ag3765.
                                                                                                                                                                                                                                                                                              2001US-0275235P.
2001US-0275579P.
2001US-0275601P.
2001US-0276000P.
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2001US-0277833P.
2001US-0278152P.
2001US-0278894P.
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2001US-0277327P.
2001US-0277338P.
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2001US-0279344P.
2001US-0280233P.
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2001US-0288148P.
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 (first entry)
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                                                                                                                                                                                      Homo sapiens.
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14-MAR-2001;
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16-DEC-2002
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inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis; asthma; inflammatory diseases; cardiovascular condition; hypertension; arthritis; restenosis; angiotensin converting enzyme; ss.

Specific; cleavage; target RNA; protein; prophylaxis; expression;

Enzymatic RNA molecule ACE mRNA target sequence.

(first entry)

(revised)

25-MAR-2003 26-JUL-1994

AAQ57329;

23 GTGTGTGTATGTGTTTGCACA 3

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AAQ57329 standard; mRNA; 24

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AAQ5732
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obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosciercosis, hypertension, soll-anderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, pancreatitis, autoimmune disease, infections, or graft-versus-host disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and amminospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation pharmacogenomics. The present nucleic acid sequence represents a PCR primer that was used in the methods of the invention for amplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polymuclectide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%; Score 17.8; DB 1; Length 23; Best Local Similarity 90.5%; Pred. No. 9.2e+02; Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                         0.5%; Score 17.8; DB 1; Length 22;
llarity 90.5%; Pred. No. 8.7e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                Sequence 22 BP; 3 A; 0 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 9 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 6976; 2627pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide polymorphism in human gene.
                                                                                                                                                                                                                                                                                                  2321 GTGTGTGTGTGTGTGTG 2341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer of the invention #3667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                                                                                                                                                                                                                             ADK97947 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-093977/10.
                                                                                                                                                                                                                                                           Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2003259875-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-2003.
                                                                                                                                                                               primer than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                       ADK97947;
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                   RESULT 577
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                              ADK97947,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                        Enzymatic RNA molecules which cleave mRNA - used to treat or prevent inflammatory, arthritic, stenotic or cardiovascular diseases or conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 17.8; DB 1; Length 24; 90.5%; Pred. No. 9.6e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multimerisation of minimal motifs using primer ZGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 3 A; 8 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3187 CAGCCTGCCCGGAGCTGGAG 3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 21; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00987132.
92US-00989848.
92US-00989849.
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                                                                                                             93WO-US006316.
                                                                                                                                                                                                                               93US-00008895.
                                                                                                                                                     92US-00916763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV55817 standard; DNA; 24
                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                Sullivan SM, Draper KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-048853/06.
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18-NOV-1998
                                                                                                             02-JUL-1993;
                                   WO9402595-A1
                                                                                                                                                                           07-DEC-1992;
                                                                                                                                                                                              07-DEC-1992;
                                                                                                                                                                                                                                     19-JAN-1993;
                                                                                                                                                       17-JUL-1992;
                                                                          03-FEB-1994
Synthetic.
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Gaps

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2335 GTGTGTGTGTGTGCACA 2355

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Sequences shown in AAV55812 to AAV55827 represent primers used in the course of the invention for the multimerisation of minimal motifs. The invention provides a method for increasing the resistence of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula onto or into the core protein a stabilising polypeptide of formula conto or into the core protein a stabilising polypeptide of formula can be anything between 1-66. X, Y and Z need not be identical from an can be anything between 1-66. X, Y and Z need not be identical from nepeat to n repeat. Alternatively a nucleic acid encoding a stabilising core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the can unused core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an Ixappab regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in canzwe/producy thereat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging. (Updated on 27-NUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single nucleotide polymorphism; SNP; single nucleotide primer extension;
              Pusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; lkappab regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; minimal motif; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP specific upper PCR primer SEQ ID 2153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 72; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2103 CACCCCCAGCTCCAGCTCCTC 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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                                                                                                                                                                                                                                                                                                                 96US-0030986P.
97US-0048945P.
                                                                                                                                                                                                                                                                              97WO-IB001508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing glycine repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                           Human herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-312463/27.
                                                                                                                                                                                                                                                                                                                                                                               (MASU/) MASUCCI M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                  WO9822577-A1
                                                                                                                                                                                                                                                                              17-NOV-1997;
                                                                                                                                                                                                                                                                                                                                      25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                   15-NOV-1996;
                                                                                                                                                                                                                                       28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       Masucci MG;
                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH39357;
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ID AAH3
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AC AAH3
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DY 14-P
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide polymorphisms SNPs. The present invention sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the presence or absence of a SNP, using the presence or a snew or amplify a single and the invention. The PCR primers are used to amplify a some or a sequence, the SNPS primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabete inspiblies, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecte and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune craneer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and
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                   Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease; osteogenesis imperfecte; autoimmune disease, acute intermittent porphyria, rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paternity analysis. The present sequence represents a PCR primer specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
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Pred. No. 9.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 1 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 60; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGCGTGT
                                                                                                                                                                                                                                                                                                                                       (ORCH-) ORCHID BIOSCIENCES INC.
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                                                                                                                                                                                                                                                      13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                                                                                                                               99US-0160096P.
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Pohl
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290930/30
                                                                                                                                                                                                                                                                                                                                                                                 Picoult-Newburg L,
                                                                                                                                                                    WO200129262-A2
                                                                                                                                                                                                                                                                                             15-OCT-1999;
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid sample.
                                                                                                                                                                                                              26-APR-2001
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect misatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one or more nucleic acid sto at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring come expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid concerned in situ hybridisation, in Southern, Northern or dotter the hybridisation to identify or detect the sequence or specific content of any gene in mapping the 5, termini of find any gene in mapping the 5, termini of find any gene in members of the monitoring of any gene in the sequence or specific mutations of any gene in members of the monitoring of any gene in members of the monitoring of any gene in members of the monitoring of any gene in the sequence or specific mutations of any gene in members of the monitoring of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequate.
                                                                                                                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
; probe; expressed sequence tag; microarray; gene expression; variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, resequence, genotype, disease, forensic, paternity testing, single nucleotide polymorphism; SNP, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human single nucleotide polymorphism (SNP) FGFR3 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 70102; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAGTGTAGATTTCTATAA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%;
                                                                                                                                                                                                                    16-MAR-2001; 2001US-0276759P
                                                                                                                                                                               15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI30472 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                       cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                     AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                            WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 19; Conserv
   EST; ss; probe;
                                                                                                            JS2003104410-A1
                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2001
                                                                                                                                                                                                                                                                                         Mittmann MP;
                                                                                                                                               05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                      genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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AA130472/
AA13 AA13
XX
AC AA13
XX
XX
DE Huma
XX
KW Huma
KW sing
   g
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The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer; parathyroid hormone type 3 receptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                       /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zebrafish PTH1R receptor coding sequence PCR primer For TM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 17.8; DB 1; Length 31; ilarity 90.5%; Pred. No. 1.2e+03; Conservative 0; Mismarch...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31 BP; 3 A; 11 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3414 AGGGGCCGGCCCTGTGCAG 3434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AGGGGCCGCCCTGCGTGCAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US011883.
                                                                                replace (16, T)
                                                                                                                                                                                                                                                                                                                                                     07-MAR-2000; 2000US-0187510P.
22-MAY-2000; 2000US-0206129P.
                                                                                                                                                                                                                                                                                                 07-MAR-2001; 2001WO-US007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA30842 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cargill M, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-522952/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         particular genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 19; Conserv
                                                                                                                                                                                       WO200166800-A2.
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Homo sapiens.
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29-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-2000
                                                                                                                                                                                                                                              13-SEP-2001
                                                                          Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA30842;
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                                                                                                                                                                                             This sequence represents a PCR primer used to isolate DNA encoding the parathyroid hormone receptor type 1 (PTHIR) receptor protein of the invention also relates to a PTHIR receptor protein.

Antagonists of PTHIR or PTHIR can be used for the treatment of diseases associated with an increase in PTHIR or PTHIR activity, respectively. The peptides are used for diagnosis or prognosis of diseases and disorders associated with PTHIR or PTHIR, such as cancer. The polypeptides can be used as a molecular weight markers on sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, including monoclonal antibodies, that bind specifically to a polypeptide. The peptides are useful during diagnosis of diseases and disorders in mammals involving PTHIR or PTHIR sequence and/or expression. Mutations that affect to PTHIR sequence and/or expression levels of PTHIR or PTHIR cornelations with disease or disorders of a developmental, by with genes associated with disease. (Updated on 15-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zebrafish, PTH1R; parathyroid hormone type-1 receptor;
developmental disorder; physiological disorder; neurological disorder;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 17.6; DB 1; Length 24; 33.3%; Pred. No. 1e+03; ve 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zebrafish PTH1R cDNA PCR primer For TM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1344 GTCTGAGATGGAGATGAAGAT 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 43; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA48458 standard; DNA; 24 BP.
           98US-0110467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                    Jueppner H, Rubin DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                          WPI; 2000-412319/35.
                               (JUEP/) JUEPPNER H. (RUBI/) RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200032775-A1.
           30-NOV-1998;
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27-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2000
                                                                                                                                                    function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA48458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The present sequence is a PCR primer for the parathyroid hormone type-1 receptor (PTHIR) gene from the zebrafish. It was used to amplify and isolate cDNA encoding this protein. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, molecular chaperone 18; cytostatic; virucidal; immunomodulatory;
antiinflammatory; haemostatic; nootropic; neuroprotective; anti-HIV;
malignant neoplasm; HIV; infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide for the diagnosis and treatment of malignant neoplasm, hemopathy, HIV infection, immunological diseases and inflammations, comprises the human molecular chaperone 18 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                           New nucleic acids encoding parathyroid hormone receptors PTH1R and useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.6; DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human molecular chaperone 18 PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1344 GTCTGAGATGGAGATGAAGAT 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 46; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001WO-CN000503.
98US-0110467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                             Jueppner H, Rubin DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611637/70.
                                                                                                                                                                                                                               WPI; 2000-412323/35.
                                                              (JUEP/) JUEPPNER H.
                                                                                          (RUBI/) RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200173072-A1.
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30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588
                                                                                                                     Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of human phosphoesterase 30. The sequences can be used in the treatment of cancer, nosohaemia, HIV infection, immunological diseases and inflammation. The present sequence is a PCR primer for the coding sequence of the invention
The invention relates to human molecular chaperone 18 with cytostatic, virucidal, immunomodulatory, antinflammatory, haemostatic, nootropic, neuroprotective and anti-HIV activity. The polympetide and encoded polymucleotide are applicable in diagnosis and treatment of malignant neoplasm, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is that of a PCR primer, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide-phosphoesterase 30 for treating various diseases, s malignant tumor, nosohemia, human immunodeficiency virus infection, immunological diseases and inflammations.
                                                                                                                                                                                                                                                                                                                                              Human; phosphoesterase 30; cancer; nosohaemia; HIV infection; immunological disease; inflammation; gene therapy; PCR primer; ss.
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0
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Pred. No. 1e+03;
0; Mismatches 4; Indels
                                                                                                                  Score 17.6; DB 1; Length 24;
Pred. No. 1e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                         Human phosphoesterase 30 coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 U; 0 Other;
                                                                                                Sequence 24 BP; 11 A; 2 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 16(Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3311 TTTTCTTTAGGAGATTTATTTTT 3334
                                                                                                                                                                     2822 GTATATATACATATATATATAA 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                    TTTGATTTAGGAAGTTTATTTTT
                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2000; 2000CN-00111518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-2000; 2000CN-00111518.
                                                                                                                     ch 0.5%;
il Similarity 83.3%;
20; Conservative (
                                                                                                                                                                                                                                                       ABA05057 standard; DNA; 24
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5
Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-018034/03.
                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                    22-FEB-2002
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ABA05945 standard; DNA; 24

RESULT 587

ABA05945 ID ABA0

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The invention relates to human endomannosidase 25 polypeptide, its recombinant production, an endomannosidase 25 antagonist and the andomannosidase encoding polymucleotide and application. The polypeptide is useful for treating cancer, haemopathy and human immunodeficiency virus infection. The present sequence is that of a PCR primer, useful to
                                                                                                          25; cancer; haemopathy; HIV; infection; enzyme; virus; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor; tyrosine kinase receptor inhibitor; epidermal growth factor receptor inhibitor; EGFR; mammary tumour; cytostatic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human endomannosidase 25 and encoding polynucleotide, useful for treating cancer, hemopathy and human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 6 A; 1 C; 4 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 18 (Disclosure); 32pp; Chinese.
                                                                       Human endomannosidase 25 PCR primer SEQ ID NO
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                                                                                                                                                                                                                                                                                                24-MAR-2000; 2000CN-00115107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                   Human; endomannosidase
                                                                                                                                     human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-056345/08.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     Xie Y;
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ABA05945;
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25-MAR-2004
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अंधिQuery Match
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Matches
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                                                                         Composition for treating mammary tumors associated with aberrant tyrosine kinase receptor activity in nonhuman animals, comprises one or more substances that inhibit the aberrant activity.
                                                                                                                                                     tumours associated with aberrant tyrosine kinase receptor activity in nonhuman animals. (C) comprises one or more substance that inhibit the aberrant tyrosine kinase receptor activity. (C) has cytostatic activity. (C) can be used as a tyrosine kinase receptor inhibitor, and an epidermal growth factor receptor (BGRR) inhibitor. (C) is especially useful for treating canine mammary tumours. The present sequence represents a PCR primer for human EGRR, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated nucleic acid (I) comprising a polynucleotide having a nucleotide sequence chosen from nucleotide sequence encoding a parathyroid hormone (PTH)/PTH-related peptide (PfHrP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parathyroid hormone; PTH; PTH-related peptide; PfHrP;
parathyroid hormone receptor; PTHR; chromosome identification; zebrafish;
PTH1R; receptor; 89; primer; PCR.
                                                                                                                                             mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Full length zebrafish parathyroid hormone receptor PTH1R primer ForTM3
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                            The present invention describes a composition (C) for treating
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                                Kleemann
                                                                                                                                                                                                                                                                         Score 17.6; DB 1; Length 24;
Pred. No. 1e+03;
0; Mismatches 4; Indels
                                Bette P,
                                                                                                                                                                                                                                                      Sequence 24 BP; 6 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
                                Van Meel J,
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                                                                                                                                                                                                                                                                                                                       1945 TACATGATCATGCGGGAGTGCTGG 1968
          (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                      Example 1; Page 21; 37pp; English
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                                F, Brandstetter I,
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                                                                                                                                                                                                                                                                                                 20; Conservative
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                                                                                                                                                                                                                                                                                      Similarity
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receptor (PTHIR receptor) having a fully defined sequence of 536 amino acids as given in the specification, PTHIR receptor, mature PTHIR receptor, PTHIR extracellular or transmembrane domain, and their complement. (I) is useful for diagnosing and treating decrease in the standard or normal level of PTHIR receptor activity in an individual, for chromosome identification. This sequence represents a primer used ioslate the full length cDNA encoding zebrafish PTHIR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
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99US-00449632
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97WO-US011687.
                 96US-00678039.
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07-JUL-1997;
                  10-JUL-1996;
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                                                      Keating MT,
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                                                                                                                    stenosis.
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                                                                                                                                                                                                                                                                                                                The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                       Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams syndrome cognitive profile; WSCP; cognition; LIM-kinase 1; LIMK1 gene; supra-vascular aortic stenosis; protein kinase; human; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                        ch 0.5%; Score 17.6; DB 1; Length 24; il Similarity 83.3%; Pred. No. 1e+03; 20; Conservative 0; Mismatches 4; Indel8
                                                                                                                    human; gene sequence; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 1 A; 2 C; 9 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 1733; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                            2329 GIGIGIGIGIGIGIGIGIGIG 2352
                                                                                                                                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Grgrgrgrgrgrgrgrargrrrcc 24
                                                                                                                             disease diagnosis; ss; PCR; primer
    24 GTCTGAGAAGAAGGTCATGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV05314 standard; DNA; 25 BP.
                                               ADH93896 standard; DNA; 24 BP
                                                                                                                                                                                                   11-DEC-2001; 2001JP-00377637.
                                                                                                                                                                                                                     11-DEC-2001; 2001JP-00377637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase domain 3' PCR primer
                                                                                                    Human gene PCR primer #741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                  (first entry)
                                                                                                                                                                                                                                                        WPI; 2003-819215/77
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                  JP2003174883-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                Homo sapiens
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                                                                                   22-APR-2004
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                                                                                                                                                                                 24-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV05314;
                                                                  ADH93896;
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This oligonucleotide was designed to amplify the region of homology in the kinase domains of PDGF receptor, HER2, HER3, FGF-FIG, FGF-BEK, insulin receptor and IRR. It was used with another kinase homology domain—based primer (see AAV05313) in the amplification of human LIM-kinase 1 (LIMK1) sequences. The LIMK1 gene is composed of 16 exons (see AAV05315 and AAT9559-T99629) and is located 15.4 kb 3' of elastin in chromosome 7. It encodes a novel protein kinase (see AAM46576). Williams syndrome cognitive profile (WSCP) is detected by determining zygosity of the LIMK1 locus, with hemizygosity being indicative of impaired visuo-spatial constructive cognition. Chromosome 7 deletion analysis allows discrimination between WSCP, SVAS (supra-vascular aortic stenosis) and Williams syndrome
                                                                                                                                                                                                 Diagnosing Williams syndrome cognitive profile from hemi-zygosity of LIMX1 - gene on chromosome 7 encoding new kinase, allowing differentiation from classic Williams syndrome and supra-vascular aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 4 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.6; DB 1;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PAPP-Ea associated 25-mer SEQ ID 1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 83.3%;
Matches 20; Conservative
(UTAH ) UNIV UTAH RES FOUND.
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                                                                     Morris CA;
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(SHAN/) SHANNON M E.
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                                                                                                                                          WPI; 1998-101185/09.
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                                                               This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, harper-E. The products of the invention have abortive and contraceptive activity and can be used for generacy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenacially. This sequence repersents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein B, hPAPPE. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPPE is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
associated plasma protein E, for preventing or aborting pregnancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated plasma protein E, for preventing or aborting pregnancy
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                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 17.6; DB 1; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 3 A; 0 C; 9 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                          1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PAPP-Ea associated 25-mer SEQ ID 1205.
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                                    Example 2; Page 233; 353pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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(SHAN/) SHANNON M E.
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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ABS75679
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the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
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Pred. No. 1.1e+03;
0; Mismatches 4; Indels
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human PAPP-E genes described in the disclosure of the
                                                                                                                                                                                                         Sequence 25 BP; 3 A; 0 C; 10 G; 12 T; 0 U; 0 Other;
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0; Mismatches 4
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Conservative
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(SHAN/) SHANNON M E.
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nes 20; Conserv
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BST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
           Human microarray DNA oligonucleotide SEQ ID NO 87311
                                                                                                                                                                                                                           15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                              16-MAR-2001; 2001US-0276759P.
                                                                                   cross-species comparison.
                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-567953/53.
                                                                                                                                                          US2003104410-A1.
                                                                                                                          Homo sapiens
                                                                                                                                                                                             05-JUN-2003.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hpapp-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the artibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                                                                                                                                                  PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 0.5%; Score 17.6; DB 1; Length 25; al Similarity 83.3%; Pred. No. 1.1e+03; 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 3 A; 0 C; 9 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                    Human PAPP-Ea associated 25-mer SEQ ID 1208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2322 TGTGTGTGTGTGCGTGTGTGTGTG 2345
     2319 GIGIGIGIGIGIGIGIGIGI 2342
                        Example 2; Page 234; 353pp; English;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001US-00827998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456P.
                                                                                                                              ABS75682 standard; DNA; 25
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-697817/75.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gu Y, Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                US2002102252-A1.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-2002.
                                                                                                                                                                                                     27-DEC-2002
                                                                                                                                                                 ABS75682;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC perfect match, perfect mismatch, antisense mismatch.

CC perfect match perfect mismatch, antisense mismatch.

CC perfect match perfect mismatch, antisense mismatch.

CC perfect match perfect mismatch, antisense mismatch.

CC in monitoring gene expression levels by hybridisation to a DNA library, in monitoring gene expression levels by hybridisation to a DNA library,

CC compounds. The nucleic acid probes are specifically designed for analysis of the nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid comparises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross species comparisen. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid mismapping the 5' termini of mRNA molecules by mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or an screening onny or genomic libraries or subclones conclaining segments of DNA that have been conclained and previously sequenced. The sequence greated is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly conclained in electronic format directly the sequence.
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human microarray DNA oligonucleotide SEQ ID NO 80270.
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                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 87311; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 CGGATGGACAAGAAGCTGCTGGCC 270
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nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACI80279 standard; DNA; 25
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ID ACI80
XX
AC ACI80
XX
XX
AC ACI80
XX
DT 14-00
XX
DE Humar
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ACI87320 standard; DNA; 25

14-OCT-2003 (first entry)

ACI87320;

RESULT 597
ACI87320/c
ID ACI873;
XX
AC ACI873;
XX
DT 14-OCT

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of taglabelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of thybridisation are least two or more nucleic acids to at least two or more nucleic acids probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Bach of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-probes is useful in in situ hybridisation, in Southern, Northern or dot-mutations of any gene, in mapping the 5' termini of mRNA molecules by prime extensions or in screening cond or the probes of supplementations of any gene, in mapping the 5' termini of mRNA molecules by the proper sequence or specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer extensions or in screening CDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been taclated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                        ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 80270; 9pp; English.
                                                                                                                                                                                                                                                                                    15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                       16-MAR-2001; 2001US-0276759P
                                                                         cross-species comparison
                                                                                                                                                                                                                                                                                                                                                                                        (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-567953/53.
                                                                                                                                                                                US2003104410-A1.
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mittmann MP;
                                                                                                                                                                                                                                05-JUN-2003.
                           EST; 88;
genetic
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ö Gaps ö 0.5%; Score 17.6; DB 1; Length 25; 33.3%; Pred. No. 1.1e+03; ve 0; Mismatches 4; Indels Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other; 83.3%; Local Similarity 83.3 nes 20; Conservative Query Match Matches ઠે

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ACH54190 standard; DNA; 25 ACH54190; ACH54190 RESULT **EXEXEXEX**

DNA target sequence #3326 useful in array for genetic analyses.

(first entry)

16-OCT-2003

Gene expression analysis; array; hybridisation; genetic variation;

Gene expression analysis; array; hybridisation; genetic variation;

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complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match. The patent, or their perfect sense match. Sense mismatch oligomucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridisation tagellabelled compounds. The probes are useful for identifying family members of a gene. The probes are useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH65260 represent the target equences of the invention. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
tag-labelled compound, gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to nucleic acid sequences that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA target sequence #7601 useful in array for genetic analyses.
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0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3677 AGGGTGGTCTCTTCTTGGGGCCCA 3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3326; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ACGGTCGTCTTCTTGGGTCCTA 25
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                                                                                                                                                                                                                                             08-AUG-2002; 2002US-00215112
                                                                                                                                                                                                                                                                                         08-AUG-2001; 2001US-0311040P
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                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-576608/54.
                                                                                                                                                                                                                                                                                                                                   (MITT/) MITTMANN M.
                                                                                                                                                        US2003082596-A1.
                                                                                                              Unidentified
                                                                                                                                                                                                 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                 Mittmann M;
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genetic alteration; pharmacogenetic reaction; genotyping; polymorphism; gene expression profiling.

single multiplex polymerase chain reaction; multifactorial disease;

vivlemore401-10.rng

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The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nuclectides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridisations, in screening compounds. The probes are useful in in situ hybridisations, in screening cDNA or genemic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic formatical and electronic provides a large of all party more in a party of the invention electronic formatical and electronic formatical and electronic electronic formatical and electronic electronic electronic electronic electronic formatical electronic elec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
tag-labelled compound; gene family; in situ hybridisation;
library screening; Southern hybridisation; northern hybridisation;
dot-blot hybridisation; gene sequence; mutation detection;
target sequence; probe; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 ACGGTCGTCTTTTTTGGGTCCTA 1
                                                                                                                                                                                                                                                                                                   08-AUG-2002; 2002US-00215112.
                                                                                                                                                                                                                                                                                                                                                       08-AUG-2001; 2001US-0311040P.
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                                                                                                                                                                                                                                                                                                                                                                                                        (MITT/) MITTMANN M.
                                                                                                                                                                                                US2003082596-A1.
                                                                                                                                              Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mittmann M;
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Designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase chain reaction, for high throughput multiplex DNA sequence amplification, comprises aligning two primers.

Disclosure; Page 34; 120pp; English.

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

WPI; 2004-340914/31.

11 7;

Li H,

07-OCT-2003; 2003WO-US031874. 07-OCT-2002; 2002US-0417009P

WO2004033649-A2.

Synthetic

22-APR-2004.

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The invention relates to a method of designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase chain reaction by aligning a first primer and a second primer. The method comprises: (a) aligning a first primer and a second primer; and (b) comprises: (a) aligning a first primer and a second primer; and (b) contain four or more bases that are perfectly matching to the 3' end does not contain seven or more bases that are perfectly matching contain four or more bases that are perfectly matching contain six or second primer, the first primer or more bases that are perfectly matching contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer, the first primer or the second primer. The method is used to sequence anywhere of the first primer or the second primer. The method is useful for designing primer or the second primer. The method is useful for designing primer or the second primer. The method is useful for designing primer or the second primer. The method is useful for designing primer or the second primer. The method is useful for designing primer or the second contain of target DNA fragments in a single multiplex polymerase contain reaction. It is also useful in the identification of multiple genes contain the primer of the designing primer or the denotyping the primer or the second primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alterations, the studies in pharmacogenetic reactions, the genotyping genetic polymorphisms in a large population, the gene expression profiling in various samples and high throughput genotyping technologies. This sequence corresponds to an example of a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.6; DB 1; Length 25; 13.3%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 6 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.3%; Pred. No. 1.1e (es 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite sequence from clone TGLA147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Aracacarrrrrrrrrrarrargie 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33728 standard; DNA; 19 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 602
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Gaps

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ss; primer; simultaneous amplification;

Single multiplex PCR primer #277.

15-JUL-2004 (first entry)

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the haemoglobin gamma G gene located at chromosomal position 11p15.5. The sequence is amplified by primers AAT66094-5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a hairpin or hammerhead ribozyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                Example 9; Col 59-60; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin B1 ribozyme binding site #135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 98; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGCGT 2336
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            89US-00341562.
91US-00754351.
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                                                           (MARS-) MARSHFIELD CLINIC.
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                                                                                                                     WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-412314/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 18; Conserv
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              21-APR-1989;
05-SEP-1991;
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                                                                                         Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA85806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rritz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                  The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (ACI)1s and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OFTTRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromsome; ds.
                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; DB 1; Length 19;
Pred. No. 8.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence found in the haemoglobin gamma G gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          Table 7; Page 221; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTGCGT 2336
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                                                                                                        92WO-US000340
                                                                                                                                      91US-00642342.
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(first entry)
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                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                     (GENM-) GENMARK.
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                                                                                                                                     15-JAN-1991;
                                           WO9213102-A1
                                                                                                      15-JAN-1992;
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18-JUN-1997
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                                                                         06-AUG-1992
                Bos taurus.
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Gaps

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1; Indels

0; Mismatches

Robbins JM;

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This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a trarget DNA of known camplification of circular single sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire single sequence repeat (SSR) alleles for amplification (GSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distinguishing between species, strains or varieties within species or identifying the presence of a disease condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, expert sequences in sequence within a single stranded DNA template and flanking regions for these target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method so also be used to obtain entire coding regions of the present method so also be used to obtain entire coding regions of the present method so also be used to obtain entire coding a degenerate
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designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simple sequence repeat; SSR; single site amplification; SSA; disease;
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                              Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSA primer 3 for amplifying A. thaliana and Z. mays DNA.
                                                                                                                                                                                                   Sequence 19 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                2550 TCGGCCTCTGCCTTTGCAC 2568
                                                                                                                                                                                                                                                                                                                                                                              AAZ89471 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                          Local Similarity 94.7
nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997;
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                                                                                                                                                                                                                                                   Query Match
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using a polymerase having strand displacement capability which can synthesize up to 10 kb fragments. This is especially useful for obtaining plant genes which are usually less than 10 kb in length. The method allows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue (less than 1 mmg). It also allows the production of a PCR template with knowledge of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with total time for target DNA development being between 4-6 months, with total time for target DNA development being between 4-6 months. AAS89469-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distinguishing between species, strains or varieties within species or identifying the presence of a disease condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker development, forensic DNA fingerprinting, etc. The method can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
nucleic acid sequence derived from amino acid sequence back translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simple sequence repeat; SSR; single site amplification; SSA; disease;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 1; Length 19;
Pred. No. 8.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSA primer 4 for amplifying A. thaliana and Z. mays DNA.
                                                                                                                                                                                                                                                                                      Sequence 19 BP; 9 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Col 9-10; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                2315 GTCTGTGTGTGTGTG 2333
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                                                                                                                                                                                                                                                                                                                               Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 606
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trom one sequence within a single stranded DNA template and flanking cregions for these target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. To cloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of genes based upon a known nucleic acid sequence or by using a degenerate nucleic acid sequence derived from amino acid sequence back translation using a polymerase having strand displacement capability which can using a polymerase having strand displacement capability which can using a polymerase having strand displacement capability which can using a polymerase usually less than 10 kb in length. The method allows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue the finally. It also allows the production of a PCR template with knowledge of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with the time for target DNA development being between 4-6 months, with the time for target DNA development being between 4-6 months, with 8X88888888888888888888888888888888

Seguence 19 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 0 Other;

Gaps ö Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 1; Indels 0; Mismatches 2315 GTCTGTGTGTGTGTGTG 2333 GIGIGIGIGIGIGIGIGI 19 0.5%; Local Similarity 94.7 nes 18; Conservative Query Match Matches В

AAC66739 standard; DNA; 19 BP 15-FEB-2001 AAC66739; RESULT 607

(first entry)

Heterologous insert sequence #2.

Probe; cytostatic; antiviral; gene therapy; ss.

Unidentified

WO200063365-A1.

26-OCT-2000.

21-APR-2000; 2000WO-US010909.

99US-0130345P 21-APR-1999;

(PANG-) PANGENE CORP.

Zarling D; Belotserkovskii B, Reddy G,

WPI; 2000-647516/62.

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure, Fig 9, 103pp, English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one homology clamp corresponding or complementary to a preselected target nucleic acid sequence and at least one anchoring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used in the present invention. The composition of the present invention can be used to modulate transcription or replication of a pre-

selected target sequence, treat a disease state of a plant or animal caused by expression of a disease gene, detect a double stranded nucleic acid target sequence, isolate either strand of a double stranded target sequence, isolate either strand of a gene family, produce a transgenic non-human organism or plant, determine the function of a double stranded nucleic acid target sequence and inhibit double stranded nucleic acid target sequence and inhibit composition may be used to produce animal models for genetic defects 8888888888

Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Gaps ö Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 0.5%; Query Match 0.5 Best Local Similarity 94.7 Matches 18, Conservative

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ઠે 용 RESULT 608 AAC66738/

AAC66738 standard; DNA; 19

AAC66738;

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15-FEB-2001 (first entry)

Heterologous insert sequence #1.

Probe; cytostatic; antiviral; gene therapy; ss.

Unidentified.

WO200063365-A1

26-OCT-2000

21-APR-2000; 2000WO-US010909.

99US-0130345P 21-APR-1999;

(PANG-) PANGENE CORP.

Zarling Reddy G, Belotserkovskii B,

WPI; 2000-647516/62.

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure; Fig 9; 103pp; English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one homology clamp corresponding or complementary to a preselected target nucleic acid sequence and at least one anchoring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used in the present invention. The composition of the present invention can be used in the present invention or replication of a preselected target sequence, treat a disease state of a plant or animal caused by expression of a disease gene, detect a double stranded nucleic acid target sequence, isolate either strand of a gene family, produce a transpent non-human organism or plant, determine the function of a transpent non-human organism or plant, determine the function of a composition nucleic acid torestion or branch migration. In addition, the composition may be used to produce animal models for genetic defects

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ; 0 Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 94.78; Query Match Best Local Similarity 94.7 Matches 18; Conservative

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2318 TGTGTGTGTGTGTGCGT 2336 rererererererer 13

ð 硆 RESULT 609

AAH60968;

BP AAH60968 standard; DNA; 19

(first entry) LO-SEP-2001

Cyclin B1 ribozyme binding site SEQ ID NO:3392.

Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; porvitasis; diabetic retinopathy; cytokine; inflammation; cell-qycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral arcpic dermattits; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.

sapiens. Synthetic. Homo

WO200130362-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US029500.

99US-0161532P. 26-OCT-1999;

(IMMU-) IMMUSOL INC.

Robbins JM, Tritz R;

WPI; 2001-300427/31.

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 318; 408pp; English.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a complete card segment encoding (I). (I) can have antiposriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating poliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detechment, and for treating and preventing prematurity and retinal detechment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAR57277 to AAR62099 represent sequences used in the

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Sequence 19 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
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Gaps ö Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 1; Indels 0; Mismatches 0.5%; Ouery Match 0.5 Best Local Similarity 94.7 Matches 18; Conservative

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RESULT 610 ABK90423

ABK90423 standard; DNA; 19 BP

ABK90423;

05-NOV-2002 (first entry)

Human UGTlal promoter polymorphism (TA)8 repeat region.

Human; ds; UGTIA1; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; TAS-103; xenobiotic.

Homo sapiens.

US6395481-B1.

28-MAY-2002.

99US-00251274. 16-FEB-1999; 99US-00251274 16-FEB-1999;

DEV CORP. (ARCH-) ARCH Di Rienzo A, Iyer L, Ratain MJ;

WPI; 2002-588597/63.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in the promoter.

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. (M1) is preferably a UGT 1 (UGTAH) gene promoter. (M1) is cusful for screening individuals for variation in glucuronidation activity, for optimising draw dosages for a patient, where the drugs cativity, for optimising are glucuronidated by UGT (preferably UGTAH) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTAH) gene promoter (UGTAH) gene promoter. Thus the DNA being amplified comprises all or part of in the promoter. Thus the DNA being amplified comprises all or part of the number of TA repeats is adetermined by a polymerase chain reaction and the number of five TA repeats (TA) 5, TAP, TAP, or sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA) 5, TAP, TAP, (TA) 6, (TA) 8, (TA) 6, (TA) 8, (TA) 6, (TA) 8, (

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The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five The repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in useful for screening individuals for variation in glucuronidation a UGT gene promoter. (M1) is useful for screening individuals for variation in glucuronidation cativity, for optimising drug desages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably UGTA1) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTIA1) gene promoter. Thus the DNA and determining the number of TA repeats in determined by a polymerase allo repart of UGTIA1 promoter. The DNA is amplified by a polymerase chain reaction and the number of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele
with expression of the UGT gene, and the individuals sensitivity to xenobiotics is effected by glucuronidation activity. The methods preferably involve determining the presence of five, six or seven TA repeats in the promoter. Defects in glucurodination is associated with Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The present sequence is the UGTIA1 promoter (TA)8 repeat region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
TAS-103; xenobiotic.
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                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%; Score 17.4; DB 1; Length 19; Best Local Similarity 94.7%; Pred. No. 8.2e+02; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human UGTlal promoter polymorphism (TA)8 repeat region.
                                                                                                                                                                                                                                                                         Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2827 TATACATATATATATA 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Col 11; 13pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TATATATATATATATA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARCH-) ARCH DEV CORP.
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ID ABK99

AC ABK90

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AC ABK90

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consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA repeats (TA)7. The promoter has any one of the genotypes (TA)5, (TA)5, (TA)6, (TA)8, (TA)7, (TA)6, (TA)8, (TA)7, (TA)8, (TA)8, (TA)7, (TA)8 or TA)6, (TA)8, (TA)7, (TA)8 or TA)8 or TA)9 or TA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.4; DB 1; Length 19;
14.7%; Pred. No. 8.2e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3462 TTATATATATCTATATA 3480
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

TA repeat polymorphism

(first entry)

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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                      Inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 19; 60pp; English.
                                                                                                                                                                             09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                       08-APR-2002; 2002IN-CH000260
                                   ISSR-related PCR primer 4.
                                                                         animal; Basmati rice; ss
                                                                                                                                                                                                                                                                                  WPI; 2003-804317/75.
                                                                                                                             WO2003085133-A2.
                                                                                                                                                                                                                                                                                                                                       animal systems
                                                                                                                                                                                                                                 (DNAF-) CENT
          15-JAN-2004
                                                                                                     Inidentified.
                                                                                                                                                       16-0CT-2003.
                                                                                                                                                                                                                                                           Nagaraju JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTIA1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful in optimising drug desages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
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                                                                                                                                                                                                                                     Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
                                          Gaps
                                                                                                                                                                                                                                                            Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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Pred. No. 8.2e+02;
                   Length 19;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                 Score 17.4; DB 1;
Pred. No. 8.2e+02;
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 3; 13pp; English.
                                                                     2827 TATACATATATATAAA 2845
                                                                                       Ratain MJ;
                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00251274.
                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2002; 2002US-00061693
                                                                                                                                                                 AAL50681 standard; DNA; 19
                                                                                                                                                                                                                   (first entry)
                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rienzo AD, Iyer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-740095/80.
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              US2002115097-A1.
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-1999;
                                                                                                                                                                                                                  16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2002
                                                                                                                                                                                           AAL50681;
                                                                                                                                         613
                                   Best Loc
Matches
                                                                                                                                                       AAL50681
                                                                                                                                                                  원
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DNA FINGERPRINTING & DIAGNOSTICS

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double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vasculation; ancient acid; siNA; downregulation; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antidrathritic; antipsoriatic; emphrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma;
                                                                                                                                                                                                                                                          ö
The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1676.
                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                / Match 0.5%; Score 17.4; DB 1; Length 19; Local Similarity 94.7%; Pred. No. 8.2e+02; local 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                          Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          2318 TGTGTGTGTGTGTGCGT 2336
                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF37387 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003070910-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF37387;
                                                                                                                                                                                                                               Query Match
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Gaps

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Indels

0; Mismatches

3462 TTATATATATCTATATA 3480

Conservative

Best Loca Matches

g ઠ

ADD69517 standard; DNA; 19

RESULT 614

ADD69517;

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WPI; 2003-679876/64.
                                                                                                                                           WO2003070910-A2
                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                 20-FEB-2002;
                                                                                                                                                                                                                                                                                                     06-JUN-2002;
                                                                                                                                                                                                                                                                                     29-MAY-2002;
                                                                                                                                                                              28-AUG-2003
                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF37400
ID ADF3
XX
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid (siMa) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a siNA that downregulates the VEGF gene; (2) kits for in vitro or or in vitro or in vit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded short interfering nucleic acid;
short interfering nucleic acid; siNA; downregulation;
vascular endothelial growth factor receptor; VEGFR; antianglogenic;
cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a double-stranded short interfering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human VEGFR1 short interfering nucleic acid (siNA) SEQ ID NO:389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 17.4; DB 1; Length 19; 14.2%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 7 A; 6 C; 4 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 1676; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                            Mcswiggen J, Beigelman L, Pavco P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1609 AAGTGCATCCACAGGGACC 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGUGCAUCCACAGAGACC 19
                                                                                                                       06-JUN-2002; 2002US-0386782P.
03-JUL-2002; 2002US-0393796P.
29-JUL-2002; 2002US-0399348P.
                                                                                                                                                                           29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
                                                                                                                                                                                                                                 04-NOV-2002; 2002US-002B7949
                                                                                                                                                                                                                                                                      15-JAN-2003; 2003US-0440129P.
                                   20-FEB-2003; 2003WO-US005022
                                                                                                        2002WO-US017674
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                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor receptor gene.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-679876/64.
                                                                                                        29-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2004
28-AUG-2003
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ID ADF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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The present invention describes a woulde-scribed wascular endothelial growth factor receptor (VBGFR) gene. Also described: (1) a single that downregulates the VBGFR) gene. Also described: (1) a single that downregulates the VBGF gene; (2) kits for in vitro or in vitro of single. Single-stranded single so is NA; (4) vectors that express single, and (5) single-stranded single so is NA; (4) vectors that express single, and is single-stranded single properties. The single hard properties. The single range of antidiabetic, nephrotropic and synacological, antiarthritic, antipsoriatic, nephrotropic and synacological, antiarthritic, antipsoriatic, nephrotropic and synacological, antiarthritic, antipsoriatic, nephrotropic and constitutes. The single are set in the single are potentially useful for treating a wide range of angiogenesis-associated conditions, useful for treating a wide range of angiogenesis-associated conditions, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiotibroma, and polycystic kidney disease. The sing may also be useful for diagnosis, and polycystic kidney disease. The sing may also be useful for diagnosis, chingle-nucleotide polymorphisms). The present sequence is used in the single-nucleotide polymorphisms). The present sequence is used in the exemplification of the present invention.
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nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New double-stranded interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates the vascular endothelial growth factor receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 9 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; SEQ ID NO 389; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen J, Beigelman L, Pavco P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGCGT 2336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2002; 2002US-0406784P-
05-SEP-2002; 2002US-0408378P-
09-SEP-2002; 2002US-0408378P-
04-NOV-2002; 2002US-0287949:
27-NOV-2002; 2002US-00306747.
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2002US-0393796P.
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Best Local Similarity 47.4%;
Matches 9; Conservative
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ADF37400;

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factor receptor gene.
                                                                                            WPI; 2003-679876/64.
                                        WO2003070910-A2.
                                    Homo sapiens.
                                                                      05-SEP-2002;
                                                                        09-SEP-2002;
                                                                            27-NOV-2002;
15-JAN-2003;
                                                                                        Mcswiggen J,
                                                        11-MAR-2002;
    12-FEB-2004
                                             28-AUG-2003
                                  Synthetic
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double-stranded short interfering nucleic acid; short interfering nucleic acid; short interfering nucleic acid; slNA; downregulation; swearlar endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; opthelmological; antiatchritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; abbetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
                                                                                                                                                                                                                                                                              Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1923.
1843 CTGGGGGCTCCCCGTACC 1861
                        1 CUGGGGGCCUCCCCGUACC 19
                                                                                                                                                   ВЪ
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2002WO-US017674.
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2002US-00287949.
2002US-00306747.
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2002US-0393796P.
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                                                                                                                                                   ADF37634 standard; RNA; 19
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                                                                                                                                                                                                                                    (first entry)
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29-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                           ADF37634;
                                                                                                         RESULT 618
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                                                                                                    double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopsthy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (downregulating) the expression of VEGFR genes. The siNh are potentially useful for treating a wide range of angiogenesis-associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthitis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The siNh may also be useful for diagnosis, dung screening, target identification and validation, genetic engineering, studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid (sink) that downregulates expression of the vascular endothelial growth factor receptor (WEGFR) gene. Also described: (1) a sink that downregulates the VEGF gene; (2) kits for in vitro or in vivo delivery of siNk; (3) conjugates and/or complexes of siNk; (4) vectors that express siNk; and (5) single-stranded siNk with similar properties. The siNks have antianglogenic, cytostatic, antidiabetic, ophthalmological, antiarbritic, antigeoriatic, nephrotropic and gynaecological activities. The siNk are useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes a double-stranded short interfering
                                                              Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 1 A; 9 C; 6 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 1689; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention.
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06-JUN-2002; 2002US-0386782P.
03-JUL-2002; 2002US-0393796P.
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                      (first entry)
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Best Local Similarity 78.9
Matches 15; Conservative
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The present invention describes a double-stranded short interfering nucleic acid (siNh) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a sink that downregulates the VEGF gene; (2) kits for in vitro or in vivo delivery of siNh; (3) conjugates and/or complexes of siNh; (4) vectors that express siNh; and (5) single-stranded siNh with similar properties. The siNhs have antiangiogenic, cytostatic, nephrotropic and opphrandlogical, antiarthritic, antipsoriatic, nephrotropic and gynaecological activities. The siNh are useful for modulating (downregulating) the expression of VEGFR genes. The siNh are potentially useful for treating a wide range of angiogenesis-associated conditions, necticularly cancers, alabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The siNh may also be useful for diagnosis,
                                                                                                                                                                                                                                    New double-stranded interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 1923; 207pp; English.
Mcswiggen J, Beigelman L, Pavco P;
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Homo sapiens.
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ADF36527/c
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                                                                                                                                                                                                                                                                            double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; abbetic retinopsthy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a double-stranded short interfering nucleic acid (siNA) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
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             (e.g. c
in the
                                                                                              Gaps
                                                                                                                                                                                                                                                         Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1936.
drug screening, target identification and validation, genetic engineering, studying gene function, and also for gene mapping single-nucleotide polymorphisms). The present sequence is used
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                                                                        0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02; tive 0; Mismatches 1; Indels
                                                   Sequence 19 BP; 2 A; 4 C; 6 G; 0 T; 7 U; 0 Other;
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                                 the present invention.
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03-JUL-2002; 2002US-0393796P.
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05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
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2002US-0363124P.
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2002US-00306747
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                                                                                   Local Similarity 94.7
nes 18; Conservative
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                                  exemplification of
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27-NOV-2002;
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                                                                         Query Match
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Matches
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ADF37647/
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delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors that express siNA; and (5) single-stranded siNA with similar properties. The siNAs have antianglogenic, cytostatic, antidiabetic, antiabetic, opphthalmological, antiathritic, antipsoriatic, nephrotropic and gynaecological activities. The siNA are useful for modulating (downregulating) the expression of VEGFR genes. The siNA are potentially useful for treating a wide range of angiogenesis-associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The siNA may also be useful for diagnosis, drug screening, target identification and validation, genetic engineering, studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the
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2002US-0408378P.
2002US-0409293P.
2002US-00287949.
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15-JAN-2003; 2003US-0440129P
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Best Local Similarity 94.7
Matches 18; Conservative
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The structure describes a contract structure of the vascular endothelial growth factor receptor (VBGFR) gene. Also described: (1) a sink that downregulates the VEGF gene; (2) kits for in vitro or in vitro and gradectic, antipaporiatic, nephrotropic and gradecological activities. The sinh are useful for modulating of downregulating) the expression of VEGFR genes. The sinh are potentially cuseful for treating a wide range of angiogenesis-associated conditions, particularly cancoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The sinh may also be useful for diagnosis, drug screening, target identification and validation, genetic or engineering, studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the
double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                 present invention describes a double-stranded short interfering
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                                                                                                                                               Example 3; SEQ ID NO 816; 207pp; English.
                                                                             factor receptor gene.
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. 0 Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 2318 TGTGTGTGTGTGTGCGT 2336 rererererererer 0.5%; Query Match
Best Local Similarity 94.7
Matches 18; Conservative 19 셤 à

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Gaps

BP

ACC79668 standard; DNA; 19 27-AUG-2003 (first entry) ACC79668; RESULT

Human, fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; mutagenesis; primer; ss. Human fibroblast growth factor 3 mutagenesis primer SEQ ID NO:3.

sapiens Homo sapier Synthetic.

JP2002272474-A.

24-SEP-2002.

22-MAR-2001; 2001JP-00083352.

22-MAR-2001; 2001JP-00083352

(ZERI) ZERIA SHINYAKU KOGYO KK

WPI; 2003-345602/33

Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.

Example; Page 8; 18pp; Japanese.

The present invention describes a method for the inspection of flat epithelial cells in which it is judged that flat epithelial cells separated from an organism can proceed to flat epithelial cancer when the

2128th base in fibroblast growth factor receptor (FGFR) gene of the cells is mutated from guanine to thywine. Also described is a method for screening treating or preventive agents for flat epithelial cancers in which a candidate substance of treating agent for flat epithelial cancer is applied to flat epithelial cancer cells producing FGFR protein in which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from guanine to thymine or the 697th amino acid is mutated from guanine to thymine or the 697th amino acid is selected by using the facts that the 2128th base in the flat epithelial cell FGFR3 gene after the application returned to guanine and that the 697th amino acid of FGFR3 protein produced returned to glycine as the indices. The method is used for the inspection of flat epithelial cells. The present sequence represents a mutagenesis primer for human FGFR3, which is used in an example from the present invention . 0 useful e.g. for treatment and down regulates expression of at least The present invention relates to a short interfering nucleic acid (siNA) that down regulates expression of at least one cyclin gene by RNA interference, siNA are used to modulate expression of cyclin genes, in. short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic; cancer; cell-proliferation disorder; restenosis; drug screening; genetic engineering; pharmacogenomics; gene mapping; single nucleotide polymorphisms; ss. Gaps ö Lower strand of cyclin D1 targeted double stranded siNA #145. 0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02; Live 0; Mismatches 1; Indels Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other; Example 3; SEQ ID NO 384; 144pp; English Thompson J, Mcswiggen J, Beigelman L; New short interfering nucleic acid, diagnosis of cancer and restenosis, 1855 CCGTACCCCGGCATCCCTG 1873 1 CCGTACCCCTGCATCCCTG 19 2002US-0406784P. 2002US-0408378P. 2002US-0409293P. ADN34364 standard; RNA; 19 BP 2002US-0363124P. 2002US-0386782P. 17-SEP-2002; 2002US-0411275P. 15-JAN-2003; 2003US-0440129P. 06-FEB-2003; 2003WO-US003662 (RIBO-) RIBOZYME PHARM INC. 01-JUL-2004 (first entry) Matches 18; Conservative WPI; 2003-689983/65. Best Local Similarity one cyclin gene. WO2003072705-A2. 20-FEB-2002; 11-MAR-2002; 06-JUN-2002;)5-SEP-2002; 09-SEP-2002; Homo sapiens. 29-AUG-2002; 04-SEP-2003 ADN34364; Query Match RESULT 622 ADN34364 889999999999988 ð

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

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cells, tissue explants or organisms, e.g. for treating a wide range of cancers and other cell-proliferation disorders such as restenosis, but also for drug screening, diagnosis, target identification and validation; genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents the lower strand of cyclin D1 targeted double stranded siNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a short interfering nucleic acid (siNA) that down regulates expression of at least one cyclin gene by RNA interference. SINA are used to modulate expression of cyclin genes, in cells, tissue explants or organisms, e.g. for treating a wide range of cancers and other cell-proliferation disorders such as restenosis, but also for drug screening, diagnosis, target identification and validation; genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents the upper strand of cyclin D1 targeted double stranded siNA which is identical to the cyclin D1 transcript target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic; cancer; cell-proliferation disorder; restenosis; drug screening; genetic engineering; pharmacogenomics; gene mapping; genetic engineering; pharmacogenomics; gene mapping; single nucleotide polymorphisms; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Upper strand of cyclin D1 targeted double stranded siNA #145.
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06-JUN-2002; 2002US-0366782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; leprosy; infectious disease; viral infection; type IV hypersensitivity; leprosy; infectious disease; viral infection; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 human; T-cell associated disease; Vbeta; autoimmune disease;
Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02;
                                         Indels
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 836; 164pp; English.
                                                                                                                                                                                                                                                                                                                                          Human Vbeta gene repeat sequence #432.
                                                                                2318 TGTGTGTGTGTGTGCGT 2336
                                                                                                                   rerererererererer
                                                                                                                                                                                                                      ADH70642 standard; DNA; 19 BP
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95US-00531241.
    0.5%;
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                                                                                                                                                                                                                                                                                                   25-MAR-2004 (first entry)
  Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-059052/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hood LE, Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast cancer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002150891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1999;
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                                                                                                                       13
                                                                                                                                                                                                                                                            ADH70642;
                                                                                                                                                                                 RESULT 624
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vivlemore401-10.rng

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This invention describes novel methods of producing double stranded nucleic acid molecules with a preselected value for a free energy parameter (e.g. a preselected T m or a preselected affinity for a nucleic acid binding ligand). The method involves preparing a first double card comprising a binding site for a nucleic acid.

List double stranded nucleic acid has a preselected relationship with a first reference value of a first free energy parameter for a reference double-stranded nucleic acid comprising a reference binding site for the light reference value of a first free energy parameter for a reference coupled in the first free energy parameter is a characteristic of the binding of a ligher than, equal to or lower than (sic). The method comprises: (a) determining a test value for a test double stranded nucleic acid, comprising a test value for a test double stranded concleic acid, comprising a test binding site for the ligand, of a second free energy parameter that is characteristic of the hybridization of the two complementary strands of double stranded nucleic acid, (b) comparing the first value to a reference value) of the cecond free energy parameter for the reference value) of the acid, and (c) if the test value and the second reference value of the
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucing double stranded nucleic acid molecules with preselected values free energy parameters such as affinity for nucleic acid binding
fungal infections such as those caused by
             the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             ö
                                                                                                                                                                     0.5%; Score 17.4; DB 1; Length 19; ilarity 94.7%; Pred. No. 8.2e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                 Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single stranded nucleic acid molecule (AT)4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Free energy parameter; thermodynamics; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 71-72; 49pp; Énglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lane MJ;
                                                                                                                                                                                                                                                  2823 TATATACATATATAT 2841
                                                                                                                                                                                                                                                                      caused by viruses such as HIV,
                                                                                                                                                                                                                                                                                                                                                                                    BP
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94US-00224840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    AAZ88880 standard; DNA;
                                                                                                                                                                                         Local Similarity
les 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-194826/17
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08-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ88880;
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This invention describes novel methods of producing double stranded nucleic acid molecules with a preselected value for a free energy parameter (e.g. a preselected T m or a preselected affinity for a nucleic parameter led, a preselected T m or a preselected affinity for a nucleic serial binding ligand). The method involves preparing a first double stranded nucleic acid comprising a binding site for a nucleic acid first double stranded nucleic acid has a preselected relationship with a first reference value of a first free energy parameter for a reference consultable stranded nucleic acid comprising a reference binding site for the ligand. The first free energy parameter is a characteristic of the binding of a ligand of interest to its binding site and the preselected comprishonship is higher than, equal to or lower than (sic). The method comprises: (a) determining a test value for a test double stranded nucleic acid, comprisens the binding site for the ligand, of a second
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second free energy parameter exhibit a test relationship that is the same as the preselected relationship, then preparing a first double stranded nucleic acid comprising all or part of the test nucleic acid, but if the test relationship is different than the preselected relationship, repeating step (a) and (b) on one or more additional test double stranded nucleic acids until an additional test double stranded nucleic acid is identified in which the test relationship is the asme as the preselected relationship, and then preparing a first double stranded nucleic acid comprising all or part of the additional test nucleic acid. AA288875-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing double stranded nucleic acid molecules with preselected values for free energy parameters such as affinity for nucleic acid binding
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                                                                                                                                                                                                                                                                                 0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02;
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                                                                                                                                                                                                                                           Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single stranded nucleic acid molecule (AT)4.
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                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lane MJ;
                                                                                                                                                                                                                                                                                                                                                            3463 TATATATATCTATATAT 3481
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94US-00224840.
94US-00260200.
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Matches 18; Conservative
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                                                                                                                                                                                                          method of the invention
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08-APR-1994;
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vivlemore401-10.rng

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free energy parameter that is characteristic of the hybridization of the two complementary strands of double stranded nucleic acid; (b) comparing the first value to a reference value (second reference value) of the second free energy parameter for the reference double stranded nucleic acid; and (c) if the test value and the second reference value of the second free energy parameter exhibit a test relationship that is the same as the preselected relationship, then preparing a first double stranded nucleic acid comprising all or part of the test nucleic acid, but if the rest relationship is different than the preselected relationship.

The reparting step (a) and (b) on one or more additional test double stranded nucleic acid is identified in which the test relationship is the same as the preselected relationship, and then preparing a first double stranded nucleic acid is identified in which the part relationship is the same as the preselected relationship, and then preparing a first double stranded nucleic acid comprising all or part of the additional test nucleic acid. AA288975-

Z88882 represent the single stranded DNA molecules used to illustrate the
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Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other;

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Gaps
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    Score 17.4; DB 1; Length 20;
Pred. No. 8.7e+02;
0; Mismatches 1; Indels
                                                  3463 TATATATATATATATAT 3481
                                                              TATATAGCTATATATAT 1
    0.5%;
Ouery Match
Best Local Similarity 94.7
Matches 18; Conservative
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AAF62964 standard; DNA; 20 BP
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RESULT 627
                                    AAP62964

IID AAP6

AAC AAP6

XXX AAP6

XXX AAP6

XXX AQ00

XXX MUSI

XXX MU
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Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113342.

Mouse; antiinflammatory; cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; phosphorothioate; ss.

Mus musculus

US6187545-B1

13-FEB-2001.

21-JAN-2000; 2000US-00488671.

21-JAN-2000; 2000US-00488671.

(ISIS-) ISIS PHARM INC

Cowsert LM; Mckay R, Butler MM, Wyatt J, WPI; 2001-190979/19. Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation.

Example 17; Col 44; 64pp; English.

30 nucleobases in length that are capable of inhibiting the expression of phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in calls or tissues. They are commonly used as research reagents and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or The present sequence is one of a number of antisense compounds of up to

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The invention relates to a map of the bread wheat D genome comprising the genome location of a microsatellite marker selected from a group of 185 genome location of a microsatellite marker selected from a group of 185 genome location of MARQ92733-ARQ92737). The invention also encompasses the use of left (ARQ92181-ARQ93103) and right (ARQ93103-ARQ93287) primers to amplify and detect the microsatellite markers, and to identify genes responsible for a phenotypic trait of interest and to identify genes a location and allohexaploid species consisting of 3 diploid genomes designated A, B and allohexaploid species consisting of 3 diploid genomes designated A, B and D, resulting from two successive intercrossings involving at least three different species. The D genome is thought to have been introduced in the most recent intercrossing, between the amphipioid AABB and Triticum to both species. Due to its polypioid genome, the large size of its genome, and its low level of polymorphism, the genetic mapping of wheat has to date been difficult. Microsatellites are tandemly repeated sequences the mainly due to polymerase slippage during replication. This high degree of polymorphism makes them especially suitable for the genetic mapping of polymorphism makes them especially suitable for the genetic mapping of
                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Map of wheat D genome comprising the genome location of a microsatellite marker, useful for e.g. identifying genes responsible for a desired phenotypic trait, especially quantitative trait loci in wheat, and
delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
                                                                                                                                                                  Gaps

    T. tauschii/wheat D genome microsatellite cfd67 right PCR primer.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite marker; wheat; D genome; mapping; genotyping; polymorphism; phenotypic trait; OTL; quantitative trait locus; disease-associated gene; development factor; quality factor; resistance factor; wheat product; identification; detection; genetically modified wheat; PCR; primer; ss.
                                                                                                                        Score 17.4; DB 1; Length 20;
Pred. No. 8.7e+02;
                                                                                                                                                                  1; Indels
                                                                            Sequence 20 BP; 2 A; 0 C; 10 G; 8 T; 0 U; 0 Other;
                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                            2325 GTGTGTGTGTGTGTG 2343
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                                                                                                                      0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                            Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003 (revised)
21-OCT-2002 (first en
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                                         deoxy gap
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                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                 RESULT
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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

CW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

CW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

CW adrenergic receptor nuclear translocator; ARNY; cathepsin S; CTSS;

CW aryl hydrocarbon receptor nuclear translocator; ARNY; cathepsin S; CTSS;

CW cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

CW cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

CW cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

CW diltathione-S-transferase 2; GST12; histamine-N-methyl transferase;

CW DP-Glucuronosyl transferase 28; UDP-Glucuronosyl transferase 28; UPC-Glucuronosyl transferase;

CW DP-Glucuronosyl transferase; UGT2B15; urokinase receptor;

CW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

CW multidrug resistance associated protein 3; cancer; prostate;

CHNR1; CHNR2; CHNR3;

Altered drug metabolism; cardiovascular function; colorectal tumour;

CM CHNR3; CHNR3; CHNR3; CHNR3; CHNR5;

CM CHNR3; CHNR3; CHNR3; CHNR3; CHNR5;

CM CHNR3; C
species which show little intraspecies polymorphism, such as wheat. In addition, microsatellites are codominant, and exhibit Mendelian.

Inheritance. The 185 microsatellite markers of the invention are developed from the ancestral diploid donor species Triticum tauschii and map to the wheat D genome, which is less polymorphic than the A or B genomes. These microsatellite markers thus help to overcome some of the problems associated with the genetic mapping of wheat. The wheat D genome invention are useful for identifying genes responsible for a phenotypic trait of interest, most notably OTLs (quantitative trait loci). In particular they may be used for analysing genes and alleles implicated in glesses and for identifying development factors, quality factors and factors conferring resistance to pathogens and xenobiotics. The microsatellite markers and associated primers may be used in microsatellite markers and associated primers may be also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping and genotyping diploid and polyploid species of Triticum, particularly Aegilops, Triticum monococcum, Triticum durum, Triticum essetivum, or related species; for identifying cultivars and hybrids of Triticum and related species; to assess whether or not a product comprises wheat or a related species; and to assess whether or not a product comprises genetically modified wheat. The present sequence represents a specifically claimed Triticum tauschii/wheat genome D microsatellite marker right per primer of the invention. (Updated on 29-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.4; DB 1; Length 20; Pred. No. 8.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Gaps ; 0

1; Indels

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This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
molecule comprising at least one base variation from that of a known
the conforme P450 Al (CYP4501A1), Gyrochrome P450 A2 (CYP4501A2),
cytochrome P450 O2E1 (CYP4501DE1), adrenergic receptor betal (ADBR1),
aryl hydrocarbon (AHR), aryl bydrocarbon receptor nuclear translocator
(ARNT), cathepsin S (CTSS), cyclooxgenaes 2 (COX2), diazepam binding
inhibitor (DB1), epoxide hydroxylase 2 (EMX2), blipoxygenase activating
protein (ELAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
transferase (HNWT), NADPH quinone oxidoreductase 2 (NQO2)
transferase (HNWT), NADPH quinone oxidoreductase 2 (NQO2)
cransferase (HNWT), nathermolabile (STM), UDP-glucuronosyl transferase 2B1 (HGT2B7), UDP-glucuronosyl transferase 2B2 (HGT2B7), UDP-glucuronosyl
transferase (HTMT), actotransferrin (LTF), multidrug resistance associated protein 3
(MRR1), lactotransferrin (LTF), craceptor (LPRA2) (HRR4 or CHRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR4 or CHRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR4 or CHRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR4 or CHRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR5) (HRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR5) (HRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR5) (HRR5) sequence
creeptor 1, 2, 3, 4, or 5 (CHRM1, CHRR2) (HRR8) (HR
                                                                                                                                     Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uscaptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 8.7e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 10 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                          Example 16; Page 131; 714pp; English.
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Best Local Similarity 94.7
Matches 18; Conservative
(DNAS-) DNA SCI LAB INC.
                                                                                                WPI; 2002-698522/75.
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human disease. The

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existing in human genes and for the diagnosis of present DNA sequence represents a human gene PCR
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                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                            The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPB). The DNA sequences of the invention are useful for detecting SNPB existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                            Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; gene sequence; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                          Claim 2; SEQ ID NO 1015; 529pp; Japanese
                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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disease diagnosis; ss; PCR; primer
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                                                                              11-DEC-2001; 2001JP-00377637
                                                                                                  11-DEC-2001; 2001JP-00377637
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                          WPI; 2003-819215/77
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                                       JP2003174883-A.
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                    Homo sapiens
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primer of the invention.
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                   Query Match
0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
                                                                       Sequence 20 BP; 2 A; 4 C; 7 G; 7 T; 0 U; 0 Other
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/note= "2'-0-methocyethyls"
16. .20
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/note= "2'-O-methoxyethyls"
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transperson because a control and an entransperson of the compounds, the forest to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to human mPGES-1 genes compounds, gas-1.

Comparison as sequence compurising 8-10 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal comparison associated with mPGES-1. MPGES-1 and antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound to can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or condition, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
sequence represents a chimeric antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:959.
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                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 11 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
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/note= "2'-O-methoxyethyls"
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modified_base
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Synthetic.
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ADM14772/c
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the present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGBS-1). The targeted to human microsomal prostaglandin E2 synthase (mPGBS-1). The human mPGBS-1 gene is located on chromosome 9, more specifically to gastan invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGBS-1, which specifically hybridise with the nucleic acid encoding mPGBS-1, which specifically hybridise with the nucleic acid encoding mPGBS-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGBS-1. MPGBS-1 chimeric antidabetic, immunomodulator, cardiant, neuroprotective, antidiametory, neuroprotective, antidiametory, neuroprotective, antidiametory, neuroprotective, antidiametory, neuroprotective, antidiametory, neuroprotective, antidiametory, neuroprotective, antiditors and cardiavascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGBS-1 entracting a disease or condition associated with mPGBS-1 entraction or can be used for preparation or can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                          New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 9 A; 8 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse B7H antisense oligonucleotide ISIS 231397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B7H; autoimmune disease; ss; antisense; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 959; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2332 TGCGTGTGTGTGTGTGT 2350
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                                   25-SEP-2002; 2002US-0413549P.
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ID ADN58895 standard; DNA; 20
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                          (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobie KW;
                                                                                                                                                                                                                                                                                                WPI; 2004-305094/28
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                                                                                                                                                                                                                Gierse JK;
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The present invention relates to measuring the copy number of a locus by amplifying and comparing test and reference loci. The invention is useful as diagnostic and prognostic tools and in correlating abnormal copy number values for specific loci with disease and effectiveness of different treatment options. The present sequence is a CA repeat fluorogenic probe used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Measuring copy number of a polynucleotide locus in sample useful as diagnostic and prognostic tool, comprises quantifying amount of test locus and reference loci in test and control subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end attached to 6-carboxy fluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.4; DB 1; Length 21;
14.7%; Pred. No. 9.2e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        Probe; Fluorescein; tetramethyl rhodamine; copy number; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "3' end attached to TAMRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray JW;
  0; Mismatches
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                                       CTGGTGACCGAGGACAACG 1663
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                  CA repeat fluorogenic probe.
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                                                                                                                                                                             AAF85976 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "5'
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                                                                                                                                                                                                                                                             (first entry)
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    Conservative
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les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginzinger DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                         modified base
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                                                                                                                                                                                                                                                           20-JUN-2001
  18;
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                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                         1645
                                                                                                                                                                                                                      AAF85976;
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ID AAH49075
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                                                                                                                                          RESULT 636
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Matches
    Matches
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                                                                                                                                                      The invention relates to a compound targeted to a nucleic acid molecule encoding B7H, where the compound specifically hybridises with the nucleic acid molecule encoding B7H and inhibits the expression of B7H. The compound is useful for modulating the expression of B7H. It is also useful for diagnosing or treating diseases associated with expression of B7H, e.g. an autoimmune disease. The present sequence represents a mouse B7H antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a compound targeted to a nucleic acid molecule encoding B7H, where the compound specifically hybridises with the nucleic acid molecule encoding B7H and inhibits the expression of B7H. The compound is useful for modulating the expression of B7H. It is also useful for diagnosing or treating diseases associated with expression of B7H, e.g. an autoimmune disease. The present sequence represents a mouse
                                   New compound targeted to a nucleic acid molecule encoding B7H and inhibits expression of B7H, useful for modulating the expression of B7H or for diagnosing or treating, e.g. autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compound targeted to a nucleic acid molecule encoding B7H and inhibits expression of B7H, useful for modulating the expression of B7H or for diagnosing or treating, e.g. autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02; ive 0; Mismatches 1; Indels
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Pred. No. 8.7e+02;
                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 16; SEQ ID NO 250; 97pp; English.
                                                                                                                     Example 16; SEQ ID NO 146; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse B7H target sequence ISIS 147955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1645 CTGGTGACCGAGGACAACG 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGACAGAGACAACG 1
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                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
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WPI; 2004-399728/37.
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Monia BP,

Query Match

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19-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (about 500 for testing for 21 specified disorders), so can be used for simultaneous testing for many diseases. Testing is quick, inexpensive. reliable and more sensitive than current physiological methods. AAH48868-AAH489166 represent oligonucleotides used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleotide support (A; gene chip) which carries a selection of oligonucleotides (I) that are identical, or complementary, to segments of reference sequences relevant to at least two genetically determined phenotypes. (A) are used for simultaneous diagnosis of at least two of the following diseases: phenylketonuria deficiency, syrup diseases, galactosemia, homocysteinuria, biotinidase deficiency, medium-chain acyl-CoA-dehydrogense deficiency, familial hypercholesterolemia, familial defective apolipoprotein-B, cystic fibrosis, Marfan syndrome, Smith-Lemil-Opitz syndrome and androgenital syndrome. Specifically they are used in neonatal or prenatal diagnosis.

(A) require a relatively small number of separate hybridization regions
                                                                             phenylketonuria; maple syrup disease; galactosemia; homocysteinuria; medium-chain acyl-CoA-dehydrogenase deficiency; blotinidase deficiency; familial hyperxholesterolemia; familial defective apolipoprotein-B; cystic fibrosis; Marfan syndrome; Smith-Lemil-Opitz syndrome; androgenital syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                          DNA chip, useful for neonatal or prenatal screening for many genetic diseases simultaneously, carries oligonucleotides complementary to phenotypically relevant reference sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                       Neonate screening; prenatal screening; gene chip; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 1; Length 21;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 6 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arteriosclerosis-detecting probe from LDLR #42.
                                               gene associated primer #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3667 GCCATGGCTCAGGGTGGTC 3685
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 63; 101pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sccarrecreassarcas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%;
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                                                                                                                                                                                                                                                      21-JAN-2000; 2000DE-01002446
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                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                 Cullen P, Seedorf U;
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457616/49.
                                                                                                                                                                                                                                                                                       SEEDORF U.
                                                                                                                                                                                                                                                                            (CULL/) CULLEN P.
                                                                                                                                                                                WO200153520-A2
                                                                                                                                                           Homo sapiens
                         12-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2003
                                                                                                                                                                                                       26-JUL-2001.
                                                  Human LDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvention
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  AAH49075;
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This invention describes a novel method for determining the genetic risk of arteriosclerosis both for clinical diagnosis and for population studies. The method comprises: (i) selecting risk-associated reference contents and sequences, including their functionally characterizing mutations, (ii) applying probes from these sequences, or their complements, to a carrier; (iii) hybridising the probes with a nucleic acid from (or synthesised from) a patient sample, and (iv) detecting and evaluating the hybridisation pattern. The method provides a quick, inexpensive and informative diagnosis, and makes possible a contaction that when present alone carry no risk but are risk mutations or mutations that when present alone carry no risk but are risk associated in presence of other mutations. The results may be combined with known risk-assessment methods to provide a more reliable diagnosis, contaction and present methods (e.g. gene therapy) that are directed against specific genes. All relevant mutations in a contaction a single test and the method is well suited to automation. ABX09147-ABX09676 represent probes used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; cytochrome P450 Al; CYP4501Al; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF; adrenergic receptor betal; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112; aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydroxylaee 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining genetic risk of arteriosclerosis, for clinical diagnosis, comprises hybridizing patient nucleic acid with an array of probes derived from risk-associated reference genes and their mutations.
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Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy; mutation; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human acetyl choline muscarinic receptor 3 polymorphic sequence #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 6 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 128; 146pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3667 GCCATGCTCAGGGTGGTC 3685
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                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2002; 2002WO-EP002780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001; 2001DE-01011925.
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Best Local Similarity 94.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-723374/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OGHA-) OGHAM GMBH
                                                                                                                                                                                                                             WO200272882-A2
                                                                                                                                                   Homo sapiens.
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HNWT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNWT; MADPH quinone oxidoreductase 2; NQO2; sulfotrandsferase thermolabile; STM; UDP-glucurcnosyl transferase 2B4; UDP-glucurcnosyl transferase 2B7; UGT2B7; UDP-glucurcnosyl transferase; UGT2B1; UPP-glucurcnosyl transferase; UGT2B15; urokinase receptor; UPA; multidrug resistance 1; lattoriansferrin; orphan nuclear receptor; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR3; CHWR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism.

Homo sapiens.

WO200257410-A2

25-JUL-2002.

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Hall J; Guida M, WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 28; Page 159; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cortochrome P450 Al (CYP4501A1), cytochrome P450 Al (CYP4501A1), aryl bydrocarbon receptor nuclear translocator cytochrome P450 02E1 (CYP4501A1), aryl bydrocarbon receptor nuclear translocator (ARNY), cathepain S (CYSS), cyclooxgenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPHX2) 5-11poxygenase activating cytochrome P450 02E1 (ARNY), Lather and the control of transferase (HNWT), MADIPH quinnen oxidoreductase 2 (NQC2), histochrome P450 CC (UGT2B1), utokinase receptor (MPA), unperguence oxidoreductase 2 (NQC2), utokinase receptor (MPA), upp-glucuronosyl transferase (UGT2B1), utokinase receptor (MPA), upp-glucuronosyl transferase (UGT2B1), utokinase receptor (MPA), orphan nuclear receptor (MPA), or securing the disorder for locating and characterising the genes that creeptor (MPA) and the invention are useful as green in an individual for a useful or treating the disorders. The nucleic acid molecules comprising the companies of their e.g., overexpression, which may be used in disgnosing metabolism. The polymorphic sequences contained in CYPH501A1, CYPH501A1, CYPH501A1, CYPH501A1, CYPH501A1, CYPH501A1, CAMP, MDR, and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYPH501A1, CYPH501A1, CAMP, MDR, and/or MDR3 are useful for screening individual for altered drug metabolism. The polymorphic sequences cont polymorphic DNA sequence of the invention

Sequence 21 BP; 9 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, and neoplastic disease. Avpersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases include multiple sclenosis and Alzheimer's disease. Hypersensitivity diseases include multiple sclenosis and Alzheimer's disease. Hypersensitivity diseases include multiple in hypersensitivities such as contact with allergens that lead to

allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by

Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a

WPI; 2004-059052/06

Rowen L;

Hood LE,

(HOOD/) HOOD L E. (ROWE/) ROWEN L.

94US-00309335. 95US-00531241. 99US-00263959

US2002150891-A1. Homo sapiens.

05-MAR-1999; 9-SEP-1994; 19-SEP-1995;

17-0CT-2002.

Disclosure; SEQ ID NO 753; 164pp; English.

Vbeta gene

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                                                                                                                                                                                                                                                          Alzheimer's disease; hypersensitivity disease; type I hypersensitivity, allergy; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                     Gaps
                                                                                                                                                                                                                 degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis;
                      ö
                                                                                                                                                                                                       human; T-cell associated disease; Vbeta; autoimmune disease;
 Length 21;
                     Indels
Score 17.4; DB 1;
Pred. No. 9.2e+02;
                      0; Mismatches
                                                                                                                                                                                  Human Vbeta gene repeat sequence #349.
                                         2823 TATATATACATATATAT 2841
                                                              19 TATATACACATATAT 1
                                                                                                                   ВР
 0.5%;
                                                                                                                   ADH70559 standard; DNA; 22
                                                                                                                                                              (first entry)
 Query Match 0.5%
Best Local Similarity 94.7%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                             oreast cancer; ds
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                                                                                                                                        ADH70559;
                                                                                                RESULT 640
                                                                                                         ADH70559,
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WPI; 2002-733635/80.
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                                                                                                                                                                                                  Mao Y, Xie Y;
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                                                                         Homo sapiens
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                                                                                                                 19-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer; ss.
                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primers AAX34328-X34331 were used to PCR amplify the gene encoding a human brain-specific tyrosine kinase (Byk; AAX34327). The coding DNA can be used in drug applications, especially to detect a nervous skin syndrome (sic) related antigen
the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used to detect
                                                                                                                                                                                                                                                                                Human; brain, tyrosine kinase; Byk; drug application; antigen; se;
nervous skin syndrome; PCR; primer; amplification.
                                                                                                                                                                                                                                                              Primer PTK3YK for human brain-specific tyrosine kinase (Byk) gene
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                                                                               0.5%; Score 17.4; DB 1; Length 22; 94.7%; Pred. No. 9.7e+02; tive 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 17.4; DB 1; Length 23; 65.2%; Pred. No. 1e+03; tive 4; Mismatches 4; Indels
                                                             Sequence 22 BP; 9 A; 0 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 4 A; 5 C; 5 G; 1 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene coding brain-specific tyrosine kinase - can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous skin syndrome related antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1618 CACAGGGACCTGGCTGCCCGCAA 1640
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                                                                                                                          2826 ATATACATATATATATA 2844
                                                                                                                                               22 ATATACATATACATATATA 4
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                                                                                                                                                                                                  AAX34331 standard; DNA; 23
                                                                                                                                                                                                                                           (first entry)
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                                                                                Query Match
Best Local Similarity 94.7'
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                               JP08256780-A.
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1995;
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                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                      AAX34331;
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AAL45613
ID AAL456:
XX
AC AAL456:
XX
DT 21-JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; zinc finger protein 234-72.38; tumour; cytostatic; diabetes; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide-human ATP dependent membrane conjugated zinc proteinase 10.45 and polynucleotide for encoding such polypeptide.
                                                                          Human, ATP dependent membrane conjugated zinc proteinase 10.45; enzyme; development disturbance; lipid metabolism disease; gene therapy; PCR;
ATP dependent membrane conjugated zinc proteinase 10-45 PCR primer #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 17 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2000; 2000CN-00116334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2000; 2000CN-00116334.
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Gaps

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nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a Tm value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept
                                                                                                          The present invention relates to human zinc finger protein 234-72.38 (see 89859122). The protein can be used for treating diseases such as tumours and diabetes. The present sequence is a PCR primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the concentration of a target nucleic acid, useful e.g. for detecting genetic mutations, comprises using a fluorescently labeled probe in which emission is reduced by binding to the target nucleic acid.
                   Polypeptide-human zinc finger protein 234-72.38 and polynucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamagata Y, Kurata S, Yamada K, Yokomaku T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the determination of the concentration of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Concentration, quantification, mutation detection, polymorphic, polymerase chain reaction, PCR; ss.
                                                                                                                                                                                                                                           Score 17.4; DB 1; Length 24; Pred. No. 1.1e+03;
                                                                                                                                                                                                        Sequence 24 BP; 10 A; 0 C; 4 G; 10 T; 0 U; 0 Other;
                                                                       Example 3; Page 17 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic deoxyribooligonucleotide poly g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NIBI-) JAPAN BIOINDUSTRY ASSOC.
(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
(KANK-) KANKYO ENG CO LTD.
                                                                                                                                                                                                                                                                                                                    3475 TATATATATATTATTGAGT 3493
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                                                                                                                                                                                                                                                                                                                                              3 TAGATATAATTTATTGAGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL56894 standard; DNA; 30 BP
                                                                                                                                                                                                                                         0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                               18; Conservative
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Furusho K;
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                                                                                                                                                                                                                                                            Local Similarity
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Koyama O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL56894;
                                                                                                                                                                                                                                            Query Match
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The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces cauced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no meterials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed, and amplification quantitation is reduced. Complex probes are not needed, and amplification can be monitored in real time. The working graph for data analysis (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribooligonucleotide that was used for investigating the base ö Determining the concentration of a target nucleic acid, useful e.g. for detecting genetic mutations, comprises using a fluorescently labeled probe in which emission is reduced by binding to the target nucleic acid. Yamada K, Yokomaku T; Gaps high (amplification of primer dimers is delayed), and the limit of Concentration; quantification; mutation detection; polymorphic; polymerase chain reaction; PCR; 88. ö 0.5%; Score 17.4; DB 1; Length 30; 77.8%; Pred. No. 1.3e+03; Indels Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other; Kamagata Y, Kurata S, 77.8%; Pred. no. Synthetic deoxyribooligonucleotide poly a. 3259 AGATATTTTATTTGCTTTGTCCTTTTT 3285 3 ATATATTTTTTTTTTTTTTTTTTTTT 29 (AGEN) AGENCY OF IND SCI & TECHNOLOGY. (KANK-) KANKYO ENG CO LTD. selectivity of a target nucleic acid Example 5; Page 21; 55pp; English (NIBI-) JAPAN BIOINDUSTRY ASSOC BP 20-APR-2000; 2000EP-00108643. 99JP-00111601 ABL56888 standard; DNA; 30 (first entry) Query Match 0.5 Best Local Similarity 77.8 Matches 21, Conservative Kanagawa T, Furusho K; WPI; 2000-657765/64. 20-APR-1999; 26-JUL-2002 EP1046717-A2 Synthetic. Kurane R, Koyama O, ABL56888; RESULT 645 ABL56888 8888888888888 8

(first entry)

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Measurement of nucleic acids, using a nucleic acid probe and analysis of
the obtained data.
                                                                                                                                                                                                                                                                                                ss; fluorochrome; nucleic acid probe; fluorescence.
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(KADK-) KADKYO ENG KK.
(KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
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ABA97618 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-1999; 99JP-00111601.
24-AUG-1999; 99JP-00236666.
30-AUG-1999; 99JP-00242693.
01-FEB-2000; 2000JP-00028896.
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                                                                                                                                                                                                                   Poly g nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2001286300-A
                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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   SO CCC CCC CCC XX B X B B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a method for measuring nucleic acids using a nucleic acid probe labelled with a fluorochrome. The nucleic acid probe decreases the fluorescence of the fluorochrome when hybridised with a target nucleic acid, the decrease in the fluorescence is measured. The method can be used for measuring a target nucleic acid
                   (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribooligonucleotide that was used for investigating the base selectivity of a target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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       monitored in real time. The working graph for data analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; fluorochrome; nucleic acid probe; fluorescence
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(KANK-) KANKYO ENG KK.
(KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN
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24-AUG-1999; 99JP-00236666.
30-AUG-1999; 99JP-00242693.
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Best Local Similarity 77.8'
Matches 21; Conservative
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99JP-00236666. 99JP-00242693.

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This invention relates to a method for measuring nucleic acids using a nucleic acid probe labelled with a fluorochrome. The nucleic acid probe decreases the fluorescence of the fluorochrome when hybridised with a target nucleic acid, the decrease in the fluorescence is measured. The method can be used for measuring a target nucleic acid
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                                                                                                          Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                       ATATATTTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe poly a for assaying nucleic acids
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3259 AGATATTTATTTGCTTTGTCCTTTTT 3285

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                                                                                                                                Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification.
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                                                                        Yamada K;
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                                                                        Kurata S,
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Pred. No. 1.3e+03;
0; Mismatches 6; Indels
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                                                                        Torimura M,
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                                   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY (KANK-) KANKYO ENG CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                          3259 AGATATTTATTTGCTTTGTCCTTTTT 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe poly g for assaying nucleic acids.
                                                                                                                                                                                                  Example 12; Page 60; 152pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kamagata Y,
                                                                       Kanagawa T, Kamagata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-2000; 2000JP-00193133.
03-AUG-2000; 2000JP-00236115.
26-SEP-2000; 2000JP-00292483.
                                                                                                                                                                                                                                                                                                                                                                                          0.5%;
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03-AUG-2000; 2000JP-00236115
26-SEP-2000; 2000JP-00292483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL95891 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
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                                                                                                           WPI; 2002-195876/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-195876/25.
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                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                    Yokomaku T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            굓,
                                                                        Kurane R,
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 649
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                                                                                                                                                        The present invention relates to nucleic acid probes, which are useful for assaying nucleic acids by hybridising with a target nucleic acid, in which a single-stranded oligonucleocide is labelled with a fluorescent substance and a quencher in a manner that the fluorescence intensity of the hybridisation reaction system is increased after completion of the hybridisation but no stem loop structure is formed. The probes are useful for assaying nucleic acids and their polymorphism and mutation, particularly useful for e.g. analytical applications, disease diagnosis and microbial identification. The present sequence was used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAQ62395-449 are primers which were used in the construction of the vector pVACI. This vector is based on the commercially available vector pRc/RSV. Leader sequences and termination signals were introduced into the vector to allow for production of fusion proteins. The vector, pSfi/Not.Tagl, was modified to replace the pelB leader with the human immunoglobulin VH1 leader sequence that permits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating immune response to a disease marker \cdot by administering a vector which expresses the disease marker to interact with the immune
Pluorescently-labeled nucleic acid probes for assaying nucleic acids their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector; pVAC1; pRc/RSV; leader sequence; termination signal; PCR; fusion protein; pSfi/Not.Tag1; pelB leader; human; immunoglobulin; single chain; Fv; murine antibody; retroviral; envelope; amplify; plasmid; vaccine; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 0.5%; Score 17.4; DB 1; Length 30; Local Similarity 77.8%; Pred. No. 1.38+03; les 21; Conservative 0; Mismatches 6: Tindala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3259 AGATATTTTATTTGCTTTGTCCTTTTT 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russell SJ, Stevenson FK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 12, Page 60; 152pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector pVAC1 construction primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 31; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ62397 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                     microbial identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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18-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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encoding of an Sfil cloning site without modification of the amino acid sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII fragment into NotI/Blunt- HindIII cut vector pRc/RSV to give pVACI. The single chain FV for an individual patient can be inserted within the VHI leader sequence. This plasmid when encoding a single chain murine antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a genetic marker for spider lamb syndrome, used to diagnose if sheep carry a gene for the syndrome, involves analyzing sheep DNA samples for mutations in fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' PCR-RFLP primer used to detect nucleotide transversion in FGFR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheep; spider lamb syndrome; SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; RFLP; restriction length polymorphism; chromosome 6; ss.
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                             0.5%; Score 17.2; DB 1; Length 22; 36.4%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                        Sequence 22 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                1e+03;
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                             853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                1 gaderecaecreerecaerere 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Col 23; 24pp; English.
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                                                                                                                                                                                                                                                86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                       19; Conservative
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                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD21616;
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                                                                                                                                                                                                                                                                       Matches
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The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
                                                                                                                                                                                                                        Solute carrier family 6 neurotransmiter transporter; sectonin 4; SLC6A4; genotyping; allele specific oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 9 gene for identifying drugs for treating disorders related to expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanchis A, Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.2; DB 1; Length 22;
Pred. No. 1e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; MLL; cancer; AF-4; CDK-6; SEPTIN6; ALL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 3 A; 8 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2395 TGCAGAGGTACCCTGGGTGTCC 2416
1852 TCCCCGTACCCCGGCATCCCTG 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 34; 152pp; English
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                            receeracersecarees 22
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                                                                                                     AAF74089 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000; 2000WO-US020638.
                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999; 99US-0146290P.
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-123317/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the protein.
                                                                                                                                                                                                                                                                                                   WO200109161-A1
                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                                                               Primer #23.
                                                                                                                                   AAF74089;
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                                                                        RESULT 652
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Gaps

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0.5%; Score 17.2; DB 1; Length 22; 86.4%; Pred. No. 1e+03; Live 0; Mismatches 3; Indels

Conservative

19;

Matches

Best Local Similarity

Query Match

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Alzheimer's disease; Parkinson's disease; graft-versus-host disease; scleroderma; hypertension; haemophilia; idiopathic thrombocytopenic purpura; immunodeficiency; AIDS; dispathic thrombocytopenic purpura; immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia; cancer-associated cachexia; multiple sclerosis; fertility; primer.
                                                                                                                                                        Human; NOVX; PCR; 88; cancer; atherosclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0340390P
2001US-0340440P
2001US-0340668P
2001US-0341144P
2001US-0341144P
2001US-034147P
2001US-034147P
2001US-0341460P
2001US-0341760P
2001US-0342592P
2001US-0342592P
2001US-0343286P
2002US-0353286P
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2001US-0338989P.
2001US-0339314P.
2001US-0339314P.
2001US-0339517P.
2001US-0339517P.
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2002US-0359914P.
2002US-0359956P.
2002US-0360924P.
2002US-0360964P.
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2002US-0361770P.
2002US-0362230P.
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                                                                15-JUL-2004 (first entry)
                                                                                                            Human NOVX PCR primer #69.
                                                                                                                                                                                                                                                                                                                                                       US2004058338-A1.
                                                                                                                                                                                                                                                                                                              Homo sapiens.
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05-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2004
                       ADO42630;
  The invention relates to amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence comprising providing a cancer-associated DNA sequence comprising providing a providing of template polymucleotide, ligating a loop-forming oligonucleotide to the 3'-end of the sense strand, annealing the loop-forming oligonucleotide to the pathandle structure, comprising the pathandle structure is subjecting the pathandle structure of a first primer homologous to the second portion, where the unknown region is amplified. In the method of comprising the known region that flanks a known region of a sancer-associated DNA sequence, the template polymucleotide comprises a sense strand, comprising the known and unknown regions. The unknown region is comprised a first or second portion. The first portion is nearer the unknown region than is the known region. The known complementary to the second portion. The first portion is nearer the unknown region for second portion is generated at the free end of the comprises ATFI (not defined) or BCR (B cell receptor). The method is useful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. The cancer-associated DNA sequence. Comprises ATFI (not defined) or BCR (B cell receptor). The method is useful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. Also disclosed as new is the use of the method in the analysis of the breakpoint region of the human MLL second on the associated with ALL and AML (acute lymphoblastic comprised acute mayorance is a poster on the pread on chromosome such as a sociated with ALL and AML (acute lymphoblastic comprised acute mayorance is a poster of the manalysis of the preakpoint region of the method is a concer-associated with ALL and AML (acute lymphoblastic concerts). The method is a concert associated with ALL and AML 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amplifying an unknown region that flanks a known region of a cancerassociated DNA sequence by subjecting the panhandle structure to extension and to PCR in the presence of a first primer homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11q23. The present sequence is a PCR primer used the method of the invention to isolate the unknown region adjacent to the BCR cancer gene.
acute lymphoblastic leukaemia, AML, acute myeloid leukaemia,
chromosomal break point, chromosome 11q23, ATF, BCR, B cell receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.2; DB 1; Length 22; 86.4%; Pred. No. 1e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 8 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 ACGTGGAGGTGAATGGCAGCAA 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATCGAGGTGAATGGGAGCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rappaport E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 42; 80pp; English.
                                                                                                                                                                                                                                                                                  97US-0056938P.
97US-0065911P.
98US-00026033.
                                                                                                                                                                                                                      09-APR-2002; 2002US-00118783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felix CA, Jones DH,
                                                                                                                                                                                                                                                                                                                                                                                            (JONE/) JONES D H. (RAPP/) RAPPAPORT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-606415/57.
                                                                                                                                                                                                                                                                                                                                                                          (FELI/) FELIX C A. (JONE/) JONES D H.
                                                                                                                              US2003096255-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          second portion
                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                19-FEB-1997;
                                         primer; PCR.
                                                                                                                                                                                                                                                                                    25-AUG-1997;
                                                                                                                                                                                                                                                                                                              17-NOV-1997;
                                                                                                                                                                                                                                                                                                                                19-FEB-1998;
                                                                                                                                                                          22-MAY-2003
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NAMES OF THE PROPERTY OF THE P

002US-0401315P 2002US-0401788P

37-AUG-2002;

ADO42630 standard; DNA; 22 BP

RESULT 654 ADO42630 ID ADO4

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Gaps

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(AGEE/)
(ALSO/)
(ANDE/)
(BERG/)
(BOLD/)
(BURG/)
(CATT/)

(ELLE/) (GANG/) (GERL/) (GORM/)

(EDIN/)

(ROTH/) (GUOX/) (HERR/)

(HALV/)

KHRA/)

KEKU/

LARO/

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The present invention describes a Trypanosoma brucei trypanosome suppressive immunomodulating factor (TSIF) protein. The present invention also describes: (1) the TSIF protein having the primary structural information of amino acids 1-553 of the 833-amino acid sequence of SEQ ID NO:2 (ADP74801) or its fragment or allelic variant having caquence of SEQ ID NO:2 (ADP74801) or its fragment or allelic variant having activity; (2) an isolated polymocleotide comprising a 2826 base pair sequence of SEQ ID NO:1 (ADP74800) which encodes the TSIF polypebtide; (3) a vector comprising the nucleic acid; (4) a genetically engineered host cell comprising the expression vector; and (5) preparing a diagnostic assay for detecting the presence of a Trypanozoon infection in a mammal. TSIF has immunosupressive activity, and can be used in gene therapy. The TSIF polypeptide or polynucleotide can be used in gene
             preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disease, soleroderma, hypertension, haemophilia, idiopathic thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used as hybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a PCR primer used in analysis of expression of a human NOVX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide derived from Trypanosomes, useful in preparing a medicament for suppressing the immune response in a mammal for treating autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma brucei; trypanosome suppressive immunomodulating factor; TSIF; immunomodulating activity; Trypanozoon infection; immunosuppressive; gene therapy; immune response; autoimmune disorder;
sequences are useful for diagnosing, treating or
                                                                                                                                                                                                                                                                                             Query Match

0.5%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                         Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                         637 CTCAAGCACGTGGAGGTGAATG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei TSIF PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 28; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2003; 2003WO-EP051082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-2002; 2002EP-00080667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beschin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP74810 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-500278/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei
                                                                                                                                                                                                                     of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Baetselier P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004056853-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP74810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human NOVX polypeptides and the polymucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polymucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo XS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P, Anderson DW, Berghs C, Boldog FL;

BA, Dipippo VA, Edinger SR, Eisen A;

EA, Gerlach V, Gorman L, Rothberg BG, G,

EN Y, Ji W, Kekuda R, Khrantsov NV;

Y DW, Li L, Macdougall JR, Miller CB, Orl

an M, Pena CRA, Peyman JM, Rieger DK;

y SG, Smithson G, Spaderna SK, Spytek KA;

vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess CE, Catterton E, Dis
Ellerman K, Gangolli EA, Gel
Herrmann JL, Halvorsen Y, J
Larochelle WJ, Lepley DM, L.
                        23-AUG-2002; 2002US-0405400P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-0405687P.
23-AUG-2002; 2002US-040563PP.
26-AUG-2002; 2002US-0406353P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PADICARU M.
PATURAJAN M.
PEYNAN C B A.
PEYNAN J A.
RIEGER D K.
ROTHENBERG M E.
SHENOY S G.
SMITHSON G.
SPADERNA S K.
SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alsobrook JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAROCHELLE W J.
LEPLEY D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACDOUGALL J R.
                                                                                                                                                      AGEE M L.
ALSOBROOK J. P.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                 EISEN A.
ELLERMAN K.
GANGOLLI E A.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GORMAN L.
ROTHBERG B G.
GUO X S.
HERRMANN J L.
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TAUPIER R J.
VERNET C A M.
VOSS E Z.
                                                                                                                                                                                                                     BERGHS C.
BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HALVORSEN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-268786/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLER C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larochelle WJ,
Padigaru M, Pat
Rothenberg ME,
Stone DJ, Taupi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZHONG M.
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Agee ML,

(STON/) (TAUP/) (VERN/) (VOSS/) (ZHON/)

SPAD/)

(PEYM/) (RIEG/)

PENA/

ROTH/) SHEN/)

(MACD/)
(MILL/)
(ORTT/)
(PADI/)

ВР.

(revised)

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AAQ23702 standard; DNA; 23
                                                                     23-SEP-2004
21-MAY-1992
                                           AAQ23702;
  AAQ23702
                                                                                                                  ô
a medicament for suppressing the immune response in a mammal for treating autoimmune disorders. The present sequence represents a PCR primer for TSIF, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                     Heavy chain; light chain; antibody; chimeric; variable; constant; domain; Fab; rescue; phagemid; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two prepns. of PCR-amplified VH genes were made. Both prepns. used an equimolar mixt. of the HUJHFOR primers; in one of the prepns, 6 separate PCR amplifications were performed with each of the HUJHBACK primers individually (1a-6a). The template was CDNA prepd. from RNA obtd. from B lymphocytes, and the prod. was further manipulated to yield the human VH domain. See also AAQ32260-349. (Updated on 25-MAR-2003 to correct PN
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of specific binding pair members - by producing libraries of polypeptide chains displayed by a package, and selection.
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                                                                                   0.5%; Score 17.2; DB 1; Length 22; 86.4%; Pred. No. 1e+03;
                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith AJH;
                                                         Sequence 22 BP; 7 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                 le+03;
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                             Human heavy chain PCL primer HuVH3aBACK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffiths AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                             602 AGGTGTACAGTGACGCACAGCC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 72; 117pp; English.
                                                                                                                                                                 1 AGGIATACACTGACGCACCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-GB001134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-GB000883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91GB-00010549
                                                                                                                                                                                                                                             AAQ32277 Standard; DNA; 23
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KS,
                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-415769/50.
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1991;
10-JUL-1991;
24-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9220791-A1
                                                                                                                                                                                                                                                                                                    25-MAR-2003
22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                         AAQ32277;
                                                                                      Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      field.)
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                                                                                                                  datches
                                                                                                                                                                                                                  RESULT 6
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The primer was used to amplify the H chain V region from a human monoclonal anti Rh-D cell line Fog-1 (Ig-k). It is one of 6 VH Back monoclonal anti Rh-D cell line Fog-1 (Ig-k). It is one of 6 VH Back monoclonal anti Rh-D cell line Fog-1 (Ig-k). It is one of 6 VH Back to primer RAQ223706-705) used together with the forward primer HulgG1-4 CHIHFOR (AAQ223716) for the H chain fragment, VK-CK, was prepd. Cragment. A corresponding light chain fragment, VK-CK, was prepd. Cragment. The PCR prod. was ligated into the vector, pJM-1-Fab Dl.3 (AAQ23857) and the ligation mixt. used to transform E. coli cells. 96 of the resulting clones were screened for anti-Rh-D activity; 40% crassembly process and the potential of this technique for one step cloning assembly process and the potential of this technique for one step cloning cells, demonstrating a high frequency of successful splicing in the assembly process and the potential of this technique for one step cloning coll human hybridomas. The pri-mers were also used to amplified a VH-CHI resulting clones, VH and vlambda genes of 15 clones were PCR amplified. 3 clifferent H chain and 2 different light chain families were PCR amplified. 3 clifferent H chain and 2 different light chain families were PCR amplified. 3 clifferent H chain and 2 different light chain families were PCR amplified. 3 clifferent Lechnique to assemble, clone and were typical of anti-Rh-D vgenes. The results demonstrate the potential of the technique to assemble, clone and isolated human Ab fragments from the technique to assemble, clone and isolated human Ab fragments from the polyclonal cell populations. See also AAQ21092-100, 103-116, 126-131;
                                                                                                                                                  Pd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revised record issued on 23-SEP-2004 : Correction to sequence location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoogenboom HRJ, Griffiths AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display
                                                                                                        Primer HuVH3aBACK for human immunoglobulin VH chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyclonal cell populations. See also AAQ21092-10
AAQ23463, 465-495, 693-719, 736-738, and 793-863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mccafferty J, Pope AR, Johnson KS, Jackson RH, Holliger KP, Marks JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page ?; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            90GB-00022845.
90GB-00024503.
91GB-0004744.
91GB-00010549.
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                                                                                                                                                                                                                                                                                                                                                                                                                            90GB-00015198
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDI-) MED RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-056862/07
                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1990;
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                                                                                                                                                                                                                                             Synthetic.
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Gaps

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0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; Ive 0; Mismatches 3; Indels

86.48;

Conservative

Best_Local Similarity Matches 19; Conserv

Query Match

Gaps

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3; Indels

0; Mismatches

86.4%;

Best Local Similarity

Query Match

19; Conservative

Matches

853 GAGGAGGAGCTGGAGGCTG 874

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RESULT 657

0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03;

vivlemore401-10.rng

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characteristics.
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15-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1993;
                                                                                                 24-MAR-1992;
24-MAR-1992;
15-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9319172-A1
                         WO9306213-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
22-APR-1994
                                                              23-SEP-1992;
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                                             01-APR-1993
                                                                                          5-SEP-1991
        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ48989;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 660
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                                                                                                                                                                                                                                                                                                                                                                            pTK genes were identified using two sets of degenerative oligonucleotide primers: a first set which amplifies all pTK DNA segments (AAQ49743-44), and a second set which amplifies highly conserved sequences present in the catalytic domain of the c-kit subgroup of pTKs (AAQ49745-46). The pTK genes identified are described in AAQ49747-57 and AAR41897-02. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; murine; Mab32; monoclonal antibody; chimeric; mouse-human antibodies; antibody; prevention; human; anti-globulin response; PCR; ss.
                                                                                                                                                                                                                                                                                                                                 New protein tyrosine kinase genes and proteins encoded by genes - are of
                                                                                                                                                      pTK; tyrosine kinase; catalytic domain; c-kit; amplification; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 0.5%; Score 17.2; DB 1; Length 23; 1 Similarity 86.4%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 8 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               Scadden D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VH domain PCR amplification primer HuVH3aBACK
                                                                                                                                                                                                                                                                            (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1801 GACGICTGGICCTITGGGGICC 1822
          874
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 60pp; English.
                                                                                                                                                                                                                                                                                                Cowley S,
                          daggraczagczagraczag 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 GACGTCTGGTCTTTGGAATTC 2
          GAGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ39335 standard; DNA; 23 BP
                                                                         BP
                                                                                                                                                                                                                                                                                                                                             human mega-karyocytic origin.
                                                                                                                                                                                                                                          93WO-US000586
                                                                                                                                                                                                                                                           92US-00826935
                                                                                                                       (first entry)
                                                                AAQ49744/c
ID AAQ49744 standard; DNA;
                                                                                                                                                                                                                                                                                                Groopman J,
                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                  WPI; 1993-320330/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                         pTK primer pTK2
                                                                                                                                                                                                                                          22-JAN-1993;
                                                                                                                                                                                                                                                            22-JAN-1992;
                                                                                                                                                                                                      WO9315201-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-JUL-1993
                                                                                                            25-MAR-2003
                                                                                                                      10-MAR-1994
                                                                                                                                                                                                                        05-AUG-1993
                                                                                                                                                                                    Synthetic.
                                                                                            AAQ49744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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AAQ39335
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The sequence is that of PCR primer HuVHJaBACK which was used, individually or in an equimolar mix of all 6 HuVHBACK primers (AAQ39333-Q39338), in the prepn. of PCR-amplified VH genes. It was used as part of a method of producing chimeric mouse-human antibodies or fragments which have the same binding specificity as a parent Ab but have increased human characteristics, preventing anti-globulin response in humans. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Producing human antibody polypeptide dimer specific for antigen comprises use of chain shuffling using phage expression, useful for reducing anti globulin responses in humans for increased human
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SBP; specific binding pair members; antibody; RGDP; replicable genetic display package; recombination; PCR; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                Winter GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                Jespers LSAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multimeric (SBP) antibody chain primer.
                                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 29; 109pp; English.
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                                                91GB-00020252.
91GB-00020377.
92GB-00006318.
92GB-00006372.
92WO-GB000883.
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92WO-GB000883.
92WO-GB001755
                                                                                                                                                                                                                                                                                                Hoogenboom HRJM, Baier M,
                                                                                                                                                                                                                      COUNCIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-117534/14.
                                                                                                                                                                                                                      (MEDI-) MEDICAL RES
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Waterhouse P;

Smith AJH,

Griffiths AD,

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The primers (AAQ48987-Q49045) are used in the amplification of Kappa and lambda-chain genes of various antibodies. These genes are then recombined into the same replicon, resulting in very diverse libraries of antibody chains, e.g. from unimmunised donors. It is also useful for chain shuffling, mutagenesis, humanising and CDR imprinting. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A set of degenerate primers (AAT03085-86) designed to amplify all protein tyrosine-kinase (pTK) sequences was used with a second set (AAT03087-88), which amplified highly conserved sequences present in the catalytic domain of the c-kit subgroup of pTKs, in a 2-step PCR to obtain probes used to screen cDNA libraries for the identification of novel pTK genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein tyrosine-kinase; agonist; cell growth; differentiation; polymerase chain reaction; primer; ss.
                                                                                                                          Prodn. of specific binding pair members, e.g. antibody chains display on surface of replicable genetic display packages.
                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein tyrosine-kinase PCR primer pTK2.
             CAMBRIDGE ANTIBODY TECHNOLOGY. MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 18; 125pp; English.
                                                                                                                                                                           Disclosure; Page 57; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                      Match 0.5%;
Local Similarity 86.4%;
les 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                              Johnson KS, Winter GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett BD, Goeddel D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-366160/47.
                                                                                            WPI; 1993-320739/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                         853
                                                                                                                                                                                                                                                                                                                                                         Query Match
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               CAMB-)
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BP.

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3; Indels

0; Mismatches

Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection and cloning of an antibody gene - using PCR, dissociating the gene into single strands and isolating the gene from a cDNA mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; amplify; primer; detection; antibody gene; antigen specific antibody; activation; lymphocyte; heavy chain; light chain; variable region; immunoglobulin; ss.
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                         Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
Sequence 23 BP; 8 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                          1801 GACGICIGGICCTITGGGGICC 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 GAGGAGCTGGTGGAGCTG 874
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                                                                                                                       23 GACGICIGGICCTITGGAATIC
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                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                          HuVH3a 5' heavy chain primer.
                               0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 86.4 les 19; Conservative
                                            Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LTTK-) LTT KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                     JP07115978-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1993;
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                                                                                                                                                                                                                                                               25-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                               Query Match
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AAX76600
ID AAX7660
XX
AC AAX7660
XX
DT 11-AUG-
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Wood WI;

Tsai SP,

Matthews W,

Lee JM,

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hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. AAC43841-Z4388 represent primers used in the amplification of a human IgG4 heavy chain which is used in the method of
                                                                                                                                                                                                              New polynuclectide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes a novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 86.4%; Pred. No. 1.1e+03; Length 23; Les 19; Conservative 0; Mismarchan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                      Turenhout EAM
                                                                                              (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                Example 2; Page 19; 61pp; English
                                                                                                                                      Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BÞ
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                  99WO-NL000285
                                                         98EP-00201543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA03074 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-616755/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                  07-MAY-1999;
                                                         08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA03074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                       This
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes methods of screening a DNA construct library for a single chain monoclonal antibody fusion reagent capable of binding a transcriptional associated biomolecule in vivo. The antibodies are useful in treating Hepatitis A and B respiratory synctial virus, HIV, Junin virus, Herpes simplex I and II, rubella, cytomegalovirus, Varicella-Zoster virus, Epstein-Barr virus, mesales, hantavirus, dengue, Ebola inter alia and cancer. Expression vectors that encode the fusion antibodies may be used in gene therapy. The methods can be used to create and isolate the fusion antibodies. The monoclonal antibody fusion reagent can be used to regulate transcription in vivo. AAX76591 to AAX76674 human sFv library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies from libraries useful in treating viral infections and cancer.
                                                     Human, sFV library, single chain monoclonal antibody fusion reagent, transcription regulation, screening, diagnosis, HIV; Hepatitis A; Hepatitis B respiratory syncitial virus, Junin virus, cytomegalovirus; Herpes simplex virus; rubella; Varicella-Zoster virus; hantavirus; Epstein-Barr virus; measles; dengue; Ebola inter alia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; IgG4; heavy chain; primer; antibody; factor VIII; hemostatic;
hemophilia A; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17.2; DB 1; Length 23;
86.4%; Pred. No. 1.1e+03;
ative 0; Mismatches 3; Indels
                    Human sFv library construction PCR primer SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 83; 132pp; English.
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                                                                                                                                                            gene therapy; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                 97WO-US021407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-371138/31.
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                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                         28-NOV-1997;
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                                                                                                                                                                                                   Synthetic
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Query Match

Matches

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Gaps

Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders. Disclosure; Page 538; 606pp; English.

The present invention relates to albumin fusion proteins, which comprise a therapeutic protein and albumin. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), renal disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. phocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. masseles), asstrointestinal disorders (e.g. infectious diseases (e.g. masseles), asstrointestinal disorders (e.g. infectious diseases) and wound healing. In the present invention, had a second allocate function masseles (e.g. masseles), assured to generate function masseles. proteins. The present sequence was used to illustrate the invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; 3; Indels 0; Mismatches 853 GAGGAGGTGGTGGAGGCTG 874 1 caccrecrecrecrecacrer 22 Query Match
Best Local Similarity 86.9%,
"...hes 19; Conservative ઠે 임

o;

Gaps

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RESULT 666

AAD20057 standard; DNA; 23 BP. AAD20057; AAD20057

18-DEC-2001 (first entry)

Human antibody VH gene amplifying PCR primer, Hu VH3-5'.

Human; albumin; HA; immune system disorder; transplant rejection; blood related disorder; myocardial infarction; glomerulonephritis; hyperproliferative disorder; childhood acute myeloid leukaemia; HH; heavy chain variable domain; renal cell carcinoma; antileukaemic; cardiovascular disorder; respiratory disorder; non-allergic rhinitis; pheorytochroma; reproductive system disorder; non-allergic rhinitis; pheorytochroma; reproductive system disorder; neuroprotective; syphilis; infectious disease; gastrointestinal disorder; wound healing; noctropic; irritable bowel syndrome; HIV; human immunodeficiency virus infection; cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant; antiarthritic; antirheumatic; renal disorder; antimicrobial; vulnerary; arrhythmia; melanoma; PCR primer; ss.

Homo sapiens,

WO200179480-A1.

25-OCT-2001.

12-APR-2001; 2001WO-US011991

12-APR-2000; 2000US-0229358P. 25-APR-2000; 2000US-0199384P. 21-DEC-2000; 2000US-0256931P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

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The invention relates to human albumin (HA) fusion proteins and their corresponding nucleic acid sequences. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders buth as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. childhood acute myeloid infarction), hyperproliferative disorders (e.g. childhood acute myeloid cleukaemia, metastatic renal cell carcinoma), renal disorders (e.g. malignant melanoma, renal cell carcinoma), renal disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome), HIV (human immunodeficiency virus) infection and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is a PCR primer used to amplify human heavy chain variable consult (VH) gene. Note: The present sequence is incorrectly reffered as
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                                                      Albumin fusion proteins comprising a therapeutic protein and albumin,
                                                                          useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human immunodeficiency virus) or infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                        Example 60; Page 315; 394pp; English
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Matches 19; Conservative
WPI; 2001-616756/71.
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멾. AAD13302 standard; DNA; 23 16-OCT-2001 (first entry) AAD13302; RESULT 667 AAD13302

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; yctostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's is sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia; PCR primer; VH domain; 88.

Human VH domain amplifying PCR primer Hu VH3-5'.

Homo sapiens.

WO200158916-A2

16-AUG-2001.

2000US-0181258P. 2000US-0187999P. 09-FEB-2001; 2001WO-US004153 09-FEB-2000; 09-MAR-2000;

22-SEP-2000; 2000US-0234336P

(HUMA-) HUMAN GENOME SCI INC

16-AUG-2001

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The invention relates to human G-protein chemokine receptor (CCR5)

CC HOGNR10 polypeptides and polynucleotides. CCR5 HOGNR10 antibodies are

CC useful for treating, preventing or ameliorating a disease or disorder

associated with inflammation, defective or aberrant chemotaxis of immune

CC astroam) or defective or aberrant T-cell antigen presenting cell

interaction. The disease or a powritus infection, a

cytomegalovirus infection such as an early stage HIV infection, a

cytomegalovirus infection, or a powritus infection, a

CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disease

CC disease or disorder may be associated with aberrant CCR5 expression, lack

disease or disorder may be associated with aberrant CCR5 expression, lack

cof CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand

cof CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand

cof CCR5 function, and protein is used as a food additive or preservative

cof increase or decrease storage capabilities. CCR5 HOGNR10 DNA are useful

cof increase or decrease storage capabilities. CCR5 HOGNR10 DNA,

cof core, tromosome identification and in gene therapy. CCR5 HOGNR10 DNA,

corporated, bone marrow, gastrointestinal tract, liver, lung,

curogenital); immune disorders (Addison's disease, allergies, autoimmune

curogenital); immune disorders (Addison's disease, allergies, autoimmune thyocaditis, diabetes mellitus, Crohn's

disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis)

credions of WH domain appedifically binds to the G-protein chemokine

credions of WH domain appedifically binds to the G-protein chemokine ö Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders. Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; receptor (CCR5) protein of the invention Li Y, Ruben SM, Example 55; Page 454; 518pp; English Local Similarity 86.4%; les 19; Conservative Roschke V, Rosen CA, Query Match

853 GAGGAGGAGCTGGTGGAGGCTG 874 22 1 GAGGTGCAGCTGGTGGAGTCTG Matches

AAD13201 standard; DNA; 23 BP 16-0CT-2001 AAD13201; RESULT 668
AAD13201
XX
AC AAD1322
XX
DT 16-OCT
XX
KW Human;
KW Cardio

Human VH domain amplifying PCR primer Hu VH3-5'. (first entry)

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; HIV; cytostatic; immunosuppressave; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma, autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia; PCR primer; VH domain; ss.

Homo sapiens

WO200158915-A2

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LIGE ALVENDATION LITERATORY CONTRESPONDATION LATERATORY CONTRIBUTION TO A LINE ALVENDATION LITERATORY CONTRIBUTION OF A LONG CALLY CONTRIBUTION OF A LONG CALLY OF A CALLY OF A LONG CALLY OF A LONG CALLY OF A LONG CALLY OF A CALCY OF A C
                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune
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                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRE) HDGNR10 polypeptide, useful for preventing or treating autoim diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human G-protein chemokine receptor (CCR5)
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                                                                                                                                                                                                                                                                       Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 55; Page 438; 495pp; English.
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                                                                                                    09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                09-FEB-2001; 2001WO-US004152.
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                                                                                                                                                                                                                                                                       Roschke V,
                                                                                                                                                                                                                                                                                                                                WPI; 2001-488965/53
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albumin fusion protein; cytostatic; anorectic; immunosuppressive; antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer; non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis; type I diabetes mellitus; rheumatoid arthritis; PCR primer; 88. growth hormone; hGH; albumin; human serum albumin; HSA; Human VH domain PCR primer Hu VH3-5' SEQ ID NO:38. ABN87305 standard; DNA; 23 (first entry) 01-AUG-2002 ABN87305; RESULT 669
ABN87305
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AC AEN8730
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DT 01-AUGXX
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Human V
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Human;
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Human;
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WO200152904-A2

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where the iraginant of variant has allowin for therapeutic processive,
antidiabetic, antirheumatic, antiarthritic and psoriatic activities.
Abbumin proteins are stabilised therapeutic proteins e.g.
antidiabetic, antirheumatic, antiarthritic and psoriatic activities.
Abbumin fusion proteins are stabilised therapeutic proteins e.g.
antibodies to C5, C242 and CD80 useful for treating various diseases and
disorders such as non-Hodgkin's lymphoma, cancer, obesity, transplant
of fisher and proteins are allitus, rheumatoid arthritis and psoriasis.
Fusing albumin to therapeutic proteins the in vitro or in vivo
protein, extends the shelf life and retains the in vitro or in vivo
protein, extends the shelf life and retains the protein
solutions with large excesses of carrier proteins to prevent loss of
therapeutic proteins due to factors such as binding to the container. The
fusion proteins are easily dispensed with a simple formulation requiring
minimal post storage manipulation. The fusion of therapeutic proteins to
albumin confers stability in aqueous or other solution. The present
sequence represents a PCR primer which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an albumin fusion protein (I) comprising a therapeutic protein: X and (a fragment or variant of) albumin comprising a the fully defined sequence in ABB79006 of 585 amino acids, (where the fragment or variant has albumin or therapeutic protein: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New albumin fusion proteins, useful for treating diseases and disorders such as cancer, comprise therapeutic protein fused to albumin.
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                         12-APR-2001; 2001WO-US011850
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Matches 19; Conservative
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                                                                                                                                              WO200179442-A2.
                                      sapiens.
                                                                                                                                                                                                                       25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                         Synthetic.
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Homo sapiens.

Synthetic.

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                                                                                                                                                                                                                                                                                                                        The invention provides a composition comprising one or more antisense oligonucleotides directed against vascular endothelial growth factor (VEGF) Where the antisense oligonucleotides inhibits profileration of between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed against VEGF for inhibiting cancer cell proliferation and angiogenesis. Preferably the oligonucleotide AAAL3031 (a modified version of AAAL2984) is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer, prostrate cancer, pancreatic cancer or melanoma. Sequences AAH23012-023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                Novel antisense oligonucleotides useful for inhibiting vascular endothelial growth factor expression, angiogenesis and for treating cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer #3 used to amplify human VH or VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 6 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1573 CAGGTGGCCCGGGGCATGGAGT 1594
                                                                                                                                                                                                                                                                                                Example 12; Page 56; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAAGTGGCCAGAGCATGGAGT 22
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                          19-JAN-2001; 2001WO-US000019
                                                                                                        19-JAN-2000; 2000US-00487023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2001; 2001US-00779879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK51873 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                     WPI; 2001-451898/48
                                                                                                                                                                      Masood R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROSE/) ROSEN C A.
                                                                                                                                       (GILL/) GILL P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002048786-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VL domain; ss
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                                           26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors
                                                                                                                                                                      3ill PS,
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ABK51873
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Matches
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Li Y, Ruben SM

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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                        Novel metalloprotease MP1 associated primer #10.
                                                                                                                                                                           examples of the present invention
                                                              Example 55; Page 150; 180pp; English
                                                                                                                                                                                                                     853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                               GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                          ABS76647 standard; DNA; 23
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                    Best Local Similarity 86.4 Matches 19, Conservative
                    Roschke V,
                              WPI; 2002-434754/46.
ROSCHKE V.
          RUBEN S M.
                                                    inflammation
                                                                                                                                                                                                                                                                               12-DEC-2002
                     Rosen CA,
                                                                                                                                                                                                                                                                    ABS76647;
     (LIYY/) I
(RUBE/) H
                                                                                                                                                                                                 Query Match
(ROSC/)
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BP.

WO200272751-A2

19-SEP-2002

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metalloprotease (MP-1). (I) is useful for preventing, treating, or metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Klainfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome, neurodegenerative diseases (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a primer associated with the novel human metalloprotease MPI polynucleotide
                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated nucleic acid molecule (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capture agent; nested sorting; gene library; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human antibody VH gene amplifying sense primer, HuVH3aBACK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                    Duclos F, Krystek S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; Page 301; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                    Chen J, Feder J, Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000; 2000US-0219183P.
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05-FEB-2002; 2002WO-US003353.
                                                      05-FEB-2001; 2001US-0266518P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD28818 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                              WPI; 2002-723329/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD28818;
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCRS) HDGNR10 and polynucleotide that bind human G-protein chemokine receptor (CCRS) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antignen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegallovitus or pox virus infections, Kaposi sarcomm, or conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS expression, ce.g. for diagnosis, prognosis and monitoring of cancer and other hyperproliferative diseases. The polynucleotide sequences encoding human G-protein chemokine receptor (CCRS) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases (e.g. parkinson's disease), and hyperproliferative diseases (e.g. cancer). ABKS1871-ABKS1906 represent PCR primers used to amplify VH and VL domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; tive 0; Mismatches 3; Indels
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Gaps ö

encoding

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The invention relates to a combination comprising capture agents which specifically bind to a polypeptide and, oligonuclectides that comprise a sequence that encodes a preselected polypeptide to which the agents bind. The anti-tag capture agents such as antibodies are used as tools for sorting proteins containing polypeptide tags for which the capture agents are specific and for a process of nested sorting. The agents are useful for functional surveys of large diversity libraries such as gene libraries. The present sequence is a PCR primer used to amplify human antibody heavy chain variable region (VH) gene. This primer is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human potassium channel beta-subunit, K+betaM3 polypeptide and polynucleotide for diagnosing, preventing and treating immune, metabolic, gastrointestinal, renal, neural and proliferative diseases or disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; potassium channel beta subunit; K+betaM3; cytostatic; anti-HIV; antiaddictive; antiarthritic; antiasthmatic; antirheumatic; antianaemic; antibacterial; immunosuppressive; antipsoriatic; dermatological; nootropic; neuroprotective; anticonvulsant; neuroleptic; antimanic; antidepressant; antiulcer; antiinflammatory; antidiartheic; antipyretic; antianphotropic; hypotensive; antianpinal; uropathnic; tocolytic; unlnerary; antiallergic; gene therapy; neural disorder; immune disorder; cancer; proliferative disorder; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes the human potassium channel beta-subunit
                                                              Combination of capture agents used as tools for sorting proteins containing polypeptide tags for which the capture agents are specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J, Jackson DG, Ramanathan C, Siemers N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K+betaM3 antibody VH domain PCR primer SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                    Disclosure, Fig 13A; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
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WPI; 2002-155051/20
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H, Ryseck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200268587-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2002
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AB082763
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AC AB08
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AC AB08
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antiasthmatic, anti-HIV, antirheumatic, antibacterial, immunosuppressive, antipacratic, dermatological, antianematic, antibacterial, immunosuppressive, antipacratic, dermatological, antianematic, neotropic, neuroprotective, antioninament, neuroprotective, antidiarematic, antidepressant, antidiarematory, antidiarematic, nephrotropic, hypotensive, antianginal, uropathic, tocolytic, antiallergic and vulnerary activities, and can be used in gene therapy. (I) can be used for diagnosing a pathological condition (or susceptibility) in a subject, and for related to aberrant neurotransmitter release or drug addiction, a disorder related to aberrant neurotransmitter release or drug addiction, a disorder related to hyper pocassium channel activity, an immune disorder related to hyper pocassium channel activity, an immune disorder related to tansplant rejection, immune disorder in which immunosuppression is desirable, a proliferative disorder related to aberrant cell cycle checkpoint, or aberrant cell cycle checkpoint, or aberrant cell cycle checkpoint, or aberrant on a proliferative disorder related to an aberration(s) in the call cycle checkpoint, or aberrant DNA damage repair. (I) can also be used for disordering, treating, prognosing, and/or preventing immune for an antiphody against K+betaM3, which is used in an example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegaloxizus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis; lymphocytopenia; PCR; primer; ss.
K+betaM3 protein (I). (I) has cytostatic, antiaddictive, antiarthritic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunoglobulin variable heavy domain PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      853 GAGGAGGAGCTGGTGGAGGCTG 874
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2001US-0297257P.
2001US-0310458P.
2001US-0328447P.
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21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2002; 2002WO-US003634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4
Matches 19; Conservative
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12-JUN-2001;
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Barber L;

Cacace A,

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antiinfertility; pulmonary; cytostatic; nephrotropic; hormonal; circulatory; gene therapy; inflammatory disorder; reproductive disorder; pulmonary disorder; renal disorder; renal disorder; endective tissue disorder; endocrine disorder; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     G protein coupled receptor; GPCR; HGPRBMY27; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                      Human HGPRBMY27 antibody VH domain PCR primer SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2002; 2002WO-US006796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2001; 2001US-0273808P.
27-MAR-2001; 2001US-0278983P.
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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The present invention describes a human G protein coupled receptor (GPCR), designated HGPRBMY27 (I). (I) has antiinflammatory, antiinferlilty, pulmonary, cytostatic, nephrotropic, hormonal and circulatory activities, and can be used in gene therapy. (I) or the protein encoded by it can be used to prevent, treat, or ameliorate a medical condition, such as inflammatory disorders, reproductive disorders, pulmonary disorders, cancer, renal disorders, connective tissue disorders, endocrine disorders, or disorders involving aberrations in tubular tissues. They can also be used to diagnose a pathological condition or a susceptibility to (I). The protein can be used to screen for candidate compounds capable of modulating activity of a GPCR polypeptide. The present sequence represents a PCR primer for the VH domain of an antibody against human HGPRBWY27, which is used in an antibody against human HGPRBWY27, which is used in an
                                                                                                                                                                   New polynucleotide encoding a human G-protein coupled receptor for preventing, treating, or ameliorating e.g. an inflammatory, reproductive, pulmonary, renal connective tissue, or endocrine disorder.
                                                                                                                                                                                                                                                                                                                                                                         Example 34; Page 298; 356pp; English.
Ramanathan C, Feder J, Mintier G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            example from the present invention
                                                                                           WPI; 2002-657945/70
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                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF37.682.55G10, XF27/283.5671, XF27/28.35G10, XF27/283.36412, XF27/283.36712, XF27/283.3712, XF27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infectious disease, an autoimmune disease such as Addison's disease, dematitis and theumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovirus or poxvirus infection, a Pneumoystis carnii infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a disease or disorder associated with Aberrant expression of novel human G-
                                                                                                                                           New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            Example 55; Page 471; 562pp; English.
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Matches 19; Conservative
                                                              WPI; 2002-643455/69.
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                                                         Gaps
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0
                          Score 17.2; DB 1; Length 23;
Pred. No. 1.18+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                               K+beta M6 related VH domain PCR primer SEQ ID No 30.
Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen J, Jackson DG,
                                                                                     853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                  1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                                                                                                                                           ABT09824 standard; DNA; 23 BP.
                               0.5%; 86.4%;
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27-MAR-2001; 2001US-0278953P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2002; 2002WO-US005674
                                                                                                                                                                                                                                                        (first entry)
                                                            19; Conservative
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                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200270727-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Chang H;
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                                Query Match
                                                                                                                                                                  RESULT 677
                                                              Matches
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New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.
New polynucleotide encoding human potassium channel beta subunit
                           Example 34; Page 281; 332pp; English.
                                                                                                                                                                                    853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                             1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                    BP.
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001; 2001WO-US011988
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                               27-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   WO200177137-A1.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2001.
               e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                 ABK93297;
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Example 60; Page 512; 2102pp; English

1 caccrecactrecresserers 22 853 GAGGAGGAGCTGGTGGAGGCTG BP. Li Y, 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001US-00779880. Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative AAD42429 standard; DNA; 23 24-FEB-2003 (first entry) Rosen CA, Roschke V, WPI; 2002-499674/53 ROSE/) ROSEN C A. ROSC/) ROSCHKE V. RUBEN S M. US2002061834-A1. Homo sapiens. 23-MAY-2002. AAD42429; RUBE/) RESULT 679 AAD42429 ઠ ö The invention relates to an isolated polynucleotide encoding a potassium channel beta subunit (K+betaM6) polypeptide or its variants. The human potassium beta subunit polynucleotide or polypeptide is useful for diagnosing, preventing, treating or ameliorating a pathological condition such as gastrointestinal, reproductive, neural, sleep, cardiovascular or pulmonary disorders, a disorder related to hyperpotessium channel activity, an immune disorder related to berrant NE activity, pineal gland associated disorders migraine headaches, disorders associated with aberrant melatonin synthesis and/or release or with low DNA repair capacities or low free-radical buffering capacity, delayed sleep phase syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis, age related disorders associated with decreased melatonin secretion, or cancer. This polynucleotide sequence represents a PCR primer relating to the potassium channel beta subunit (K+betaM6) of the invention polypeptide, useful for diagnosing, preventing, treating or ameliorating Gaps Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; disorder; disorder; disorder; immune disorder; endocrine disorder; haematopoietic disorder; natial disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antiinflammatory; antiulcer; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic; VH domain; PCR; primer; ss. .; 0 Ouery Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels PCR primer #3 for amplifying human antibody VH domain. Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's limmunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoprosis, arthritis). ABK93295-ABK93304 represent PCR primers used to amplify DNA encoding human antibody VH domains in the examples of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; heavy chain variable domain; PCR; primer; VH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HDGNR10 antibody VH domain amplifying PCR primer, Hu VH3-5'.
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                                                                                                                                                                                                                                                                                                                                                                                                Score 17.2; DB 1; Length 23;
Pred. No. i.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0. Other;
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defective or aberrant chemotaxis of immune cells or T cell antigen-
presenting cell interaction, viral infections (specifically human immune
deficiency (including its early stages), cytomegalo or pox viruses),
autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
carinii infection, Kaposi's sarcoma or any condition associated with
aberrant expression of CCR5 or their ligands. They are also used for the
detection, diagnosis, prognosis and monitoring of cancers or other
hyperproliferative diseases. The present sequence is a PCR primer used to
amplify human HDGNR10 antibody heavy chain variable (VH) domain
                   888888888888888
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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0
Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; es 19; Conservative 0; Mismatches 3; Indels
                                                                                      853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                1 GAGGTGCAGCTGGTGGAGTCTG 22
        Query Match
                              Best Loca
Matches
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Gaps

Human K+betaM2 antibody VH domain amplifying 5' PCR primer, VH3 AAD46081 standard; DNA; 23 BP (first entry) 27-DEC-2002 AAD46081; RESULT 680 AAD46081

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Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder; reproductive disorder; metabolic disorder; premature puberty; nephritis; endocrine disorder; memory disorder; neuroendocrine condition, asthma; spermatogenesis; renal disease; learning deficiency; Alzheimer's disease; neuroendocrine condition, asthma; spermatogenesis; renal disease; learning deficiency; Alzheimer's disease; carcinoid tumour; blood coagulation disease; blood platelet disease; rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy; graft-versus-host disease; organ rejection; antisterility; thrombolytic; antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive; nephrotropic; cytostatic; nootropic; hypotensive; vulnerary; PCR; primer;

WO200266601-A2. Homo sapiens.

29-AUG-2002.

24-JAN-2002; 2002WO-US002332

24-JAN-2001; 2001US-0263872P. 14-FEB-2001; 2001US-0269794P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Lee L, Chen J, Jackson D, Ramanathan C, Siemers N; Carroll P; Feder J, 1 Chang H, (

WPI; 2002-691617/74.

New potassium channel beta-subunit, K+betaM2, proteins and nucleic acids, useful for diagnosing, treating and/or preventing e.g. reproductive, neural, metabolic, endocrine, memory, neurodegenerative disorders or

Example 19; Page 358; 366pp; English.

diseases.

The present invention relates to human potassium channel beta-subunit (K+betaM2) proteins and polynucleotides encoding such proteins. The K+betaM2 sequences are useful for diagnosing, treating and/or preventing reproductive disorders, neural disorders, disorders related to aberrant potassium regulation or hyper potassium channel activity, metabolic

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growth hormone synthesis and/or secretion), memory disorders, disorders of the testis (e.g. spermatogenesis), neuroendocrine condition related to aberrant thyroid hormone release, renal disease or disorders (e.g. aberrant thyroid hormone release, renal disease or disorders (e.g. chephritis), disorders related to aberrant higher brain function (e.g. disease), proliferative disorders (e.g. carcinoid tumour) and disorders (c.g. involving excessive smooth muscle tone or excitability (e.g. asthma).

They may be used to modulate haemostatic or thrombolytic activity, to treat or prevent blood coagulation diseases or disorders, blood platelet diseases, wounds, autoimmune diseases or disorders, blood platelet or rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection or graft-versus-host disease, and hyperproliferative diseases. K+betema cor graft-versus-host disease, and hyperproliferative diseases. K+betema cor graft-which is used for amplifying the VH domain of antibodies of directed against human K+betaM2 DNA. This sequence is used in the
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disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the invention
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Best Local Similarity 86.4
Matches 19, Conservative
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Human; glycine receptor alpha subunit 4; HGRA4; HGRA4sv; splice variant; cardiovascular disorder; reproductive disorder; neural disorder; cardiant; antiarrhythmic; antianginal; antidiarrhelc; antiuloer; nootropic; neuroprotective; antibacterial; virucide; protozoacide; nervous system disorder; gastrointestinal disorder; gene therapy; infection; PCR; primer; 88. Anti-HGPR4 antibody VH domain PCR primer SEQ ID NO: 40. Unidentified.

AAL49669 standard; DNA; 23 BP

AAL49669

27-NOV-2002 (first entry)

AAL49669;

#0200266606-A2.

29-AUG-2002

13-FEB-2002; 2002WO-US004329.

16-FEB-2001; 2001US-0269535P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Ramanathan C, Chen J, Jackson DG, Lee L, Feder J, Chang H; Chang

WPI; 2002-674925/72.

New isolated nucleic acid molecules encoding human glycine receptor A4 (HGRA4) polypeptides, useful for preventing, treating and ameliorating conditions, e.g. neural or gastrointestinal disorders.

Example 24; Page 341; 349pp; English.

The present invention provides the protein and coding sequences of the human glycine receptor alpha 4 (HGRA4) and its splice variant HGRA4sv. The sequences can be used in the treatment of neural disorders, gastrointestinal disorders, disorders related to hyper glycine receptor

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activity, cardiovascular disorders, reproductive disorders, or bacterial, viral and parasitic infections. The present sequence is a PCR primer used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                    0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
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                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  853 GAGGAGGAGCTGGTGGAGGCTG 874
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11-SEP-2000; 2000GB-00022216
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The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stronal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a PCR primer described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                   Human, FAPalpha, fibroblast activating protein alpha, antibody, Ab, gene therapy, cancer, wound healing, inflammation, cytostatic, PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mersmann M;
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Pred. No. 1.1e+03;
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                                                                                                                                                                      Human V gene library PCR primer HUVHB3.
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1 GAGGTGCAGCTGGTGGAGTCTG 22
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il Similarity 86.4%;
19; Conservative
                                                                           AAK98469 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-041180/05.
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Best Local Similarity
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                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                       08-AUG-2002
                                                                                                                                                                                                                                   primer; ss.
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                                                                                                          AAK98469;
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Schmidt 1
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                                              RESULT 683
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ID ADJ3
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AC ADJ3
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DT 15-P
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Gaps

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Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels

853 GAGGAGGAGCTGGTGGAGGCTG 874

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New isolated K+betaM4 or K+betaM5 nucleic acid molecule, useful for preventing, treating or ameliorating a medical condition related to hyper potassium channel activity such as cancer, immune, neural and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroprotective; antiinflammatory; immunosuppressive; cytostatic; neural; nephrotropic; cardiant; human G-protein receptor; HGRBMY28; HGRBMY29;
                              hyper potassium channel activity; hepatic disorder; neural disorder; gastrointestinal disorder; reproductive disorder; immune disorder; cardiovascular disorder; renal disorder; immune disorder; apoptosis; infectious disease; inflammatory disorder; cancer; Hepatotropic; Cerebroprotective; Neuroprotective; Gastrointestinal; Gymecologica; Immunomodulator; Cardiovascular; Immunostimulant; Immunosuppressive; Nephrotropic; Antinflammatory; Cytostatic; Gene Therapy; human; VH; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K+betaM4 and K+betaM5, CDNA sequences (I, ADJ33294 and ADJ33316), and encoded proteins sequences (II, ADJ33295 and ADJ33317). The invention is useful for preventing, treating or ameliorating a medical condition by administering (I) or (II) to a mammalian subject, where the medical condition is a disorder related to hyper potassium channel activity selected from a hepatic, neural, gastrointestinal, reproductive, immune, cardiovascular or renal disorder, or an immune disorder related to aberrant apoptosis or innate immunity, an infectious disease, an inflammatory disorder and cancer. The present sequence is a primer used in an example from the invention for amplifying VH domains, for the ktbetaM5 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human potassium channel beta subunits,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siemers N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 0.5%; Score 17.2; DB 1; Length 23; I Similarity 86.4%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee L, Chen J, Jackson DG, Ramanathan C, Carroll P;
                    Potassium channel beta subunit; K+betaM4; K+betaM5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorders.
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                                                                                                                                                                                                                                                        WO200268604-A2.
                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                              primer; 88
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Best Local S
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ID ABT4
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AC ABT4
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DT 17-S
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DE Huma
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XW Neur
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Gaps

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This invention relates to an isolated nucleic acid molecule comprising a polynucleotide encoding a human G-protein receptor, including HGRBMY28, CC HGRBMY29, HGRBMY29, DO HGRBMY29, ZO PyPeptides. The HGRBMY28 or HGRBMY29 polypeptides and nucleic acids are useful for treating, preventing or ameliorating a medical condition, e.g. an immune disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, a parameter, a gastrointestinal disorder, a neural disorder, a pulmonary cisorder, a gastrointestinal disorder, a disorder related to aberrant p27 regulation, a disorder related to aberrant p27 regulation, a disorder related to aberrant DNA repair regulation, a disorder related to aberrant DNA repair regulation, a disorder related to aberrant capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder of the lymph capoptosis regulation, a disorder of the spleen, a disorder, a renal disorder, a cardiovascular disorder, a proliferative disorder, and a disorder of the spleen, a disorder of the colon, cervix, lung, squamous cells or tissues, a renal disorder, a cardiovascular disorder, a placental disorder, and a disorder of the isolated polymucleotides of the invention may be used to treat disorders by gene therapy. This
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HGPRBMY29v1; HGPRBMY29v2; HGRBMY28; HGRBMY29; immune disorder; pulmonary;
                      inflammatory; haematopoietic; gastrointestinal; small intestine; cancer; proliferative; aberrant p27 regulation; FRM1; cell cycle; DNA repair; apoptosis; spleen; lymph node; reproductive; oesophageal; metabolic; endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular; placental; testis; heart; gene therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their variants, useful for treating, preventing or ameliorating e.g. hematopoietic, neural, pulmonary, gastrointestinal, inflammatory or proliferative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGPRBMY28 PCR primer relating to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feder J, Mintier G, Ramanathan C,
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                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001; 2001US-0283161P.
03-MAY-2001; 2001US-0288468P.
25-JUN-2001; 2001US-0300619P.
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Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001US-0283145P
                                                                                                                                                                                                                                                                                                           11-APR-2002; 2002WO-US011525
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                                                                                                                                                                                                                   WO200283856-A2
                                                                                                                                                                      Homo sapiens.
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ID AALS
XX
AC AALS
XX
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(first entry) 27-AUG-2003 Human antibody VH domain amplifying primer, Hu VH3-5'

Human, TNF-related apoptosis-inducing ligand; Kaposi's sarcoma, cancer, hyperproliferative disorder, rheumatoid arthritis, Parkinson's disease, neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disorder; myasthenia gravis; autoimmune disorder; Huntington's disease, vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury; infectious diseases; myelodysplastic syndrome; cardiovascular disorder; graft-versus-host disease; toxin-induced liver disease; cachexia; AIDS; errebrovascular disorder; incombotic microangiopathy; aplastic anemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis; asthma; AIDS; therapy; TRAIL receptor; tumour necrosis factor; TRAIL-R; PCR; primer; ss.

Homo sapiens

WO2003042367-A2

22-MAY-2003.

13-NOV-2002; 2002WO-US036431

14-NOV-2001; 2001US-0331309P. 07-MAY-2002; 2002US-0377973P. 15-AUG-2002; 2002US-0403376P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA; Salcedo T, Roschke V, Ruben SM,

WPI; 2003-449572/42

Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor polypeptide

Example 5; Page 325; 405pp; English.

The Invention Figures to antibodies of the invention are useful for treating treceptors (TRAIL)

receptors (TRAIL-R). Antibodies of the invention are useful for treating, preventing or ameliorating cancer (e.g. cancers of pancreas, uterine, breast, colon, lung and gastrointestine and Kaposi's sarcoma) and other hyperproliferative disorders, neurodegenerative disorders (e.g. brakinson's disease, Alzheimer's disease and Huntington's disease), autoimmune disorders (e.g. thups, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, Hashimoto's disease and immunodeficiency syndrome), inflammatory disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immune deficiency syndrome; AlbS, herpes viral infections and other viral infections), myelodysplastic Syndromes (e.g. aplastic anaemia), graftversus-host disease, ischaemic injury, liver injury, toxin-induced liver disease, septic shock, cachesia, anorexia and proliferative disorders.

Antibodies of the invention are also useful for treating cardiovascular disorders, cerebrovascular disorders, thrombotic microangiopathies, and ulcerative collitis and for wound healing. The invention is also used to prepare vaccines. The primer is used to amplify human antibody VH domain. This primer is used in the exemplification of The invention relates to antibodies that immunospecifically bind to the invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps .. 0 Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels

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1 GAGGTGCAGCTGGTGGAGTCTG 22

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ABQ76996 standard; DNA; 23

ABQ76996;

03-APR-2003 (first entry)

Human anti-VEGF2 antibody VH domain PCR primer HuVH3-5'

cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic; antiartheritic; antidabetic; ophthalmological; antiallergic; vulnerary; immunosuppressive; dermatological; antipsoriatic; proliferative disorder; cancer; cardiovascular disorder; arrhythmia; cerebrovascular disorder; acrebral anoxia; inflammatory disease; infectious disease; angligenesis; autoimmune disease; systemic Lupus Erythematosus; wound healing; vasculmar tissue repair; gene therapy; vaccine; PCR; primer; ss. Human; VH domain; VL domain; vascular endothelial growth factor; VEGF-2;

Homo sapiens.

WO200283850-A2.

24-OCT-2002.

12-APR-2002; 2002WO-US011405.

13-APR-2001; 2001US-0283408P.

(HUMA-) HUMAN GENOME SCI INC.

Wager RE; Ruben SM, Rosen CA, Albert VR,

WPI; 2003-093008/08.

New isolated polynucleotide encoding an antibody which inhibits vascular endothelial growth factor (VEGF)-2 polypeptide, useful for diagnosing or treating diseases associated with aberrant VEGF-2 expression or function, e.g. cancer.

Example 32; Page 236; 344pp; English.

This invention describes a novel isolated polynuclectide encoding a first antibody comprising an amino acid sequence selected from at least one, two or three complementarity determining (CDR) region(s) of a VH and/or UL domain of a second antibody that immunospecifically binds to a vacular endothelial growth factor (VEGF)-2 polypeptide. The products of the invention have cytostatic, cardiovascular, antibheumatic, vulnerary, antibatinamatory, antiarthritic, antidiabetic, ophthalmological, cardiant, antiallergic, immunosuppressive, dermatological and antipositatic activity. The polynuclectide is useful in diagnosing, treating, preventing, prognosing, ameliotating or monitoring diseases associated with aberrant VEGF-2 or VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function, such as cancer and other proliferative disorders (e.g. cerebral anoxia), inflammatory diseases, or reference disorders (e.g. cerebral anoxia), inflammatory diseases, infectious diseases, autoimmune diseases (e.g. rheumatoid arthritis, systemic Lupus Erythematosus, allergies), diabetic retinopathy or soriasis. The polynucleotide, polypeptide and antibodies described in the invention may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polynucleotide and polypeptide may also be used for in vitro purposes related to scientific research, and thousantism of the invention of the contraction of the contract diagnostics and therapeutics e.g. gene therapy and in vaccines to treat human diseases. This sequence represents a PCR primer used in the isolation and amplification of polynucleotides described in the disclosure of the invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

853 GAGGAGCTGGTGGAGGCTG 874

vivlemore401-10.rng

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The invention relates to an isolated antibody comprising a first amino acid sequence having 95 % identity to a second amino acid sequence of either variable heavy chain or light chain-complementarity determining regions (VHCDR1)/VLCDR2 or VHCDR3/VLCDR3 appearing as ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF (tumour necrosis factor) related apoptosis-inducing ligand receptor, also known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that produces the antibody, an antibody that binds the same epitope on a TR4 polypeptide as the antibody that binds the same epitope on a TR4 polypeptide or detecting, diagnosing, prognosing or monitoring cancers, and other hyperproliferative disorders) using the antibodies, a hybridoma cell line selected from the hybridoma cell lines selected from the hybridoma cell lines selected from the hybridoma cell lines solataled in the antibodies expressed by these hybridoma cell lines. The antibodies of the invention are useful for diagnosing or treating a disease or disorder associated with increased or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antibody for treating, or preventing disease or disorder, comprises amino acid sequence having identity to other amino acid sequence of either variable heavy/light chain-complementarity determining regions.
                                                                                                                                                                                                                                                                                                                                                                                    PCR; ss; primer; human; TRAIL receptor; tumour necrosis factor; TNF; TNF-related apoptosis-inducing ligand; antibody; VH; cancer; heavy chain variable region; TRA; TRS; TRX; TR10; apoptosis; hyperproliferative disorder; hybridoma cell line; Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease; AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder; Alzabainer's disease; autoimmune disorder; Alzabainer's disease; autoimmune disorder; inflammatory disease; rheumatoid arthritis; psoriasis; wound healing; cardilovascular disorder; amplogenesis; immune response;
                                            Gaps
                                          ;
0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                  Human anti-TRAIL receptor antibody VH PCR primer Hu VH3-5'
                                          Indels
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                                          0; Mismatches
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                                                                                  853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                  GAGGTGCAGCTGGTGTTG 22
                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000; 2000US-0246612P.
16-NOV-2000; 2000US-0248847P.
27-NOV-2000; 2000US-025904P.
04-UTN-2001; 2001US-0255018P.
09-OCT-2001; 2001US-0327359P.
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                                                                                                                                                                                                                              ABX08573 standard; DNA; 23
                                                                                                                                                                                                                                                                                                          (first entry)
                                          19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemotherapeutic agent.
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                       Best Local Similarity
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                                                                                                                                                                                                                                                                      ABX08573;
  Query Match
                                          Matches
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decreased apoptosis, e.g. cancer (such as colon, breast, uterine, pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-
host disease (GVHD), infectious disease, acquired immunodeficiency
syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
disease, Parkinson's disease), autoimmune disorders like multiple
consists, Behcet's disease, lupus erythematosus, inflammatory diseases
cuch as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in
promoting angiogenesis, wound healing, and in the specification. The
antibody is administered in combination with a chemotherapeutic agent
cantibody is administered in combination with a chemotherapeutic agent
continued in immunoassays for qualitatively and target the
polypeptides, and in immunoassays for qualitatively and quantitatively
consequence is
consequence of a primer used to amplify a nucleic adid encoding the heavy chain
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consequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vascular endothelial growth factor; VEGF-2; inflammatory disease; proliferative disorder; tumour; breast; cancer; brain; prostate; colon; lymphangions; infection; Kaposi's sarcoma; psoriasis; immunosuppressive; rheumatoid arthritis; diabetic retinopathy; gene therapy; antimicrobial; cytostatic; ophthalmological; autoimmune disease; VH; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to vascular endothelial growth factor (VEGF)-2 antibodies. VEGF-2 antibodies are useful for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases or disorders, proliferative disorders, tumours, tumour metastasis, breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vascular endothelial growth factor (VEGF)- 2 antibodies, for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases, proliferative disorders, autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human VH gene amplifying PCR primer, Hu VH3-5'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy.
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Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD49552;
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        88888888888888888888888888888888888
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cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid arthritis, psoriasis, diabetic retinopathy, a disease or disorder associated with aberrant VEGF-2 (receptor) expression, or a disease or disorder associated with the lack of VEGF-2 (receptor) function. The antibody is also useful for detecting, diagnosing, prognosing, or monitoring cancers and other hyperpoliferative disorders. VEGF-2 is also used in gene therapy. The present sequence is a PCR primer used for amplifying human VH gene. This sequence is used in the exemplification of
      8866666666688888
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                   853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                  1 caccrecrecrecrecres 22
                  86.48;
                  Local Similarity 86.4
hes 19; Conservative
     Query Match
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ABX99237 standard; DNA; 23 ABX99237; RESULT 690 ABX99237

(first entry) 21-MAY-2003 Anti-CAN-12 antibody VH region PCR primer Hu VH3.

Human; ss; PCR; CAN-12; calpain; cysteine protease; cytostatic; protein co-ordinate data; antiinflammatory; neuroprotective; primer; immunosuppressive; inotropic; vulnerary; analgesic; gene therapy; vaccine; neurodegenerative condition; musculo-degenerative condition; cancer; multiple sclerosis; a blood disorder; autoimmune disorder; oseophagitis, oseophagitis, oseophagitis, cancer; multiple disorder; autoimmune disorder; chromosome 2p16-p21, antibody; heavy chain variable region; light chain variable region.

Homo sapiens

WO200288303-A2.

07-NOV-2002

02-APR-2002; 2002WO-US010419.

03-APR-2001; 2001US-0281253P. 04-MAY-2001; 2001US-0298768P.

25-JUN-2001; 2001US-0300620P

(BRIM) BRISTOL-MYERS SQUIBB CO

Chen J, Duclos F, Feder JN, Nelson TC, Seiler S,

WPI; 2003-156689/15.

New isolated nucleic acid molecule for diagnosing, treating or preventing disorders, e.g. neuro- and musculo-degenerative conditions or cancer, related to the CAN-12 or CAN-12v2 polypeptides.

Example 35; Page 454; 737pp; English.

The invention relates to an isolated nucleic acid molecule comprising a polynucleotide having a sequence that is at least 95% identical to the human cDNAs for CAN-12 or its variants (CAN-12v1 and CAN12v2), including various functional fragments defined in the specification. CAN-12 is a calpain family cysteine procease, the gene for which is located on chromosome 2p16-p21. Also included are the encoded CAN-12 proteins (including fragments), CAN-12 recombinant vectors, host cells, anti-CAN-

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a molecule or a molecule complex which comprises the structural coordinates of CAN-12 and CAN-12 would be specification, a method for identifying a mutant with altered biological properties, tentofic function or activity of CAN-12 and CAN-12v2 models given in the specification, a method for identifying a mutant with altered biological properties, function or activity of CAN-12 and CAN-12v2 and a method for designing or selecting compounds as potential modulators of CAN-12 and CAN-12v2. The nucleic acid molecule and the polypeptide are useful in diagnosing, treating and/or preventing various diseases and disorders related to the CAN-12 or CAN-12v2 polypeptides, particularly neuro- and musculocid degenerative conditions, such as cancer, multiple sclerosis, blood disorders, autoimmune disorders, osesphagitis or other osesphagal motility disorders. Many other diseases and disorders are listed in the specification. The methods may be used in identifying agonists and antagonists of the above polypeptide and polynucleotide. The present sequence is a PCR primer used to clone DNAs encoding the VH and VL (heavy and light chain variable regions) molecules of anti_CAN-12 antibodies
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5555555555555555555555888

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

ö 0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels Best Local Similarity 86.4%; Matches 19; Conservative Query Match Best Local Similarity

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à

ACC48653 standard; DNA; 23 RESULT 691 ACC48653

BP.

ACC48653;

11-AUG-2003 (first entry)

Human antibody heavy chain variable region PCR primer Hu VH3-5'.

antianginal; neuroprotective; osteopathic; cytostatic; immunosuppressive; antibacterial; antipsoriatic; antinflammatory; gynaecological; immunostimulant; antirheumatic; antiarthritic; antiansemic; haemostatic; dermatological; antiateriosclerotic; virucide; vulnerary; antiasthmatic; gene therapy; antibody; PCR; primer; 88. Human; potassium channel; K+betaMB; cardiovascular; vasotropic; cardiant;

WO2003020910-A2

13-MAR-2003

04-SEP-2001; 2001US-0317087P.

04-SEP-2002; 2002WO-US028180

(BRIM) BRISTOL-MYERS SQUIBB CO.

Chang H; Lee LM, Feder JN,

WPI; 2003-290187/28.

New human potassium channel beta subunit (K+betaM8) polypeptide or polynucleotide, useful for preventing, treating or ameliorating e.g. breast or colon cancer, arthritis, asthma, multiple sclerosis, ostecarthritis or ischemia.

Example 32; Page 284; 308pp; English.

The present sequence is PCR primer Hu VH3-5', which is designed to amplify human antibody heavy chain variable regions (VH). It is one of a set of primers (see ACC48651-86) used in the identification and cloning of VH and VL domains of antibodies directed against the novel human

Vaughan TJ

Dobson CL,

Rosen CA, Albert VR,

Salcedo T, Ruben SM,

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potassium channel beta subunit, K+betaNB (see ABR41902). The VH and VL domains can be used to generate expression vectors. Antibodies directed to K+betaNB are useful for affinity purification of the polypeptide, in diagnostic assays and imaging, in immunophenotyping, and in therapeutic applications, including the use of nucleic acids encoding the antibodies in antibody-based gene therapy. Disorders that may be treated include a male reproductive disorder, a testicular disorder, a disorder related to aberrant calcium, potassium or potassium channel regulation, a pullmonary disorder, an immune system disorder associated with mis-regulation of NPKB, an inflammatory calcium, disorder, an innate immunity disorder, a disorder associated with a failure to initiate and/or sustain an adequate inflammatory response, in the static and a static and a static and a subject of the sustain an adequate inflammatory response, an innate immunity disorder, a disorder associated with a failure to initiate and/or sustain an adequate inflammatory response, an innate inman and a subject associated with a failure to initiate and/or sustain an adequate inflammatory response, and a such a subject associated with a subject associated with a failure to initiate and/or sustain an adequate inflammatory response, and a such a subject associated with a su
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                                         8X88888888888888888
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                   853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                1 caccrecacirecrecación 22
                                                  Matches
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Gaps

AAD54813 standard; DNA; 23 BP AAD54813; RESULT 692

26-JUN-2003 (first entry)

Human TR4 antibody VH domain amplifying PCR primer, Hu VH3.

TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; hyperproliferative disorder; neurodegenerative disorder; immune disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; Habilmoto's thyroiditis; methiniston's disease; Habilmoto's thyroiditis; whilary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder; glomerulonephritis; immune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; inflession acquired immunodeficiency syndrome; viral infection; inflammatory disorder; rheumatoid arthritis; septic shock; inflammatory disorder; rheumatoid arthritis; septic shock; inflamine disorder; myolodysplastic syndrome; plastic anaemia; schaemic injury; myocardial infarction; reperfusion injury; cachexia; erroke; cardiovascular disorder; peripheral artery disease; mimb ischaemia; arrhythmia; congestive heart failure; neovascularisation; myocular disorder; wound healing; angiogenesis; transplantation; primer; PCR; human; ss

Homo sapiens

WO200297033-A2 05-DEC-2002. 07-MAY-2002; 2002WO-US014268

02-AUG-2001; 2001US-0309176P. 21-SEP-2001; 2001US-0323807P. 09-OCT-2001; 2001US-0327364P. 14-NOV-2001; 2001US-0331310P. 20-DEC-2001; 2001US-0341237P. 05-APR-2002; 2002US-0369860P. 2001US-0293473P. 2001US-0294981P. 2001US-0331044P. 25-MAY-2001; 04-JUN-2001; 07-NOV-2001;

(HUMA-) HUMAN GENOME SCI INC.

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The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating, preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in detecting, diagnosing, preventing or ameliorating cancers and other hypercreating, preventing or ameliorating neurodegencative disorders (e.g. proliferating preventing or ameliorating neurodegencative disorders (e.g. Alzheimer's disease, multiple amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease), retinitis pigmentosa, cerebellar degeneration and Huntington's disease), immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, slogren's syndrome, biliary cirrhosis, disease, Crohn's disease, polymyositis, immune-related glomentlonephritis, mysathenia gravis, discasses (e.g. acquired immunodeficiency syndrome, infections and other viral infections) and proliferative disorders viral infections and other viral infections and other viral infections and thining myelodysplastic scheme of moreatial infarction and reperfusion injury), septic shock, cachexia, and contining callowands and proliferation and toxin-induced liver diseases (e.g. astromasis), ischemic injury (such as that caused by stroke, anorexia and toxin-induced liver diseases (e.g. acheanic) injury), septic shock, cacheanic anorexia and toxin-induced liver diseases (e.g. acheanic) injury diseases such as limb ischaemic an errery diseases such as limb ischaemic an errery diseases such as limb ischaemic and properfusion and reperfusion injury), applied as alcohol). They are also useful for treating cardiovasis and reconstant and experience and provinced and provinced and anorexial inferience and such as alimb ischaemic and provinced and provinced and anorexial and toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artery diseases such as limb ischaemia, arrhythmia including peripheral failure and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and coular disorders, for wound healing, for promoting angiogenesis and as adjuvants to enhance immune responsiveness to specific antigen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 antibody VH domain amplifying PCR primer. This sequence is used in the exemplification of the invention
                                                                                                                     Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                Example 5; Page 224; 301pp; English.
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Human; antigen; platelet glycoprotein; GPIIIa; fibrin; ss; PCR; primer; anti-platelet binding protein; heavy chain variable region; phage display library; platelet aggregation thrombus formation; thromboembolism; unstable angina; saphenous vein bypass graft; percutaneous transluminal coronary angioplasty; atrial fibrillation; valvular heart disease; cerebrovascular disease; Trousseau's syndrome; peripheral vascular disease; arterial thromboembolism; acute diseaminated intravascular coagulation; extracorporeal device; prosthetic heart valve; auxiliary-subclavian venous thrombosis. Human heavy chain variable region gene cDNA library PCR primer #3. 25-SEP-2003 (first entry)

ВР.

ACD28137 standard; DNA; 23

ACD28137;

1 GAGGTGCAGCTGGTGGAGTCTG 22

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Homo sapiens.
  06-FEB-2003
      Filpula DR;
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The invention relates to a nucleic acid molecule, or its complement, that encodes an anti-platelet binding protein, isolated from a phage display clibrary by an in vitro selection process that comprises screening a diverse human antibody variable domain expression library against at least one human platelet antigen, and the human antibody variable domain expression library expresses single-chain proteins. Also included are an expression vector comprising the nucleic acid operably lined to a promoter, a host cell comprising the nucleic acid operably lined to a promoter, a host cell comprising the nucleic acid operably lined to a promoter, a host cell comprising the nucleic acid operably lined to a comprising protein encoded by the nucleic acid that binds to activated or non-activated human platelet glycoprotein IIb/IIIa receptor (and inhibites platelet adaption or thrombus formation), a substantially isolated and purified human antibody (or its fragment) that binds to a platelet binding protein, and a conjugate comprising a non-antigenic polymer covalently linked to the single-chain antigen-binding polymer covalently linked to the single-chain antigen-binding protein, and a conjugate comprising and polypeptide (i.e. the anti-platelet binding protein). The host cell and the anti-platelet binding protein is protein as useful for inhibiting platelet platelet binding protein for wholes blood. The vector is useful for inhibiting platelet to platelet mediated thrombus formation in a blood vessel, the blood vessel having an endothelial lining in need of treatment. The vector, the host cell, the anti-platelet binding protein or the vector is useful for preventing or traating conditions such as venous transluminal corronary angioplasty, atrial fibrilaria, vector, the host cell, the anti-platelet binding protein or platelet mediated formation of glosase, peripheral vascular disease, secondary prevention of arterial thromboembolism, unstable angina, acceptance of secular disease, peripheral intravascular disease, periphera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      programment of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid molecule encoding anti-platelet binding protein which is useful for inhibiting platelet aggregation or platelet mediated thrombus formation in blood and for treating venous thromboembolism.
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                            platelet binding protein antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-2000; 2000US-0185628P.
                                                                                                                                                                                                                                                                                                                                             27-FEB-2001; 2001US-00794189
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US2003027207-A1.
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Human, protein coordinate data; heavy chain variable domain; VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptoals-inducing ligand; Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; glioblastoma; graft versus host disease; antibody therapy; nootropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated antibody or its fragments such as VHCDR1 (heavy chain variable domain complementarity determining region), VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tunour necrosis factor; TNF-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL: RE), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or graft versus host disease, ALDS (acquired immune deficiency syndrome) or a neurodegenerative disorder. The invention is useful in antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragment, useful for treating, preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy. The present sequence is human VH domain amplifying PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lu
gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
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                                                                                                                                                              Human VH domain amplifying PCR primer, Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 241; 301pp; English.
                                        BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2002; 2002US-0369877P.
04-JUN-2002; 2002US-0384828P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2002; 2002US-0396591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2002; 2002US-0425737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2002; 2002WO-US040597
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                                      AAL62799 standard; DNA; 23
                                                                                                                         (first entry)
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Best Local Similarity 86.4<sup>†</sup>
Matches 19; Conservative
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                                                                                                                       06-OCT-2003
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                                                                                 AAL62799;
RESULT 694
                     AAL62799
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Gaps

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Indels

0; Mismatches

853 GAGGAGGAGCTGGTGGAGGCTG 874

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Gaps

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0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels

86.48;

Local Similarity 86.4 les 19; Conservative

Query Match Best Local S Matches

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21-FEB-2001; 2001US-0270134P.
27-MAR-2001; 2001US-0278952P.
                                                                                                                 21-FEB-2002; 2002US-00081775
                   ACD91445 standard; DNA; 23
                                                                                                                                                    Ramanathan CS, Feder JN,
                                                                                                                                    (RAMA/) RAMANATHAN C S.
                                                                                                                                         (FEDE/) FEDER J N.
(MINT/) MINTIER G A.
                                                                                                                                                            WPI; 2003-521919/49.
                                                                                                 US2003060409-A1.
                                                                                          Homo sapiens
                                  22-SEP-2003
                                                                                                         27-MAR-2003
                                                                                                                                                                                cancer.
                           ACD91445;
           RESULT 695
                ACD91445
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Example 35; Page 106; 149pp; English.
                                            874
                                                                                         1 GAGGTGCAGCTGGTGGAGTCTG 22
                                            853 GAGGAGGAGCTGGTGGAGGCTG
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27-MAR-2001; 2001US-0278927P.
                                                                                                                                                                                                                                                                                                                      ADA09673 standard; DNA; 23
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(RAMA/) RAMANATHAN C
(MINT/) MINTIER G A.
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(BARB/) BARBER L E.
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                                                                                                                                                                                                                                                                                                                                                                                                   ADA09673;
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                                                                                                                                                                                                                                            RESULT 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRBMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disease; arthritis; asthma; AIDS; psoriasis; graft-versus-host disease; systemic lupus erythematosus; reproductive disorder; varicocele; orchitis; neural disorder; Alzheimer's disease; Parkinson's disease; depression; schizophrenia; cardiovascular disorder; hypertension; acute heart failure; pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia; pone disorder; osteoporosis; pain; cancer; chromosome identification; gene therapy; PCR; primer; ss; variable heavy chain; VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein coupled receptor; HGPRBMY25; immune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human heavy chain variable region related PCR primer #3.
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1 GAGGTGCAGCTGGTGGAGTCTG 22
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Gaps ö

Local Similarity 86.4 les 19, Conservative

Query Match Best Loca Matches

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The invention relates to an isolated nucleic acid molecule encoding a G protein-coupled receptor HGPRBMY26. The nuclectide sequence comprises sequential nuclectide deletions from either the C-terminus or the N-terminus. Also included are a isolated polypeptide encoded by the nucleic acid, a recombinant vector comprising the nucleic acid, making a crecombinant host cell comprising the nucleic acid, making a pathological condition or a susceptibility to a pathological condition in testicular tissue of a subject, identifying a compound that modulates the biological activity of a human G-protein coupled receptor HGPRBMY26 (and a member consisting of NPAT/GRE or NPAT alpha 15, all undefined), and careening for candidate compounds capable of modulating activity of the HGPRBMY26 polypetide. The HGPRBMY26 polypetides, polypeutides, polypuncleotides, compounds or pharmaceutical preparations comprising HGPRBMY26 are useful for preventing, treating or ameliorating a male reproductive condition; can amine disorder or a condition, a testicular cancer, choriocarcinoma, nonseminoma, seminoma,
                                                                                                                                        male reproductive condition; amine disorder; testicular disorder; male resticular acancer; choricoarcinoma; nonseminoma; seminoma; seminoma; spermatogenesis; infertility; filmfelter's syndrome; XX male; epididymitis; genital wart; germinal cell aplasia of the testis; cryptorchidism; varicocele; immotile cilia syndrome; viral orchitis; premature puberty; incomplete puberty; Kallman syndrome; Cushing's syndrome; hyperprolactinaemia; haemochromatosis; congenital adrenal hyperplasais, follicle stimulating hormone deficiency; granulomatous disease; PCR; primer; antibody; heavy chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human G-protein coupled receptor HGPRBMY26 polypeptides and nucleic acids, useful for preventing, treating or ameliorating e.g. testicular disorder, choriocarcinoma, infertility, viral orchitis, or Cushing's
                                                                                                     Human anti-HGPRBMY26 antibody heavy chain PCR primer Hu VH-3 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barber LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feder JN, Ramanathan CS, Mintier GA, Cacace A,
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RESULT 698
                                                                                                                                                                                    Matches
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spermatogenesis, infertility, Klinefelter's syndrome, XX male, epididymitis, genital warts, germinal cell aplasia of the testis, cryptorchidism, varicocele, immotile cilia syndrome, viral orchitis, premature puberty; incomplete puberty, Kallman syndrome, Cushing's syndrome, hyperprolactinaemia, haemochromatosis, congenital adrenal hyperplasia, follicle stimulating hormone (FSH) deficiency and granulomatous disease. The present sequence is a PCR primer used in the isolation sequences encoding heavy or light chains (VH or VL) of anti-HGPRBMY26 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor; GPCR; HGPRBMY14; neuropeptide Y receptor; proliferative disorder; testicular cancer; NF-KB; disbetes mellitus; autoimmune disorder; male reproductive disorder; appetite disorder; VH; eating disorder; neurodegenerative disorder; human; PCR; primer; se.
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, useful for preparing a composition for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder e.g., testicular cancer, autoimmune or neurodegenerative
disorders, or diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HGPRBMY14 antibody VH gene amplifying primer, Hu VH3-5'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryseck
                                                                                                                                                                                               Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kornacker M,
                                                                                                                                                                   Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 30; Page 111; 166pp; English.
                                                                                                                                                                                                                                                                 853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                               GAGGTGCAGCTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                   0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2002; 2002US-00067649
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16-OCT-2001; 2001US-0329897P
                                                                                                                                                                                                   Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                             AAD59740 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2003 (first entry)
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Barber LE;
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RAMANATHAN C S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NELSON T C.
KORNACKER M.
RYSECK R.
CACACE A.
BARBER L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-687761/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peder JN,
                                                                                                                                                                                                                                                                                                                                                                                                              AAD59740;
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(KORN/) 1
(RYSE/) 1
(CACA/) (
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(RAMA/)
                                                                                                                                                                                                                                                                                                                                               RESULT
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identifying its binding partners, including agonists and antagonists. Antagonists to the polypeptide is useful in treating a disorder related to aberrant NF-kB activity or a proliferative disorder. HGPRBMY14 DNA and protein are also useful in treating neurodegenerative or autoimmune disorders, or diabetes mellitus. The present sequence is a RT-PCR primer used for amplifying human HGPRBMY14 antibody VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a human chemokine betal (Ckbl) protein (I) comprising a deletion in amino acid residues from the amino terminus and/or carboxy terminus of the 31 residue amino acid sequence (S1, see ADD06466). (I) has anti-HIV, neuroprotective, antithyroid, antiarthritic, antirheumatic, immunosuppressive, noctropic, antianifammatory, antiathatic, antiallergic, osteophatic, nephrotrophic, tuberculostatic, virucide, antiatherosclerotic and antimicrobial activities. (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic; antirheumatic; immunosuppressive; nootropic; antiinflammatory; antisathmatic; antiallergic; osteopathic; nephrotrophic; tuberculostatic; antiallergic; osteopathic; antiinflorbal; tuberculostatic; antiatherosclerotic; antimicrobial; infection; HIV; immune disorder; haematopotetic disorder; autoimmune disorder; multiple sclerosis; Grave's disease; arthritis; rheumatorid arthritis; transplant rejection; neurodegenerative disorder; hazheimer's disease; inflammatory disease; athma; allergic disorder; inflammatory kiney disease; glomerulomephritis; infectious disease; tuberculosis; hepatitis infection; herpes viral infection; viral infection; viral infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human chemokine betal protein comprising deletion in amino acids from amino and/or carboxy terminus, and is a fusion protein further comprising human serum albumin, is useful for treating multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; chemokine betal; Ckbl; anti-HIV; neuroprotective; antithyroid;
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                            Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human serum albumin; HSA; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 46; SEQ ID NO 35; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human VH domain PCR primer SEQ ID NO:35
                                                                                                                                                                                                                                                                                  853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                            1 GAGGTGCAGCTGGTGGAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
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                                                                                                                                                                                              0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD06499 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                         19; Conservative
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                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200297038-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                 Query Match
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for preventing infection, preferably viral (human immunodeficiency virus (HIV)) infection, in a cell, by contacting the cell with (I). (I) is also useful for treating a disease, such as HIV infection or immune disorders, haematopoietic disorders, autoimmune disorders multiple sclerosis, carve's disease, arthritis, rheumatoid arthritis, transplant rejection, Grave's disease, inflammatory disease, asthma, allergic disorders, inflammatory bowel disease, osteoarthritis, collitis, inflammatory kidney diseases, glomerulonephritis, infections, ustal infection, proliferative disorders or abherosclerosis, infection, viral infection, proliferative disorders or aberosclerosis, in an individual. (I) inhibits or abolishes the ability of HIV to bind to, viral infection, proliferative disorders or arberosclerosis, in an individual. (I) inhibits or abolishes the ability of HIV to bind to, viral sloacts a CCRS agonists or antagonists, stimulate chemotaxis of CCRS-expressing cells, inhibit CCRS ligand binding to a CCRS expressing cells, inhibit CCRS ingand binding to a CCRS molecule, or upregulate or downregulate CCRS expression. (I) is useful as an immunological probe for the differential identification of the tissues or cell-types. (I)-human serum albumin (HSA) fusion proceins are useful for diagnosing, treating and preventing various disorders in mammals, cell-types. (I)-human serum albumin (HSA) fusion proceins are useful for electrophoresis techniques, for raising antibodies, and to test the electrophoresis techniques, for raising antibodies, and to test the biological activities of the CKbl protein. (I)-HSA fusion protein portein portein cuseful for screening for molecules that bind to the CKbl protein portein portein cuseful for screening for molecules that bind to the CKbl protein portein portein portein cuseful the contact of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTRPC3 VH domain PCR primer, SEQ ID 272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-2004 (first entry)
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The present invention relates to novel proteins and their coding sequences (ADC83405) encoding human transient receptor potential condences (ADC83400-ADC83405) encoding human transient receptor potential channels. The coding sequences are useful for preparing a medicament for preventing, treating or ameliorating a medical condition, such as renal disorders, a disorder related to abbarrant calcium regulation; neural disorders, various choroid plexus neoplasms, prion disorder; cerebellum disorders, various choroid plexus neoplasms, prion disorders; movement disorders, a disorder that maps to or is associated with chromosome locus 9421.11-21.31; amyotropic lateral calcionis, early onset pulverulent cataract; infantile nephronophthisis, hypomagnesemia with secondary hypocalcemia; osteoporosis; DNA-repair deficiencies; xeroderma pigmentosum; UV sensitivity; gamma irridation sensitivity; pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's conditions involving increased levels of apurinic/apyrimidinic/abasic sites; disorders related to aberrant signal transduction; and disorders related to misregulation con this man evaruable from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                  useful in preventing, treating or ameliorating a medical condition, such as renal disorder, neural disorder e.g., Alzheimer's disease, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albumin fusion protein; therapeutic protein; HIV; osteoporosis; cancer;
                                                                                                nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wound; autoimmune disease; cardiovascular disease; hepatitis; multiple sclerosis; psoriasis; graft-versus-host disease; stroke; atherosclerosis; inflammation; anti-HIV; osteopathic; cytostatic; vulnerary; cardiant; hepatotropic; neuroprotective; antipsoriatic; immunosuppressive; cerebroprotective; antiatrateriosclerotic; antiinflammatory; human; VH domain; PCR; primer; ss
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  Bol
                                                                                                New human transient receptor potential channel (LTRPC3)
Lee L, Blanar MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which was used in an example from the invention
                                                                                                                                                                               Example 34; Page 436; 508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human VH domain DNA, PCR primer #3.
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  Wu S,
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2004 (first entry)
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(HASE/) HASELTINE W A.
                      Sun L;
                                                          WPI; 2003-278394/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS2003125247-A1
    Chen J,
                         Levesque PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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  Lee N,
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The present invention relates to albumin fusion proteins comprising any of the therapeutic proteins listed in the specification, or their fragments or variants, and an albumin protein or its fragments or variants. The invention also discloses pharmaceutical compositions comprising the albumin fusion proteins, a kit comprising the albumin fusion proteins, a kit comprising the albumin patient, that is modulated for treating a disease or disorder in a patient, that compositions and methods of the invention are useful in variant. The compositions and methods of the invention are useful in such as HIV, osteoporosis, cancer, wounds, autoimmune diseases, cardiovascular diseases, hepatitis, multiple sclerosis, psoriasis, graftversus-host disease, stroke, atherosclerosis and inflammation. The
                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a PCR primer. Note: The present sequence is given in the Sequence listing but is not mentioned elsewhere in the specification. The present sequence given as SEQ ID No:38 in the Sequence
                                                                                            diseases (e.g. HIV, cancer, atherosclerosis or stroke) comprises a therapeutic protein (e.g. cathepsin K or vascular endothelial growth
                                                                             New albumin fusion protein for diagnosing, preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        listing differs from that given on page 129
                                                                                                                                                         Disclosure; SEQ ID NO 38; 180pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2004 (first entry)
               Haseltine WA;
                                                                                                                            factor) and an albumin.
                                             WPI; 2003-810996/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003109021-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2003
             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 701
ઠે
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1 gaggrecageregregagrere 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD67296 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2003; 2003WO-US002397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2002; 2002US-0352011P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POIN-) POINTILLISTE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003062402-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD67296;
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 702
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD67296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINCE SERVICE SERVICE
                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                            a
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; metalloprotease; MMP-29; immune disorder; reproductive disorder; testicular disorder; gastrointestinal disorder; cardiovascular disorder; ovarian disorder; hepatic disorder; pulmonary disorder; renal disorder; metabolic disorder; neural disorder; immunary disease; sclerosis; skeletal muscle disorder; amyotrophic lateral sclerosis; gene therapy; immunomodulatory; antiinfertility; cytostatic; hepatotropic; pulmonary; nephrotropic; cardiant; vascular; neuroprotective; nootropic; muscular;
                                                                                                             Gaps
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MMP-29 antibody VH domain amplifying 5' PCR primer, VH3.
0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                  853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                 GAGGTGCAGCTGGTGGAGTCTG
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and polymucleotides encoding such proteins. Sequences of the invention are used to diagnose a pathological condition or a susceptibility to a medical condition in a subject. They are useful for preventing, treating, or ameliorating medical conditions such as immune condition or disorders, cancitions, female reproductive disorders, male reproductive disorders, orally disorders, posticular disorders, male reproductive disorders, cancer, hepatic disorders, pulmonary disorders, metabolic disorders, renal disorders, pulmonary disorders, metabolic disorders, renal disorders, pulmonary disorders, metabolic disorders, renal disorders, inflammatory diseases inflammatory diseases where proteases are either directly or indirectly involved in disease progression, sclerosis, amyotrophic lateral sclerosis or a disorder associated with aberrations of chromosome 2432 MMP-29 sequences are also useful in gene therapy. The present sequence is human MMP-29 antibody VH domain amplifying PCR primer. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                present invention relates to novel metalloprotease (MMP-29) proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                     New nucleic acid encoding a metalloprotease (MMP-29) useful for diagnosing a pathological condition or a susceptibility to a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                           Krystek SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                                  Example 37; Page 134; Opp; English
                                              Lee L,
                                              Feder JN,
                                                                                                                                   New nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 86.4
                                                                                                                                                                                        condition in a subject.
(KRYS/) KRYSTEK S R.
                                                                                       WPI; 2003-801269/75.
                                              Chen J,
                                              Wu S,
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apparatus combination; binding site collection; pattern recognition; profiling; screening; ss; PCR primer. Human antibody related PCR primer SEQ ID NO:14. 15-JAN-2004 (first entry)

New combination comprising an addressable collection of binding sites, software comprising instructions for pattern recognition and an imager for detecting patterns, useful for profiling a sample.

WPI; 2003-636736/60.

Ault-Riche D,

26-APR-2001; 2001US-0286764P

WU S. CHEN J. FEDER J N. LEE L.

(CHEN/) (FEDE/) H

WUSS/)

Siemers NO;

Ramanathan CS,

Jackson D,

Seguence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 19-JUN-2001; 2001US-0299378P 25-JUN-2001; 2001US-0300614P (FEDE/) RESULT 703
AAD62328
XX
AC AAD623:
XX
AC AAD623:
XX
DT 15-JAN
XX
DT 15-JAN
XX
CW HUMAN;
KW 3691ci
KW 16cod
KW 16cod
KW neuro
KW PCR;
XX
OS HOMO
XX
COS HOMO
XX
COS HOMO
XX
XX
COS HOM
XX
CO Matches

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Feder JN, Lee L, Chen J, Jacke
Chang H, Duclos F, Krystek SR;
(CHAN/) CHANG H.
(DUCL/) DUCLOS F.
(KRYS/) KRYSTEK S R.
                                                                                                                                                                                    WPI; 2003-810910/76
        The present invention describes a combination of apparatus (1)

Comprising: (a) an addressable collection of binding sites; and (b)

Software comprising instructions for pattern recognition and/or an imager

Comprises: (a) capture agents, where each capture agent is preselected to

specifically bind to a pre-selected tags; and (b) tagged reagents, each

Comprises a molecule and erage; where each locus in the

comprises a molecule and a tags, each tag is pre-selected to specifically

bind to a capture agent, where each agis pre-selected to specifically

comprises a molecule and a tags, each tag is bound to a capture agent,

bind to a capture agent, where each tags is bound to a capture agent,

comprises a molecule and a tag, each tag is bound to a capture agent,

comprises a tagged reagent with the capture agent, where

comprises a capture argued reagent with the capture agent, where

comprises a teach locus comprises the same pre-selected tag. Also

described: (1) a system for profiling samples; (2) a method for profiling

che database produced by the method of profiling a sample;

comprising capture system that displays a collection of binding

comprising capture agents bound to a solid support and tagged reagents;

and (6) a method for screening samples. The combination (1) is useful for

comprising a sample. The present sequence is used in the exemplification
                                   Disclosure; SEQ ID NO 14; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention.
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0
0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                              3; Indels
                                0; Mismatches
                                                              853 GAGGAGGTGGTGGAGGCTG 874
                                                                                           19; Conservative
                   Best Local Similarity
   Query Match
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AAD62328 standard; DNA; 23 BP.
                                                                                     15-JAN-2004 (first entry)
                                           AAD62328;
```

PCR primer used to amplify human HEAG2 VH domain, Hu VR3.

Human; HEAG2; potassium channel; aberrant amygdala function; autism; fear; neurodevelopmental disorder; psychopathologogical; schizophrenia; aggression; memory; emotional disorder; aberrant hypothalamus function; leptin receptor disorder; enargy-expenditure disorder; motion sickness; food intake disorder; bone remodeling disease; bone disorder; neurophysin-related disorder; aporter; contropic; neurophysin-related disorder; anorectic; antiemetic; VH domain; primer; PCR; ss.

19-JUN-2002; 2002US-00174613 US2003114354-A1. Homo sapiens. 19-JUN-2003.

LEE L.
CHEN J.
JACKSON D.
RAMANATHAN C S.
SIEMERS N O. (JACK/) (RAMA/) (SIEM/) (LEEL/)

FEDER J N.

2002US-0359370P. 2002US-0360000P. 2002US-0367500P.

2002US-0370227P. 2002US-0378950P. 2002US-0382617P.

08-APR-2002; 10-MAY-2002; 24-MAY-2002;

27-MAR-2002;

2002US-0350358P. 2002US-0351360P.

24-JAN-2002; 28-JAN-2002; 26-FEB-2002; 28-FEB-2002;

21-DEC-2001;

23-DEC-2002; 2002WO-US040891.

WO2003060071-A2.

24-JUL-2003.

ö The present invention provides novel polynucleotides encoding HEAG2 (human potassium channel) polypeptides, fragments and homologues thereof. The invention is useful for producing three-dimensional representation of a molecule or molecular complex comprising the structural coordinates of the PAS domain of HEAG2. The invention is also useful for treating conditions such as disorder associated with aberrant amygdala function, fear, neurodevelopmental psychopathological disorders, schizophrenia, autism, aggression, memory, emotional disorders, aberrant hypothalamus function, leptin receptor disorders, food intake disorders, energy-expenditure disorders, bone canceling functions, neurophysin-related disorders, bone disorders, bone remodeling disease, appetite suppression and motion sickness. The present sequence is PCR primer used to amplify human HEAG2 VH domain. This sequence is used in the exemplification of Computer for producing three-dimensional representation of molecule o molecular complex of PAS domain of potassium channel protein, useful designing compounds as potential modulators for treatment of Gaps ; 0 albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; PCR; primer; ss; human. 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; tive 0; Mismatches 3; Indels Human albumin fusion protein-related PCR primer SeqID1058. Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 853 GAGGAGGAGCTGGTGGAGGCTG 874 Example 32; Page 108; Opp; English. 1 GAGGTGCAGCTGGTGGAGTCTG 22 ADF15971 standard; DNA; 23 BP neurodevelopmental disorders 12-FEB-2004 (first entry) 19; Conservative Query Match Best Local Similarity Matches 19; Conserv the invention Homo sapiens. ADF15971; RESULT 704 ADF15971 g ठ

Ruben SM;

Li Y,

Roschke V,

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antibody (ABI) comprising an amino acid sequence of at least one, two or three complementarity determining regions (CDR) of a heavy chain variable (VH) domain of an antibody (AB2) that immunospecifically binds to a protein chemokine receptor (CCRS), at least one, two or three CDR regions of a light chain varaible (VL) domain of AB2 or at least one, two or three CDR regions of both a VH and a VL domain of AB2. The antibody is useful for detecting, diagnosing, prognosing or monitoring cancers and other hyperproliferative disorders and for treating, preventing or
                                                                                                                                                                                                                                                                                    New polypeptide comprising domains of an antibody that binds G-protein chemokine receptor CCRS is useful to detect, diagnose, prognose or monitor cancers and other hyperproliferative disorders and to treat or prevent a disease or disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ameliorating a disease or disorder. This sequence represents a primer used in the isolation of an immunoglobulin heavy chain variable region from antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a new isolated polynucleotide that encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                   Example 55; SEQ ID NO 25; 179pp; English.
                                                                        09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
         01-MAY-2002; 2002US-00135839.
                                                    09-FEB-2000; 2000US-0181258P.
                                                                                                                   09-FEB-2001; 2001US-00779879
                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                WPI; 2003-898066/82
                                                                                                                                                                                                     Rosen CA,
         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a PCR primer which was used in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Turner AJ, Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 107; SEQ ID NO 1058; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                               DELTA BIOTECHNOLOGY LTD.
28-MAY-2002, 2002US-0383123P.
05-JUN-2002, 2002US-0385708P.
10-JUL-2002, 2002US-0394625P.
24-JUL-2002, 2002US-0394625P.
13-AUG-2002, 2002US-040213IP.
11-AUG-2002, 2002US-041355P.
18-SEP-2002, 2002US-0411426P.
18-SEP-2002, 2002US-0411426P.
23-OCT-2002, 2002US-041191P.
23-OCT-2002, 2002US-041191P.
                                                                                                                                                                                                                                                                                                                 (DELZ ) DELTA BIOTECHNOLOGY L?
(PRIN-) PRINCIPIA PHARM CORP.
                                                                                                                                                                                                                                                05-NOV-2002; 2002US-0423623P
                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-598517/56
                                                                                                                                                                                                                                                                                                                                                                               Ballance DJ,
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protease-42; thiol protease; protein co-ordinate data; C2 family;
calpain superfamily; hepatotropic; nephrotropic; gynaecological;
KW antiinflammatory; cytostatic; vasotropic; cardiant; ophthalmological;
M auditory; gene therapy; vaccine; hypercalpain activity;
M auditory; gene therapy; vaccine; hypercalpain activity;
KW demale reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW female reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW female reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW paccatur menopause; pelvic inflammatory disease; tubal pregnancy;
KW chlamydial infection; neural disorder; hepatic disorder; immune disorder;
M nematopoletic disorder; renal disorder; pulmonary disorder;
M inflammation; gastrointestinal disorder; colon disorder;
M proliferative disorder; colon; gastrointestinal tissue; colon cancer;
CW proliferative disorder; colon; gastrointestinal tissue; colon cancer;
M hearing loss; multiple sclerosis; cataract; myocarditis; human; PCR;
M primer; ss; VH domain.
                                            ö
                                            Gaps
                                            ö
                                                                                                                                                                                                                                                                                                                                                                      Human protease-42 protein-related VH domain PCR primer SeqID70.
0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                                       874
                                                                                                                               1 gaggrecageregregaerere 22
                                                                                       853 GAGGAGGAGCTGGTGGAGGCTG
                    86.4%;
                                                                                                                                                                                                                                           ADF70252 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                              (first entry)
                      Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                12-FEB-2004
                                                                                                                                                                                                                                                                                     ADF70252;
    Query Match
                                                                                                                                                                                                RESULT 706
                                                                                                                                                                                                                    ADF70252
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ઠે 셤 ADF72145 standard; DNA; 23 BP.

Homo sapiens.

cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5; cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring; cancer; hyperproliferative disorder; human; HDGNR10; PCR; primer; ss; immunoglobulin; heavy chain; variable region.

US2003166024-A1

04-SEP-2003

Homo sapiens

Human immunoglobulin variable heavy chain primer seq id 25.

(first entry)

12-FEB-2004

RESULT 705
ADP72145
AC ADP72145
XX AC ADP7214
XX DT 12-FEB
XX CACCE
XX CACCE
XX CACCE
XX CACCE
XX CACCE
XW CACCE
XX CACC

ADF72145;

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(NELS/)
(KORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEDE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel DNA sequences encoding protease-42

Eamily and the calpain superfamily. Calpains have been associated with

Camily and the calpain superfamily. Calpains have been associated with

numerous disease states. The invention may allow development of compounds

with hepatotropic, nephrotropic, gynaecological, antinflammatory,

cytostatic, vasotropic, cardiant, ophthalmological or auditory

cytostatic, row advances provided may be useful for preparing a

composition for diagnosing, preventing, treating or ameliorating a

calpain activity, a disorder associated with deficiencies in

calpain activity, a disorder associated with deficiencies in

calpain activity, a disorder associated with deficiencies in

calpain activity, a disorder related to aberrant cell cycle

conterine bleeding, dysfunction, a disorder related to

aberrant calcium regulation, a disorder related to

aberrant calcium regulation, a disorder related to

conterine bleeding, dysfunction, pelvic inflammatory disease, tubal

conterine bleeding, dysfunction, pelvic aromatase deficiency, premature

conterine bleeding, dysfunction, pelvic aromatase deficiency planenary

conterine disorders, haematopoletic disorders, renal disorders, pulmonary

disorders, an inflammatory condition, an inflammatory disease

conterine disorders haematopoletic disorders, renal disorders, pulmonary

disorders, an inflammatory condition, an inflammatory disease

conservation, either directly or indirectly, are involved in disease

conservation, either directly or indirectly, are involved in disease

conservation, increased an inflammatory condition, an inflammatory disorders, polon disorders, polon disorders, pelvic 
                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a human cysteine protease, useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                              a composition for diagnosing, preventing or treating e.g., neural, hepatic, immune, hematopoietic, renal or pulmonary disorders.
                                                                                                                                                                                                                                                                                               Nayeem A, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 33; SEQ ID NO 70; 449pp; English.
                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                            Chen J, Feder JN,
                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                               14-MAR-2003; 2003WO-US007984
                                                                                                                                                                                      14-MAR-2002; 2002US-0364941P
                                                                                                                                                                                                                                                                                                                                              WPI; 2003-767513/72
                           WO2003078594-A2
                                                                             25-SEP-2003
                                                                                                                                                                                                                                                                                            Duclos F,
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ö
                                   Gaps
                                   ö
ch 0.5%; Score 17.2; DB 1; Length 23; 1 Similarity 86.4%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 3; Indels
                Local Similarity
Query Match
                                 Matches
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AAD63842 standard; DNA; 23 AAD63842; RESULT 707 AAD63842

ВЪ.

(first entry) 12-FEB-2004

Human HGPRBMY14 antibody VH domain amplifying PCR primer, Hu VH3-5'.

Human; G-protein coupled receptor; GPCR; hyper immune activity; melanoma; eating; appetite disorder; male reproductive disorder; testicular cancer; autoimmune disorder; hypercongenital condition; birth defect; vulnerary;

ADF18235 standard; DNA; 23 BP.

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RESULT 708 ADF18235

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid molecule encoding G-protein coupled receptor (GPCR). The methods and compositions of the present invention are useful for preventing, treating and/or ameliorating a disorder related to aberrant MTR-kB activity, disorder related to aberrant neuropeptide Y receptor activity, a disorder directly linked to aberrant neuropeptide X receptor activity, an eating or appetite disorder, a disorder linked to aberrant DNA synthesis, male reproductive disorder, immune activity, hypercongenital conditions, birth defects, necrotic lesions, wounds, disorders related to aberrant signal transduction, the skin, melanoma, foetal lung disorder, disorder of the breast cancer, in addition to other proliferative diseases and/or disorders in the activity and disorder disorder disorder cancer, in addition to other proliferative diseases and/or disorders in the activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and disorders related to abnormal populations of cells or activity and ac
necrotic lesion, signal transduction, proliferative disorder, anorectic, foetal lung disorder, proliferative disease, dermatological, anti-HIV, gene therapy, cancer, angiogenesis, gynaecological, relaxant, PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissues in the G1 or G2 phase of the cell cycle, disorders related to abnormal populations of cells or tissues in the S or M phase of the cell cycle, disorders related to aberrant smooth muscle contraction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acids encoding G-protein coupled receptor polypeptide, useful for diagnosing, treating, ameliorating and/or preventing disorders, such as cancer, and autoimmune, gynecological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenesis. The invention is useful in gene therapy. The present sequence is a PCR primer used to amplify human HGPRBMY14 antibody VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson TC, Kornacker MG, Ryseck R;
DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001US-026525P.
16-OCT-2001; 2001US-0329897P.
05-FEB-2002; 2002US-00067649.
                                                                                                                                                                                                                                                                                                             14-NOV-2002; 2002US-00295693.
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Barber LE, Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEDER J N.
RAMANATHAN C S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NELSON T C.
KORNACKER M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYSECK R.
CACACE A.
BARBER L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenic diseases.
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                                                                                                                                                                                                US2003198976-A1
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                        23-OCT-2003,
                                                                                       primer; ss.
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(CACA/) C
(BARB/) F
(BOLD/) E
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gene therapy; vaccine; scFv; TR01G03; PCR; primer; ss.
                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                WPI; 2003-853871/79.
                                                     WO2003086301-A2.
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                                                                               23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; ss.
                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG30372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 710
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                                                                                          Human; TL5; cytostatic; anti-HIV; immunosuppressive; immunostimulant;
virucide; dermatological; antiinflammatory; antirheumatic; antiarthritic;
neuroprotective; muscular-gen.; antiasthmatic; antiallergic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of PCR primer Hu VH3-5' for the human heavy chain variable region (VH). A set of primer sequences ADF18313-ADF18268 was used in the identification and cloning of VH and VL domains from antibody-expressing cell lines. The invention relates to antibodies that specifically bind to TL5. These are used in the diagnosis, prevention or reatment of a disease or disorder such as an autoimmune disease, transplant rejection, cancer (especially colon cancer, lymphadenopathy, transplant rejection, cancer (especially colon cancer, breast cancer, und Kaposi's sarcoma), an immunodeficiency syndrome, or an inflammatory disease such as asthma or allergy.
                                                                                                                                                                                                                                                                                                                                                                                                       New antibody that specifically bind to TL5, useful for diagnosing, preventing, treating or ameliorating diseases (e.g. cancer, autoimmune disease, inflammation or transplant rejection), and in immunophenotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TR2; orphan nuclear receptor; cytostatic; immunosuppressive; virucide; immunostimulant; dermatological; antiinflammatory; antirheumatic; antiathritic; neuroprotective; muscular; antiasthmatic; antiallergic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; es 19; Conservative 0; Mismatches 3; Indels
                                                                 Antibody heavy chain variable region PCR primer Hu VH3-5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-TR2 antibody VH domain amplifying primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 13; 195pp; English.
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                                                                                                                                                                                                                                            10-APR-2003; 2003WO-US010956
                                                                                                                                                                                                                                                                     15-APR-2002; 2002US-0372087P
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                                        12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-854097/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope mapping.
                                                                                                                                                                                     WO2003089575-A2.
                                                                                                                                   PCR; gene; ss.
                                                                                                                                                               Homo sapiens.
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               ADF18235;
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The invention relates to an isolated antibody (A1) that specifically binds orphan nuclear receptor TR2 or that competitively inhibits the binding of an antibody to TR2. The antibody and methods are useful in inhibiting the growth of or K11ling orphan nuclear receptor TR2 expressing cells and treating, preventing or ameliorating a disease or disorder selected from an autoimmune disease, graft-versus-host disease, transplant rejection, cancer, herpes simplex virus infection and an immunodeficiency, e.g. lupus erythematous, rheumatoid arthritis, multiple sollerosis, mysathenia gravis, or inflammatory disorders (e.g. asthma or allergies). The antibody may also be used in immunoassays for qualitatively and quantitatively measuring levels of TR2 polypeptides in biological samples, in immunophenotyphing of cells lines and biological samples, or in epitope mapping. Sequences ACFS8401-436 represent PCR primers for amplifying the VH and VL domains of an anti-TR2 antibody
                                                                                                                                                                                                                                                                                               New antibodies that specifically bind to orphan nuclear receptor useful for diagnosing, preventing, treating or ameliorating diseases, e.g. cancer, autoimmune diseases, inflammation or viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMAD; VH; CDR; complementarity determining region; VL; scFv; single chain antibody; antidiabetic; type II diabetes; human; PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer Hu VH3-5' used to amplify human VH domain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 156; Opp; English.
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                                                        12-APR-2002; 2002US-0371722P.
10-APR-2003; 2003WO-US010955
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Matches 19; Conservative
                                                                                                                 (HUMA-) HUMAN GENOME SCI
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Gaps

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The invention describes a new isolated nucleic acid molecule comprising:

a polynucleotide fragment or complement of the cDNA sequence; a performance of the cDNA sequence; a comprising nucleotides described a comprising nucleotides 4-1404 or 1-1404 of the polynucleotide sequence encoding a polypeptide, or its fragment, domain or epitope. The polynucleotide sequence does not thyridise to a nucleotide sequence having only A or I residues. The polypeptide comprises a fully defined 335-amino acid sequence, or its amino acids 2-335 without the start methionine or 1-335 including the start methionine or 1-335 including the start methionine or 1-335 including the start methionine acitivity, a disorder associated with deficiencies in methionine activity, a disorder associated with hypermethionine activity, a confidence of paramethy activity, a disorder associated with hypermethionine activity, a disorder associated with hypermethionine activity, a confidence of the colon or ovarian cancer. This sequence of represents a primer used to isolate DNA encoding a human heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotide useful for detecting single nucleotide polymorphisms
                              New nucleic acid encoding a human methionine aminopeptidase, useful for preparing a composition for diagnosing, preventing or treating e.g., neural, metabolic, vascular, immune or inflammatory disorders or ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable domain of antibodies directed against novel human methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; single nucleotide polymorphism; microarray; side effect; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single nucleotide polymorphism detection primer, SEQ ID No 1688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                   Example 34; SEQ ID NO 38; 183pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 GAGGAGGTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2002; 2002JP-00034717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aminopeptidase, Protease-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%;
Best Local Similarity 86.4%;
Matches 19; Conservative
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ID ADF88105 standard; DNA; 23
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WPI; 2003-900678/82.
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                                                                                                                                                                                                                                                  The invention relates to a novel antibody that specifically binds to a GMAD polypeptide comprising a first amino acid sequence that is at least 95% identical to a second amino acid sequence of a VH CDR (complementarity determining region) or VL CDR of an scPv (single chain antibody molecule). The antibody of the invention demonstrates antidiabetic activity and may be useful for diagnosing, monitoring, treating, preventing or ameliorating type II diabetes. The current sequence is that of the PCR primer which was used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gynaecological; antiinflammatory; cytostatic; vasotropic; neuroprotective; gene therapy; vaccine; methionine activity disorder; methionine activity deficiency; hypermethionine activity; protease regulation; cell cycle regulation; neural disorder; metabolic disorder; vascular disorder; immune disorder; inflammatory condition; proliferative disorder; colon cancer; ovarian cancer; human; methionine aminopeptidase; Protease-39;
                                                                                                                                   New antibody that specifically binds to GWAD polypeptide, useful for diagnosing, monitoring, treating, preventing or ameliorating type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heavy chain variable domain primer seq id 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                    Claim 2; SEQ ID NO 5; 410pp; English.
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                                                            Chowdhury P;
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08-MAR-2002; 2002US-0362872P.
                        (HUMA-) HUMAN GENOME SCI INC
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NELSON T C.
BASSOLINO D A.
KRYSTEK S R.
NAGLICH J.
                                                            Albert VR,
                                                                                                 WPI; 2003-804305/75
                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS2003204070-A1
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                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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(NELS/)
(BASS/)
(KRYS/)
(NAGL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEN/)
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Matches
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                       The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1202 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene is neeful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism one of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human growth factor; epidermal growth factor-8; BGS-8; immunosuppressive; haemostatic; grasecological; antiinfertility; hepatotropic; cardiant; cytostatic; BGF agonist; gene therapy; immune disorder; cardiant; haematopoietic disorder; reproductive disorder; reproductive disorder; hepatic disorder; cardiovascular disorder; proliferative disorder; cancer; aberrant growth factor regulation; wound repair; angiogenesis regulation; epithelial cell growth regulation; epidermal cell growth regulation; EGF receptor; proliferative condition; lymph node; uterus; pancreas; liver; heart; stomach; lung; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding a human epidermal growth factor, BGS-8, useful for preventing, treating or ameliorating immune, hematopoietic, male or female reproductive, hepatic, cardiovascular, or proliferative
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human growth factor protein BGS-8-related PCR primer SeqID29.
                                                                                                                                                                                                                                                                             0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                   Sequence 23 BP; 5 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          0; Mismatches
Claim 2; SEQ ID NO 1688; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 32; SEQ ID NO 29; 330pp; English
                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                     1652 CCGAGGACAACGTGATGAAGAT 1673
                                                                                                                                                                                                                                                                                                                                                        23 CTGAGAACAACGTGGTGAAGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG16167 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2001; 2001US-0298340P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2002; 2002WO-US019442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                          Local Similarity 86.4 es 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu S, Feder J, Lee LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-167439/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2002102319-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG16167;
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         713
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 71
ADG16167
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This invention relates to a novel DNA sequence encoding a human growth factor with homology to epidermal growth factor-8 (BGS-8). The invention may be useful for the development of compounds with an immunosuppressive, haemostatic, gynaecological, antiinfertility, hepatotropic, cardiant or cytostatic activity which act as BGF agonists. In addition the genetic acquences of the invention may be useful for gene therapy. The invention may be useful for preventing, treating or ameliorating medical conditions, such as immune disorder, haematopoietic disorder, a hepatic disorder, a male or female reproductive disorder, a hepatic disorder, a cardiovascular disorder, a proliferative disorder, cancer, or a disorder related to aberrant growth factor regulation, wound repair, a disorder related to aberrant growth factor regulation, wound repair, or regulation, epithelial or epidermal call growth regulation or the BGF receptor, or a proliferative condition involving one or more lymph node, uterus, liver, heart, stomach, lung and pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; human serum albumin; HSA; therapeutic protein; helf-life; in vitro biological activity; in vivo biological activity; metabolic disorder; endocrine disorder; diabetes; type 1; type 2; diabetes-related condition; hyperglycaemia; neural disorder; neuropathy; extinopathy; cardiovaecular disorder; heart disease; renal disorder; obesity; glucose level maintenance; weight loss; antidiabetic; cardiant; anorectic; ophthalmological; gene therapy; antibody; VH domain; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human antibody VH domain PCR primer Hu VH3-5', SEQ ID NO:344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH21547 standard; DNA; 23 BP.
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2002US-0360000P.
2002US-0367500P.
2002US-0370227P.
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2002US-0402708P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-2002; 2002WO-US040892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003059934-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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28-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2002;
08-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2002;
24-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH21547;
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WPI; 2003-598501/56 RESULT 715 ADG68058 Matches 셤 ઠ

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The invention relates to fusion proteins comprising human serum albumin (ADH21530) and a therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein protein may be fused to the N-terminus, the C-terminus or both termin of albumin via a linker. The albumin component of the fusion proteins or prolongs the shelf-life and the in vitro and vivo biological activity of the proteins compared with those of the corresponding therapeutic proteins on their own. The invention also relates to nucleic acids of albumin fusion proteins, vectors and host cells comprising an albumin fusion protein, the method of extending the shelf-life of a long and protein, the method of extending the shelf-life of a cherapeutic protein, the method of extending the shelf-life of a cherapeutic protein protein with albumin fusion proteins may be used using an albumin fusion protein in the albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes. The albumin fusion proteins may be used to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders (especially heart disease, renal disorders and obesity. The proteins may also be used in a method of maintaining a basal glucose level in a gating and in a method for losing weight. The present sequence is
New albumin fusion protein, useful for preparing a composition for
                                                                                                                                                                             Example 91; SEQ ID NO 344; 1086pp; English.
                                                       treating diabetes mellitus
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New TRP-PLIK2 nucleic acid and its splice variants, useful for manufacturing a medicament for preventing, treating or ameliorating a medical condition, e.g. renal, inflammatory or reproductive disorders.

Example 33; SEQ ID NO 274; 457pp; English.

Blanar M,

Chang H, Lee L,

Chen J, Feder J, Wu S,

Lee N,

WPI; 2003-148463/14.

(BRIM) BRISTOL-MYERS SQUIBB CO

22-MAY-2001; 2001US-0292599P. 08-MAR-2002; 2002US-0362944P. 22-MAY-2002; 2002WO-US016164.

28-NOV-2002

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                                                                                               Gaps
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                                           Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; les 19; Conservative 0; Mismatches 3; Indels
Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                          853 GAGGAGGTGGTGGAGGCTG 874
                                                   Query Match
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neuron degeneration; neurogenic inflammation; allergy; immunodeficiency; excessive immune activation; visual defect; hearing disorder; pain; cancer; hypertension; cardiovascular disease; Calcium homeostasis; osteoporosis; hypercalcuric stone disease; chronic renal failure; prollferative disorder; ischaemia-reperfusion injury; heart failure; immuno-compromised condition; HIV infection; NF-kappa-B regulation; apoptosis regulation; NF-kappa-B activity; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                 gynaecological; immunomodulatory; cardiant; cytostatic; neuroprotective; antiviral; anti-HIV; gene therapy; immune disorder; haematopoietic disorder; inflammatory disorder; renal disorder; reproductive disorder; hepatic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis;
                                                                                                                                                                                                                                                                                               RP-PLIK2; transient receptor potential channel; antiinflammatory;
                                                                                                                                                                                                                                                       Human TRP-PLIK2 gene-related Ab VH domain PCR primer SegID274.
                                                                                                                                                                                                                                                                                                                                                                                                      hyper transient receptor potential activity, prostate cancer, testicular cancer, chromosome 9q21 aberration, amyotrophic lateral sclesosis, frontchemporal dementia; early-onset pulverulent cataract; infantile nephronopthisis;
1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                             ADG68058 standard; DNA; 23 BP
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypomagnesaemia;
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                                                                                                                                                                                                                   11-MAR-2004
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WO200294999-A2

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This invention relates to a novel isolated human TRP-PLIK2 (transient receptor potential channel) nucleic acid sequence and the protein encoded by it. The invention may be useful for the development of compounds with an antitinfilammatory, graaecological, immunomodulatory, cardiant, crytostatic, neuroprotective, antiviral or anti-HIV activity. In addition, the DNA sequence may be useful for gene therapy. The invention may therefore be useful for manufacturing a medicalement for preventing, treating or ameliorating a medical condition, for example immune disorders, hemptopietic disorders, inflammatory disorders, renal disorders, reproductive disorders, hepatic disorders, a disorder related consorder related consorder related to chromosome 9g21.2-22 aberrations, testicular cancer, diseases related to chromosome 9g21.2-22 aberrations, amyotrophic lateral scalerosis with frontotemporal dementia, early-onset curvor protein a familial hamophagocytic lymphonistiocytosis, amyotrophic ataract, infanilial hamophagocytic lymphonistiocytosis, neuron degeneration, neurogenic inflammation, visual defects, hearing disorder, pain, cancer, hypertension, oratiovascular diseases, diseases associated with disturbances in Calcium homeostasis including costeoporosis, hypercalcular, stone disease, chronic renal failure, immuno-compromised conditions, HIV infection, disorders associated with aberrant compromised conditions, HIV infection, disorders associated with aberrant capoptosis regulation, disorders associated with aberrant capoptosis regulation, disorders associated with destrable.

C decreasing or increasing IRB activity would be therapeutically desirable and disorders in which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human VEGF-2 related PCR primer SEQ ID No 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 checrechecrecrechen 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5
Best Local Similarity 86.4
Matches 19; Conservative
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New isolated polynucleotide encoding an antibody which inhibits a VEGF-2 polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant VEGF-2 expression or function, e.g. cancer or
infectious disease; autoimmune disease; rheumatoid arthritis; Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis; angiogenesis; wound healing; vascular tissue repair; human; PCR; primer;
                                                                                                                                                                                 Wager RE;
                                                                                                                                                                                                                                                                        Example 32; Page 240; 425pp; English
                                                                                                                                                                                Albert VR, Ruben SM,
                                                                                                             12-APR-2002; 2002WO-US011474.
                                                                                                                               13-APR-2001; 2001US-0283385P.
24-JAN-2002; 2002US-0350366P.
                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                    WPI; 2003-092991/08.
                                                                     WO200283704-A1
                                                                                                                                                                                                                                                      inflammation.
                                                 Unidentified.
                                                                                         24-OCT-2002.
                                                                                                                                                                                Rosen CA,
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The invention relates to an isolated polynuclectide encoding a first antibody at least 91.00% identical to a second antibody comprising an emino acid sequence selected from at least one, two or three CDR region(s) of a VH or VL domain where the first antibody in the CDR immunospecifically inhibits a VEGF-2 polypeptide. The isolated polynuclectide is useful in diagnosing, treating, preventing, prognosing, ameliorating or monitoring diseases associated with aberrant VEGF-2 or VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function, csuch as cancer and other proliferative disorders (e.g. cerebral disorders (arrhythmias), cerebroacular disorders (e.g. cerebral anoxia), inflammatory diseases, infectious diseases, autoimmune diseases (e.g. rheumatoid arthritis, Systemic Lupus Erythematosus, allergies), diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and antibodies may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polynucleotide and polypeptide may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors, and for the production of diagnostics and therapeutics to treat human diseases. This polynucleotide sequence represents a PCR primer used in the exemplification of the invention

Gaps ö Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 0; Mismatches 86.48; 19; Conservative Query Match Best Local Similarity Matches

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ACA54716 standard; DNA; 23 ACA54716; RESULT 717

05-JUN-2003 (first entry)

Human NF-kappaB associated antibody VH domain PCR primer #3.

Human; nuclear factor-kappaB; NP-kappaB; immune disorder; cancer; inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;

intrucings integrated and integrated by the stroke integrated by the st hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV; X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti; influenza; rheumatoid arthritis; inflammatory bowel disease; colitis; haematopoietic tumour; hyper-IgM syndrome; viral infection; asthma; antiarteriosclerotic, PCR; primer; ss.

Homo sapiens.

WO200286076-A2.

31-OCT-2002

19-APR-2002; 2002WO-US012636,

19-APR-2001; 2001US-0284962P. 26-APR-2001; 2001US-0286645P.

09-JAN-2002; 2002US-0346986P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Carman J, Feder J, Nadler S;

WPI; 2003-093119/08

Novel NF-kappaB-associated polypeptides and polynucleotides useful for diagnosing, treating and preventing cancer, hepatic disorders, aberrant apoptosis, viral infections, autoimmune disorders, asthma and stroke.

Example 33; Page 407; 608pp; English.

The present invention relates to the isolation of human nuclear factorkappaB (NF-kappaB) associated polypeptides and polynucleotides. The NFkappaB associated polypeptide and polynucleotide sequences are useful for
preventing, treating or ameliorating various disorders including immune
disorders, inflammatory disorders, cancers, disorders relating to
aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
hematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal
dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
hepatitis B, hepatitis C, Epstein Barr virus (EBN), influenza),
rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
cheumatoid arthritis, activity disorders related to aberrant acute phase
contemporate immune activity, disorders related to aberrant acute phase
contemporate immune activity, disorders related to aberrant signal
chapter immune activity, disorders related to aberrant signal
chapter immune activity, disorders related to aberrant signal
chapter and phyperpoliferative disorders related to aberrant signal
chapters and phyperpoliferative disorders diseases of the pancreas disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial infections, cardiovascular disorders, infertility, psoriasis and haemolytic anaemia. The present sequence represents a PCR primer used in the examples of the present invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps .. 0 0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; Indels 86.4%; Preu. ... 19; Conservative Best Local Similarity Query Match Matches

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The present invention relates to the isolation of a novel member of the immunoglobulin (Ig) superfamily, human antigen presenting cell expression (APEXX4, and variants (APEXX401) thereof.

The polypeptides of the invention are useful for treating, preventing or ameliorating medical conditions, such as immunological disorders (e.g. rheumatoid arthritis, inflammatory bowel disease, sepsis, acne or host versus graft disease), haematopoietic disorders, disorders related to aberrant leukcoyre proliferation, differentiation, migration or activation, disorders related to aberrant activation of natural killer cells, disorders of the spleen, inflammatory disorders, and proliferative disorders (e.g. neoplasms). APEX4, APEX4v1 and APEXsv1 polypeptides, and proliferation, migration, migration and activation in various cells, tissues and organisms. The polynucleotides sequences are are useful in Chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New APEX (antigen presenting cell expression) 4 and APEX4v1 proteins and nucleic acids, useful for treating or preventing e.g. immunological disorders, hematopoeitic and/or proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organisms. The polynucleotides sequences are are useful in chromosome identification, chromosome mapping, as molecular weight markers, and in gene therapy. The present sequence represents a PCR primer used in the examples of the present invention
                                                                                                                                                                                                                                     PCR primer #3 for DNA encoding VH domain of anti-APEX4 human antibody.
                                                                                                                                                                                                                                                                        Human; immunoglobulin superfamily; Ig; APEX4; sepsis; acne; antigen presenting cell expression 4; immunological disorder; rheumatoid arthritis; inflammatory bowel disease; activation; host-versus-graft disease; haematopoietic disorder; migration; leukocyte proliferation; differentiation; T-cell activation; B-cell activation; natural killar cell; splean disorder; inflammatory disorder; proliferative disorder; neoplasm; immunosuppressive; antinflammatory; antiarthritis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 28; Page 296; 368pp; English.
1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2001; 2001US-0281223P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-2002; 2002WO-US008721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001; 2001US-0278037P
                                                                                                                     23
                                                                                                                                                                                                    (first entry)
                                                                                                                     ABX08633 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-040582/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200277173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                  20-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finger J;
                                                                                                                                                             ABX08633;
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The invention comprises the amino acid and coding sequence of B7-related (BSL2) fusion proteins. The B7-related fusion proteins of the invention are useful for modulating the activation of immune or inflammatory response cells (e.g. T cells). The B7-related fusion proteins are useful for treating or preventing: transplantation rejection; graft versus host disease; asthma; chronic obstructive pulmonary disease; cancers; viral infections (e.g. HIV, herpes or encephalitis); and autoimmune disease (e.g. rheumatoid arthritis, multiple sclerosis or psoriasis). The present DNA sequence represents a PCR primer that was used to amplify the DNA encoding the variable domain of an antibody that is specific for a B7-
                                                                                                                                                          PCR, ss; gene therapy; B7-related fusion protein; BSL2; viral infection; immune response modulation; inflammatory response modulation; cancer; transplantation rejection; graft versus host disease; asthma; herpes; chronic obstructive pulmonary disease; HIV; encephalitis; pooriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated B7-related nucleic acid fusion molecules and fusion polypeptides, useful for diagnostic applications, modulating the activation of immune or inflammatory response cells, preventing or treating cancer or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 17.2; DB 1; Length 23;
86.4%; Pred. No. 1.1e+03;
tive 0; Mismatches 3; Indels
                                                                                                                         B7-specific antibody VH domain PCR primer - SEQ ID No 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Page 161; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
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               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2001; 2001US-00875338.
15-FEB-2002; 2002US-00077023.
                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2002; 2002WO-US018049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC78591 standard; DNA; 23
               ABT15964 standard; DNA; 23
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mikesell GE, Shen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-140629/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related protein
                                                                                                                                                                                                                                                                                                                     WO200299119-A2
                                                                                          28-MAR-2003
                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                      12-DEC-2002.
                                                    ABT15964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC78591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 720
ACC78591
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ABT15964
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Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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Gaps

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The invention relates to an albumin fusion protein comprising a therapeutic protein.X, and albumin, its variant or fragment. The albumin therapeutic protein.X and albumin, its variant or fragment. The albumin fusion protein to regament, L is a peptide linker and R2 is albumin. The albumin fusion protein is useful for treating a disease or disorder that is modulated by therapeutic protein.X (claimed), such as cancer; infections (bacterial, viral, fungal, parasitic); or immune (AIDS, asthma); hematopoietic (leukemia, sepsis); reproductive (cystic fibrosis, endometriosis); musculoskeletal (osteoporosis, osteoarthritis); cardiovascular (congestive heart failure, atherosclerosis); neural/sensory (ataxia, attention deficit disorders, autism); respiratory (emphysema, bronchitis); endocrine (goiter, glomerulonephritis); chiquestive (ulcer, cirrhosis); or connective/epithelial (lupus, keloids) disorders. Sequences ACC78589-624 represent PCR primers for amplifying human VH and VL domains, that can be used to create multifusion proteins
                                                                         Albumin, HA; cytostatic; antibacterial; virucide; fungicide; anti-HIV; antiasthmatic; osteopathic; antiarthritic; antiinflammatory; nootropic; neuroprotective; anti-thyroid; anti-ulcer; hepatotropic; vulnerary; protein therapy; growth hormone; hGH; VL; VH; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ss; PCR; VEGF; vascular endothelial growth factor; human; cancer; angiogenesis; neoplastic proliferation; primer; RT-PCR; reverse transcriptase PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New albumin fusion protein comprising a therapeutic protein:X, and albumin, its variant or fragment, useful for treating a cancer, AIDS asthma, leukemia, sepsis, endometriosis, osteoporosis, atherosclerosis, autism, or emphysema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                        Human VH domains amplifying forward primer VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 60; Page 391; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 daggrecageregredagrere 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human VEGFR-1 RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX90509 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                    05-OCT-2001; 2001US-0327281P.
                                                                                                                                                                                                                                                                                            04-OCT-2002; 2002WO-US031794.
                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 86.4%;
nes 19; Conservative
  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-468174/44.
                                                                                                                                                                                                                   WO2003030821-A2.
                                                                                                                                                                              Homo sapiens.
18-AUG-2003
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                                                                                                                                                                                                                                                         17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
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Matches
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The invention relates to a composition comprising an antisense oligomucleotide directed against vascular endothelial growth factor (VEGF). The antisense oligomucleotide is useful for preparing a composition treating cancer, neoplastic proliferation, abnormal cellular proliferation and preventing angiogenesis. The present sequence is a proliferation and preventing angiogenesis. The present sequence is a carearse transcriptace (RT)-PCR primer for a VEGF or related gene, used to clone the coding region for expression in tumour cell lines. The cell lines were used to test prospective antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                              New composition comprising an antisense oligonucleotide directed against vascular endothelial growth factor, useful for preparing a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; G-protein coupled receptor; HGPRBMY39; cancer; PCR; primer; male reproductive disorder; testicular disorder; immune disorder; inflammatory disorder; developmental disorder; leukaemia; VH; bone marrow disorder; testicular cancer; proliferative disorder; neural disorder; Alzheimer's disease; prion disorder; antibody; bone metabolism disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HGPRBMY39 antibody VH domain PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 6 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1573 CAGGTGGCCCGGGCCATGGAGT 1594
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 12; Page 19; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 chagicachagagachigadi 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                   31-JAN-1997; 97US-0037004P.
30-JAN-1998; 98US-00016541.
2AN-2000; 2000US-00487023.
19-JAN-2001; 2001WO-US000193.
                                                                                                   13-MAR-2001; 2001US-00805761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002; 2002WO-US028582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001; 2001US-0317793P.
27-NOV-2001; 2001US-0333658P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACA61414 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  for treating cancer.
                                                                                                                                                                                                                                                                                                             WPI; 2003-255224/25
                                                                                                                                                                                                                                                                           Masood R;
                                                                                                                                                                                                                        (GILL/) GILL P S. (MASO/) MASOOD R.
                                US2002165174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003023007-A2
 Homo sapiens.
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                                                                  07-NOV-2002
                                                                                                                                                                                                                                                                         Gill PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA61414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 722
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vivlemore401-10.rng

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The invention relates to. an isolated nucleic acid encoding a human G-
protein coupled receptor HGPRBMY39 (or its fragment domain or epitope),

tis complement or a polynucleotide capable of hybridising under stringent

conditions to it. Also included are a HGPRBMY39 recombinant vector, a

conditions to it. Also included are a HGPRBMY39 recombinant vector, a

recombinant host cell comprising the vector sequences (used to express

cond make the protein), an isolated HGPRBMY39 polypeptide, and an anti-
HGPRBMY39 antibody. The HGPRBMY39 polypeptide, and an anti-
HGPRBMY39 antibody. The HGPRBMY39 polypeptide is

cuseful for preventing, treating or ameliorating e.g. a (male)

reproductive disorder; a testicular disorder or cancer; a disorder

cuseful for preventing, treating or ameliorating or encare; a clasorder

cuseful for preventing, resticular disorder related to aberrant G-

protein coupled receptor dependent phosphatidylinositol-calcium

controlling, a disorder related to aberrant G-

proinflammatory signal; aberrant N-formyl peptide signalling; aberrant

cuseful activation; a disorder associated with below normal neutrophil activation;

a disorder related to aberrant intracellular and/or extracellular

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a disorder related to aberrant neutrophil activation;

a disorder related to aberrant intracellular and disorders;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a 
                                                                                                                                                                                                             New human G-protein coupled receptor, HGPRBMY39, useful for treating or preventing e.g. immune, inflammatory, developmental, proliferative, neural, reproductive, bone marrow or prion disorders.
                                                                                      Gopal S, Mintier G, Feder JN;
                                                                                                                                                                                                                                                                                                                                                  Example 37; Page 313; 359pp; English.
                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                     WPI; 2003-313245/30.
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(BRIM) BRISTOL-MYERS SQUIBB CO.

WPI; 2003-577292/54. Feder J, Lee L,

19-JUL-2001; 2001US-0306577P. 19-JUL-2002; 2002WO-US023407.

WO2003050235-A2 Homo sapiens.

19-JUN-2003

Gaps .. 0 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 0; Mismatches 86.4%; Query Match 0.5 Best Local Similarity 86.4 Matches 19; Conservative

853 GAGGAGGTGGTGGAGGCTG 874 1 GAGGTGCAGCTGGTGGAGTCTG 22 ద

ADJ79912 standard; DNA; 23 06-MAY-2004 (first entry) ADJ79912; ADJ79912
XX
XX
ADJ79912
AC
ADJ7991
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DT
O6-MAYXX
XX
XX
XX
XX
Immunos
XW
Antiart
XW
An

ВР.

immunosuppressive, antidepressant; nephrotropic; tranquilizer; antidadictive; nootropic; antinfertility; virucide; cytostatic; antidarticic; anti-HIV; antiasthmatic; antidiabetic; anti-HIV; antiasthmatic; antidiabetic; antidiamatory; antilipemic; osteopathic; potassium agonist; potassium antagonist; gene therapy; potassium camelalpha subunit; diagnosis; rheumatorid arthritis; asthma; leukemia; psoriasis; neutropenia; diabetes; panotratitis; osteoporosis; hypertriglyceridemia; infertility; testicular cancer; viral orchitis; memory disorder; osteoporosis; hypertriglyceridemia; infertility; testicular cancer; viral orchitis; memory disorder; osteoporosis; hypertriglon; serotonin regulation; dysphoria; depression; irritability; anxiety; immunophenotyping; phosphorylation; Primer #3 for VH region of anti-human K channel K+alphaM2 antibody gene. ss; primer

The invention relates to an isolated human potassium channel alpha
subunit, K+alphaMZ polypeptide. The K+alphaMZ polypeptide and
subunit, K+alphaMZ polypeptide. The K+alphaMZ polypeptide and
colymuclostide are useful for diagnosing, preventing, treating or
ameliorating a medical condition, such as a neural disorder, an immune
disorder (e.g. rheumatoid arthritis, AIDS, asthma, leukemia, psoriasis or
centropenia), a disorder related to aberrant potassium regulation,
metabolic disorder (e.g. diabetes, pancreatitis, osteoporosis or
hypertriglyceridemia), a reproductive disorder, a renal disorder, a male
creproductive disorder (e.g. infertility, testicular cancer or viral
orchitis), a memory disorder, an obsersative/compulsive disorder, an
addiction, a disorder related to aberrant dopamine or serotonin
regulation, desphoria, depression, irritability, anxiety, or depression,
irritability or anxiety associated with treating drug addiction, learning
irritability or anxiety associated with treating drug addiction,
irritability or price are useful for the affinity purification of the
colypeptides from recombinant call culture, in diagnostic assays to
detect the presence or quantification of the polypeptides, or for
immunophenotyping. Vectors and host cells containing the gene are useful
containing the polypeptides. This sequence corresponds
corrections and host cells containing the gene are useful New isolated human potassium channel alpha subunit, KalphaM2 polypeptide, useful for diagnosing, preventing, treating or ameliorating a medical condition, for example a neural disorder, an immune disorder or a metabolic disorder. Gaps ; 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; to a PCR primer to amplify a heavy chain variabl human potassium channel K+alphaM2 antibody gene. Example 31; SEQ ID NO 43; 313pp; English. 853 GAGGAGGAGCTGGTGGAGGCTG 874 1 GAGGTGCAGCTGGTGGAGTCTG 22 Query Match 0.5%; Best Local Similarity 86.4%; Matches 19; Conservative RESULT 724 ઠે

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ds; gene; immunosuppressive; cardiant; antiinflammatory; cytostatic; anti-HIV; antirheumatic; antiarthritic; antibacterial; antiseborrheic; dermatological; antipsoriatic; neuroprotective; nootropic; antipartinsonian; antidiabetic; ophthalmological; antiasthmatic; antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive; anorectic; metabolic; virucide; osteopathic; antianginal; vulnerary; Anti-human GCRP HGPRBMY30 antibody VH region PCR primer Hu-VH3 06-MAY-2004 (first entry) ADJ93146;

ADJ93146 standard; DNA; 23 BP.

ADJ93146

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Novel human G-protein coupled receptor, HGPRBMY30 polypeptide useful for preventing and treating e.g. immune disorders, cardiovascular disorders
gene therapy; G-protein coupled receptor protein; HGPRBMY30; immune disorder; cardiovascular disorder; inflammatory disorder; metabolic disorder; reproductive disorder; testicular cancer; neural disorder; endocrine disorder; gastrointestinal disorder; Alzheimer's disease; Parkinson's diseases; diabetes; dwarfism; asthma; schizophrenia; obesity; anorexia; osteoporosis; angina pectoris;
                                                                                                                                                                                                                                                                                                Example 37; SEQ ID NO 49; 343pp; English.
                                                                                                                                                                                                              Ramanathan C;
                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                 30-MAY-2002; 2002WO-US017085.
                                                                                                                                                                      30-MAY-2001; 2001US-0294411P.
                                                                                                                                                                                                                                                                             or inflammatory disorders.
                                                                                                                                                                                                              Feder JN, Mintier GA,
                                                     schizophrenia, obesity
myocardial infarction
                                                                                                                                                                                                                                   WPI; 2003-140445/13.
                                                                                                        WO200296946-A1
                                                                                    Homo sapiens.
                                                                                                                            05-DEC-2002
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The invention relates to an isolated human G-protein coupled receptor, HGPRBMY30 polypeptide or a sequence having 95% identity to the above mentioned sequences. (I) is useful for preventing or treating a medical condition, selected from an immune disorder; a cardiovascular disorder; an inflammatory disorder in which G-protein coupled receptors are either disorder; a reproductive disorder; a metabolic disorder; a metabolic disorder; a metabolic disorder; an eneral disorder; a male reproductive disorder; certicular cancer; a neural disorder; and redoctine disorder; prognosing, preventing, and/or ameliorating the diseases such as hematopoletic and pulmonary disorders, Alzheimer's, Parkinson's diseases, diabetes, dwarfism, color blindness, retinal pigmentosa, asthma, expression, schizophrenia, sleeplessness, hypertension, anxiety, stress, renal failure, acute heart failure, hypotension, obesity, anorexia, HIV infections, osteoporosis, angina pectoris, and myocardial infarction. (I) and (II) are useful for modulating signal transduction activity. (I) and (II) are useful for modulating signal transduction activity. (I) and (II) are useful for modulating signal transduction activity. (I) and (II) are useful for modulating signal transduction activity. (I) and (II) are useful for modulating signal transduction of body healpht, weight, hair color, eye color, skin, percentage of dipose tissue, pigmentation, size and shape, to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, corpaspillities, hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities. This sequence corresponds to a porner. primer for the var HGPRBMY30 protein

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels Best Local Similarity 86.4 Matches 19; Conservative Query Match

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GAGGAGGTGGTGGAGGCTG 874 GAGGTGCAGCTGGTGGAGTCTG 22 853

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ADE83880 standard; DNA; 23 BP RESULT 725 ADE83880 ID ADE8386 XX

antipporiatic; dermatological; antiinflammatory; immunosuppressive; antirheumatic; antiarthritic; cerebroprotective; cytostatic; anti-HIV; vulnerary; dermatitis; autoimmune disease; rheumatoid arthritis; Chemokine beta-4 binding antibody PCR primer Hu VH3-5' SEQ ID NO:39 systemic lupus erythematosus; autoimmune encephalitis; cancer; HIV infection; wound; inflammatory disorder; human; psoriasis; chemokine beta-4; CK-B4; single chain Fvs; scFvs; 29-JAN-2004 (first entry) PCR primer; ss antibody; ADE83880;

Homo sapiens. Synthetic

WO2003092597-A2.

13-NOV-2003

30-APR-2003; 2003WO-US013414.

01-MAY-2002; 2002US-0376561P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2004-022614/02.

New antibody that specifically binds to a chemokine beta-4 polypeptide, useful for diagnosing, treating, preventing or ameliorating psoriasis, rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection and wounds

Example 2; SEQ ID NO 39; 181pp; English.

The present invention describes an antibody (I) that specifically binds to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first amino acid sequence at least 95% identical to a second amino acid sequence comprising a VH complementarity determining region (CDR) or VL cDR of any of the single chain Fvs (scFvs) from any of 17 fully defined sequences of 245-253 amino acids (ADB83861 to ADB8387). Also described: (I) a kit comprising the isolated nucleic acid molecule encoding (I); (3) a vector comprising the isolated nucleic acid of (2); (4) a host coll comprising the vector of (3); (5) a cell line engineered to express (I); (6) an antibody that binds the same epitope as (I); (7) an antibody that competitively inhibits the binding (I) to a CK-B4 polypeptide; (8) a method for detecting aberrant expression of CK-B4 polypeptide; (8) a method for detecting aberrant expression of CK-B4 polypeptide; (8) a sasaying the level of CK-B4 polypeptide expression in a first biological sample of an individual using at least one of (I), and comparing the standard level of CK-B4 polypeptide expression or level of CK-B4 polypeptide in a second, normal biological sample, where an increase or decrease in the assayed level of CK-B4 polypeptide in the first biological sample compared to the standard level is indicative of biological sample. diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or an autoimmune disease such as rheumatoid arthritis, systemic lupus erythematosus and autoimmune encephalitis. They can also be used in administering (I) to the animal. (I) has antipsoriatic, dermatological, antinflammatory, immunosuppressive, antirheumatic, antiarthritic, cerebroprotective, cytostatic, anti-HIV and vulnerary activities. The methods and compositions of the present invention are useful for cancer, HIV infection, wounds and inflammatory disorders. The present sequence is used in the exemplification of the present invention. aberrant expression, and (9) a method of treating, preventing or ameliorating psoriasis, dermatitis or an autoimmune disease, comp

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; Best Local Similarity Query Match

Wager RE;

Ruben SM,

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The invention comprises a DNA sequence encoding an antibody which immunospecifically inhibits vascular endothelial growth factor 2 (VEGF-2) protein. The antibody of the invention is useful for detecting,
                                                                                                                                                                                                                                                                                                    diagnosing, monitoring, treating or preventing cancers or other hyperproliferative disorders, inflammatory disorders, autoimmune disease, rheumatoid arthritis, psoriasis, and diabetic retinopathy. The present DNA sequence represents a PCR primer that was used in an example of the
                                                                                                                                                                                                     New polynucleotide encoding VEGF-2 antibody, useful in detecting, diagnosing, prognosing, monitoring, treating or preventing e.g. cancers.
                                                                                                                                                                                                                                             Example 32; SEQ ID NO 38; 410pp; English
                                                                                   19-AUG-2002; 2002WO-US026246.
                                                                                                          12-APR-2002; 2002WO-US011474.
                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                           Albert VR,
                                                                                                                                                                                  WPI; 2004-022839/02.
                                   WO2003097660-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003186267-A1
           Unidentified.
                                                          27-NOV-2003
                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                            Rosen GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG75494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or precedence; and the present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody that specifically binds neurokinin B, useful for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; vascular endothelial growth factor 2; VEGF-2; cancer; hyperproliferative disorder; inflammatory disorder; autoimmune disease; rheumatoid arthritis; psoriasis; diabetic retinopathy; PCR; ss; primer; VH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                           antibody, neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB; ss; PCR; primer.
                                                                                                                                                                                    Human neurokinin B antibody VH PCR primer HuVH3-5' SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VEGF-2-specific antibody VH domain PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 43; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGCTGGTGGAGGCTG 874
                          874
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                          853 GAGGAGGAGCTGGTGGAGGCTG
                                                   1 GAGGTGCAGCTGGTGGAGTCTG
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                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                        29-MAY-2003; 2003WO-US016802
                                                                                                                                                                                                                                                                                                                                                  30-MAY-2002; 2002US-0383802P
                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH13834 standard; DNA; 23
                                                                                                               ADG34320 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19, Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-053456/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                          WO2003102136-A2
                                                                                                                                                              26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004
                                                                                                                                                                                                                                                                                                  11-DEC-2003
   19;
                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention
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                                                                                                                                       ADG34320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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     Matches
                                                                                                  ADH13834
                                                                                        RESULT
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                                                                                                                                          Gaps
                                                                                                                                             ;
0
                                                                   Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-HLLRCR-1 antibody VH domain PCR primer #3.
                                                                                                                                                                                                                    853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2002; 2002US-00271078.
                                                                          Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG75494 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-2004 (first entry)
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Isolated nucleic acid molecule for e.g. diagnosing and treating cardiovascular condition, comprises polynucleotide encoding human leucine-rich repeat cardiac receptor-1 protein having amino acid sequence of
                                    Mintier G;
    11-OCT-2001; 2001US-0328478P.
                                    Feder JN, Ramanathan CS,
               FEDER J N.
RAMANATHAN C S.
                                              WPI; 2004-031999/03.
                         MINTIER G.
                                                                        specific length.
                    (RAMA/)
(MINT/)
               (FEDE/)
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The invention relates to an isolated nucleic acid molecule comprises a polynucleotide encoding the full-length human leucine-rich repeat cardiac receptor-1 (HLLRCR-1) protein appearing as ADG75441and ADG75443. Also included are a recombinant vector comprising the isolated nucleic acid molecule, a recombinant vector comprising the vector sequences, the isolated polypeptide, an isolated mithody that binds per a pecifically to the isolated polypeptide, making an isolated polypeptide, and recovering the polypeptide, making an isolated polypeptide or a pecifically to the isolated polypeptide, making an isolated polypeptide or deveraining the polypeptide, making an pathological condition or a susceptibility to a pathological condition in a subject (by determining the presence or absence of a mutation in the polymelecule, and diagnosing a pathological condition or a susceptibility to a pathological condition or a subsence of the mutation) and preventing, treating or ameliorating a pathological condition or a beence of the mutation) and preventing, treating or ameliorating a cardiovascular medical condition by administering a polypeptide or its modulator to a disorder, neural disorder, reproductive disorder, neural disorder, reproductive disorder, neural disorder, reproductive disorder, neural disorder, related proliferated condition of the lung, colon cancer, related proliferated condition of the lung, colon cancer, related proliferated condition of the colon, memory, establishment of short term memory, establishment of short term memory, establishment of short term memory, establishment of long term memory, dementia, complition, learning, development of long term memory, desorders associated with heurom attrition, Alzheimer's disorder short accompany severe trauma to the brain, disorder sasociated with the brain, particularly memory disorders, movement (ansociated with aberrant signal transduction, or aberrant call-to-call continuication, aberrant signal transduction, or aberrant call-to-carciniment (many other disea specification). The invention provides human sequence that encodes a leucine-rich repeat containing protein with homology to the leucine-rich repeat containing protein known as NoGo receptor that is primarily expressed in the brain and is thought to be responsible for modulating neurite growth. The present sequence is a PCR primer used to isolate nucleic acid encoding a VH or VL chain of an anti-HLLRCR-1 antibody. Example 34; SEQ ID NO 55; 164pp; English.

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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 0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03;
                                        3; Indels
                                      0; Mismatches
                                                                          853 GAGGAGGAGCTGGTGGAGGCTG 874
Query Match 0.5%;
Best Local Similarity 86.4%;
                                        19; Conservative
                                        Matches
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1 gaggracagcragargagarcra 22

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Gaps

ADH61821 standard; DNA; 23 RESULT 729

ADH61821 ADH61821 ID ADH6 XX AC ADH6

(first entry)

Human G protein chemokine receptor-related PCR primer SegID15.

G-protein chemokine receptor; HSATU68; cytostatic; anti-HIV; anti-HIV; neutinification challed the company pressive; nootropic; neutoroprotective; vaccine; gene therapy; infectious disease; silicosis; sarcoidosis; adult respiratory syndrome; ARD5; brain tumour; hyperproliferative disorder; lymphoblastic leukaemia; brain tumour; breast cancer; Raposi's sarcoma; Hodgkin's garcoma; myeloid leukaemia; urethral cancer; gastrointestinal disorder; gastric reflux; peptic oseophagitis; liver disorder; intrahepatic cholestasis; hepatoromal syndrome; pancreatic disease; neoplasm; pancreas cell tumour; islet cell tumour; gallbladder disease; bile duct tumour; cardiac osedema; pulmonary heart disease; reproductive disorder; cardiac osedema; pulmonary heart disease; reproductive disorder; testicular atrophy; gonorrhoea; renal disorder; kidney failure; diabetes insipidus; immunoresponsiveness; B-cell function; lymphoid tissue regeneration; protein co-ordinate data; PCR; primer; ss.

US2003224426-A1. Unidentified.

04-DEC-2003

11-APR-2003; 2003US-00411284.

11-JAN-1996; 96WO-US000499. 21-DEC-1998; 98US-00101518. 12-APR-2002; 2002US-0371725P.

LIYY/) LI Y.

Li Y;

WPI; 2004-033959/03.

Novel isolated human G-protein chemokine receptor HSATU68 polypeptide, useful for preventing, treating or ameliorating medical conditions such as leukemia.

Example 13; SEQ ID NO 15; 168pp; English.

This invention relates to a novel isolated human G-protein chemokine receptor polypeptide (HSATU68) and the DNA sequence which encodes it. The receptor polypeptide (HSATU68) and the DNA sequence which encodes it. The invention may be useful for the development of compounds with a cytostatic, anti-HTV, anti-inflammacrory, anti-diabetic, immunosuppressive, cytostatic, anti-HTV, anti-inflammacrory, anti-diabetic, immunosuppressive, contropic or neuroprotective activity which act as agonists of the receptor of the invention can susceptibility to a pathological condition and for developing methods for treating, preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the receptor of the invention such as infectious diseases which includes silicosis, sarcoidesis. The captractory syndrome (ARDS), hyperproliferative disorders such as acute colludowed lymphoblastic leukaemia, brain tumours, breast cancer, Kaposi's sarcoma, Hodgrin's sarcoma, myeloid leukaemia and urethral cancer, capastrointestinal disorders such as gastric reflux and peptic consophagitis, liver disorders such as gastric reflux and peptic consophagitis, liver disorders such as such as neoplasms or pancreas and islet cell tumours, gallbladder diseases such as bile duct tumour, chearing such as cardiac oedema, pulmonary heart disease, reproductive disorders such as cardiac oedema, pulmonary heart disease, uch as diabetes consolative, diabetes insipidus, for stimulating B-cell responsivenes to boost immunoresponsiveness emong individuals having an acquired loss of B

vivlemore401-10.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated nucleic acid molecule encoding a human neurotransmitter transporter. The invention further comprises: a recombinant vector comprising the above nucleic acid molecule; a method of making a recombinant host cell comprising the above nucleic acid molecule; an isolated polypeptide comprising a sequence selected from: the full length protein or a polypeptide fragment, domain or epitope of a sequence having 727 amino acids or the encoded sequence included in ATCC Deposit Number PTA-4803, having neurotransmitter transporter activity; a polypeptide comprising amino acids or the sequence having 727 amino acids minus the start methionine; and a polypeptide comprising amino acids 1-727 of the sequence having 727 amino acids in isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide; a method of making an isolated polypeptide; a method for preventing,
                  present
                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; neuroleptic; neuroprotective; hypotensive; hypotrensive; hypotrensive; and algesic; anorectic; antablic; antiparkinsonian; noctropic; tranquilizer; antiadictive; hypnotic; gene therapy; dopamine; opioid peptide; serotonin; GABA; glutamate; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human neurotransmitter transporter polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating for e.g. disorders related to aberrant neurotransmitter transport or affective or
-cell function and as therapy for generation and/or regeneration of lymphoid tissues following surgery, trauma or genetic defect. The presen sequence is that of a degenerate PCR primer which was used to amplify a region of a VH or VL gene during the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                  human neurotransmitter transporter; HNTTBMY1; PTA-4803; antidepressant;
                                                                                                                                               Gaps
                                                                                                                                               ;
0
                                                                                                              Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee LM;
                                                                                                                                               3: Indels
                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feder JN,
                                                                                                                Score 17.2; DB 1;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                      HNTTBMY1 antibody VH domain primer, SEQ ID 61.
                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Westphal R,
                                                                                                                                                                               853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                            GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2002; 2002US-00319315.
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                                                                                                                0.5%;
                                                                                                                                                                                                                                                                                           ADH76560 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                       22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramanathan CS,
                                                                                                            Query Match
Best Local Similarity 86.4'
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHARMA R.
RAMANATHAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psychotic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-010866/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WESTPHAL R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003219774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEE L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-2003.
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                                                                                                                                                                                                                                                                                                                         ADH76560;
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(FEDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LEEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RAMA/)
                                                                                                                                                                                                                                                            RESULT 730
                                                                                                                                                                                                                                                                             ADH76560
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conditions antiparkinsonian, nootropic, transqualizer, antiaddictive, anabolic, antiparkinsonian, nootropic, transquilizer, antiaddictive, anabolic, antiparkinsonian, nootropic, transquilizer, antiaddictive, and hyponotic. The human neurotransmitter transporter nucleic acid can be used in gene therapy to treat disorders. The composition and methods are useful in diagnosing, preventing or traating a pathologic or medical condition selected from a disorder related to aberrant neurotransmitter transport; affective disorders, immune-related disorders, neuropathic pain, obesity, anorexia, bulimia, Parkinson's disease, dementias, behavioral disorders; memory disorders; organitive disorders, neuropathic pain, obesity, anorexia, bulimia, Parkinson's disease, dementias, behavioral calsorders; memory disorders; organitive disorders associated with aberrant serotonin expression and/or activity; anxiety, fear, depression, sleep, pain, disorders associated with aberrant maintenance of an attentive or alert states attention deficit disorders affecting the ceffecting the release of neurotransmitters such as affecting the release of neurotransmitters such as affecting the establishment of long term potentiation; circadian rhythm disorders; disorders; neuronal confers neuronal confers neuronal caramisation system disorders, and pain. This polynucleotide sequence represents a primer used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
condition; and methods of diagnosing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv; inflammatory bowel disorder; ulcerative colitis; Crohn's disease; diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibody, useful for treating, preventing or ameliorating inflammatory bowel disorder, cancer of the gastrointestinal tract or diabetes (non-insulin dependent diabetes).
                                                                                      pathological condition or a susceptibility to a pathological condition a subject. The human neurotransmitter transporter nucleic acid has the following activities: antidepressant, immunosuppressive, neuroleptic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                        neuroprotective, hypotensive, hypertensive, analgesic, anorectic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.2; Dilarity 86.4%; Pred. No. 1.1e Conservative 0; Mismatches
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                                           or ameliorating a medical
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